In this file, full sequence alignments are provided for the proteins noted in the text as having clear indications for (or against) microcompartment targeting. The aligned sequences are in FASTA format. The aligned sequences for a given protein family can be viewed by 'copying' and 'pasting' the sequences into Jalview or a similar program. Aligned sequences are provided for 11 protein families believed to be involved in compartmentalized enzymatic reactions: PduC, PduD, PduE, PduG, PduH, PduO, PduP, EutB, EutC, EutG, and Pfl2. Each protein family is indicated by a "%%" label and the protein family name, followed by a set of aligned sequences. Each protein sequence begins with the label ">gi". Genes that were identified as being associated with microcompartment function based on their chromosomal proximity to BMC shell genes are denoted by a "++" after the ">gi" label. The NBCI gene accession ID and annotation follow the ">gi" or ">gi++" label. For analyzing a family of aligned sequences in a viewing program (e.g. Jalview), the text to be copied and pasted should begin with the ">gi" label for the first sequence from the family, and should end prior to the "======================" label that separates distinct protein families from each other.

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%%  PduC [targeting tail not implicated]

>gi++|215487213|ref|YP_002329644.1| propanediol dehydratase, large subunit,
AdoCbl-dependent [Escherichia coli O127:H6 str. E2348/69]
-------------MRSKRFEALAKRPVNQDGFVKEWIEEGFIAMESPNDPKPS-IKIVNG
VVTELDGKPANQFDLIDHFIARYGINLARAEEVIAMDSVKLANMLCDPNVKRSDIVPLTT
AMTPAKIVEVVSQMNVVEMMMAMQKMRARRTPSQQAHVTNIKDNPVQIAADAAEGAWRGF
DEQETTVAVARYAPFNAIALLVGSQVGRPGVLTQCSLEEATELKLGMLGHTCYAETISVY
GTEPVFTDGDDTPWSKGFLASSYASRGLKMRFTSGSGSEVQMGYAEGKSMLYLEARCIYI
TKAAGVQGLQNGSVSCIGVPSAVPSGIRAVLAENLICSSLDLECASSNDQTFTHSDMRRT
ARFLMQFLPGTDFISSGFSAVPNYDNMFAGSNEDAEDFDDYNVIQRDLKVDGGLRPVREE
DVIAIRNKAARALQAVFAGMGLPPITDEEVEAATYAHGSKDMPERNIVEDIKFAQEIIHK
NRNSLEVVKALAQGGFTDVAQDMLNMQKAKLTGDYLHTSAIIVDDGQVLSAVNDVNDYAG
PATGYRL-----------------------------------------------------
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------------------------------------------------------------
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>gi++|218782820|ref|YP_002434138.1| Glycerol dehydratase [Desulfatibacillum
alkenivorans AK-01]
-----------MQKRQKRFEVLEQRAVNKDGFIKEWAEVGLVAMDSPYDPKPG-LKIENG
KVVEMDGIPCAEFDMIDTFIANHCIDVNVAAEAMAIDSLEFAKKLVDINVSGAEIKRLVP
GLTPAKILDILKKMNVVELMMAMQKLRCRKTPANQAHITNVKDTPALLAADSAEGSFRGF
QELETTVGIARYAPMNAIALLIGGQVGCRGTLTQCAVEEAMELQMGMKGLTAYAETVSVY
GTDQVFVDGDDTPWSKAFLASAYASRGIKMRFTSGTGSEVQMGYANKKSMLYLEIKCIMI
TKGAGVQGLQNGSISCIGVPGAVPGGIRAVLAENVATVLLDLEVASGNDQTFTHSPIRNT
ARMLMQFLPGTDYVFSGYSGVPNYDNMFAGSTHDSDDFDDMLVLQRDLQCDMALRPVTEE
QIIAVRNKAARAMQAVFQEVGFPAITDEEVEAATYAHGSKDMPDRNQPEDLRAIEEFLKS
GKTGLDIVRALHKHGFQDVAESVLGMLKQKVSGDYLHTSAIVDENFNVKSAVNDRNDYMG
PGTGYRLEGER--WELLKNIPQAIS-----------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------PEDI---------
>gi++|218705533|ref|YP_002413052.1| Glycerol dehydratase large subunit [Escherichia
coli UMN026]
-------------MRSKRFEALAKRPVNQDGFVKEWIEEGFIAMESPNDPKPS-IKIVNG
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VVTELDGKPANQFDLIDHFIARYGINLARAEEVIAMDSVKLANMLCDPNVKRSDIVPLTT
AMTPAKIVEVVSQMNVVEMMMAMQKMRARRTPSQQAHVTNVKDNPVQIAADAAEGAWRGF
DEQETTVAVARYAPFNAIALLVGSQVGRPGVLTQCSLEEATELKLGMLGHTCYAETISVY
GTEPVFTDGDDTPWSKGFLASSYASRGLKMRFTSGSGSEVQMGYAEGKSMLYLEARCIYI
TKAAGVQGLQNGSVSCIGVPSAVPSGIRAVLAENLICSSLDLECASSNDQTFTHSDMRRT
ARFLMQFLPGTDFISSGFSAVPNYDNMFAGSNEDAEDFDDYNVIQRDLKVDGGLRPVREE
DVIAIRNKAARALQAVFAGMGLPPITDEEVEAATYAHGSKDMPERNIVEDIKFAQEIINK
NRNSLEVVKALAQGGFTDVAQDMLNMQKAKLTGDYLHTSAIIVDDGQVLSAVNDVNDYAG
PATGYRLQGER--WEEIKNIPGALD-----------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------PNEID--------
>gi++|218549343|ref|YP_002383134.1| Glycerol dehydratase large subunit [Escherichia
fergusonii ATCC 35469]
-------------MRSKRFEALAKRPVNQDGFVKEWIEEGFIAMESPNDPKPS-IKIVNG
AVTELDGKSVSQFDLIDHFIARYGINLARAEEVITMDSVKLANMLCDPNVKRRDIVPLTT
AMTPAKIVEVVSHMNVVEMMMAMQKMRARRTPSQQAHVTNVKDNPVQIAADAAEGAWRGF
DEQETTVAVGRYAPFNAIALLVGSQVGRPGVLTQCSLEEATELKLGMLGHTCYAETISVY
GTEPVFTDGDDTPWSKGFLASSYASRGLKMRFTSGSGSEVQMGYAEGKSMLYLEARCIYI
TKAAGVQGLQNGSVSCVGVPSAVPSGIRAILAENLICAALDLECASSNDQTFTHSDMRRT
ARFLMQFLPGTDFISSGFSAVPNYDNMFAGSNEDAEDFDDYNVIQRDLKVDGGLRPVREE
DVIAIRNKAARALQAVFAGMGLPPITDEEVEAATYAHGSKDMPERNIVEDIKFAQEIINK
NRNGLEVVKALAKGGFTDVAQDMLNIQKAKLTGDYLHTSAIIVGNGEVRSAVNDVNDYAG
PATGYRLQGER--WEEIKNIPGALD-----------------------------------
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------------------------------------------------------------
-----------------------------------PNELG--------
>gi++|205353185|ref|YP_002226986.1| glycerol dehydratase large subunit [Salmonella
enterica subsp. enterica serovar Gallinarum str. 287/91]
-------------MRSKRFEALAKRPVSQDGFVKEWIEEGFIAMESPNDPKPS-IKIVNG
AVTELDGKPVSEFDLIDHFIARYGINLNRAEEVMAMDSVKLANMLCDPNVKRSEIVPLTT
AMTPAKIVEVVSHMNVVEMMMAMQKMRARRTPSQQAHVTNVKDNPVQIAADAAEGAWRGF
DEQETTVAVARYAPFNAIALLVGSQVGRPGVLTQCSLEEATELKLGMLGHTCYAETISVY
GTEPVFTDGDDTPWSKGFLASSYASRGLKMRFTS--GSEVQMGYAEGKSMLYLEARCIYI
TKAAGVQGLQNGSVSCIGVPSAVPSGIRAVLAENLICSSLDLECASSNDQTFTHSDMRRT
ARLLMQFLTGTDFISSGYSAVPNYDNMFAGSNEDAEDFDDYNVIQRDLKVDGGLRPVREE
DVIAIRNKAARALQAVFAGMGLPPITDEEVEAATYAHGSKDMPERNIVEDIKFSQEIINK
NRNGLEVVKALAQGGFTDVAQDMLNIQKAKLTGDYLHTSAIIVGDGQVLSAVNDVNDYAG
PATGYRLQGER--WEEIKNIPGALD-----------------------------------
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------------------------------------------------------------
-----------------------------------PNEID--------
>gi++|125717397|ref|YP_001034530.1| glycerol dehydratase large subunit pduC,
putative [Streptococcus sanguinis SK36]
-------------MRSKRFEVLSERPINQDGFVKEWVEEGLVAMESPNDPKPS-IKIQNG
KVVELDGKPKEEFDLIDQFIANYGIDLSLAEEVIQMDSREIANKILTPSVPRTEIIKLTK
AMTPAKIIEVVNQMNVVEIMMCLQKMRTRKQTATQAHVTNVNDNPVQIAADAAEGALRGF
AEQETTVAVVRYAPFNALSLMIGSQVGRPGVLTQCSLEEATELEFGMRGFTAYAETISVY
GTEDVFTDGDDTPWSKAFLASAYASRGLKMRFTSGTGSEVQMGQAEGKSMLYLEARCLYV
TKAAGVQGTQNGSVSCIGIPAAVPSGIRAVVAENLIASMLDLECASSNDQTFTHSDLRRS
VRTLMQFAPGTDFINSGYSATPNYDNMFAGSNWDAEDFDDYNVLQRDLRVDGGLRPVREE
EVVKVRNKAARVMQALFKGLGLPQITDEEVEAATYAHGSKDMPERDKVEDIKAAQGILER
GVQGADLIKALANNGFPEVANELLNLFKQRVAGDFLQTSAIFDRDWNVISAVNSPNDYVG
VGTGHRLVGEE--WEKVKDIPKAID-----------------------------------
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------------------------------------------------------------
-----------------------------------PRDV---------
>gi++|123442946|ref|YP_001006921.1| putative propanediol utilization protein:
dehydratase, large subunit [Yersinia enterocolitica subsp. enterocolitica 8081]
-------------MKSKRFEALAKRPVNQDGFVKEWIEEGFIAMESPNDPKPS-IKIVNG
VVTELDGKPQSSFDLIDHFIARYGINLAHAEEVMKMDSIKLANMLCDPNVSRRTIVPLTT
AMTPAKIVEVVSHMNVVEMMMSMQKMRARRTPSQQAHVTNVKDNPVQIAADAAEGAFRGF
DEQETTVAVARYAPFNAIALLVGSQVGRPGVLTQCSLEEATELKLGMLGHTCYAETISVY
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GTEPVFTDGDDTPWSKGFLASSYASRGLKMRFTSGSGSEVQMGYAEGKSMLYLEARCIYI
TKAAGVQGLQNGSVSCVGVPSAVPSGIRAILAENLICSALDLECASSNDQTFTHSDMRRT
ARLLMQFLPGTDFISSGYSAVPNYDNMFAGSNEDAEDFDDYNVMQRDLKVDGGLRPVLEA
DVVAIRNKAARALQAVFAGMGLPPITDEEVIAATYAHGSKDMPERNIVEDIKFAQEIISK
NRTGLEVVKALAQGGFEDVAQDMLNIQKAKIAGDYLHTSAIIKGDNQVLSAVNDVNDYAG
PATGYRLEGAR--WEEIKNIPNALD-----------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------PNELG--------
>gi++|152971724|ref|YP_001336833.1| propanediol utilization: dehydratase, large
subunit [Klebsiella pneumoniae subsp. pneumoniae MGH 78578]
-------------MRSKRFEALAKRPVNQDGFVKEWIEEGFIAMESPNDPKPS-IRIVNG
AVTELDDKPVEQFDLIDHFIARYGINLARAEEVMAMDSVKLANMLCDPNVKRSDIVPLTT
AMTPAKIVEVVSHMNVVEMMMAMQKMRARRTPSQQAHVTNIKDNPVQIAADAAEGAWRGF
DEQETTVAVARYAPFNAIALLVGSQVGRPGVLTQCSLEEATELKLGMLGHTCYAETISVY
GTEPVFTDGDDTPWSKGFLASSYASRGLKMRFTSGSGSEVQMGYAEGKSMLYLEARCIYI
TKAAGVQGLQNGSVSCIGVPSAVPSGIRAVLAENLICSALDLECASSNDQTFTHSDMRRT
ARLLMQFLPGTDFISSGYSAVPNYDNMFAGSNEDAEDFDDYNVIQRDLKVDGGLRPVREE
DVIAIRNKAARALQAVFAGMGLPPITDEEVEAATYAHGSKDMPERNIVEDIKFAQEIINK
NRNGLEVVKALAKGGFPDVAQDMLNIQKAKLTGDYLHTSAIIVGEGQVLSAVNDVNDYAG
PATGYRLQGER--WEEIKNIPGALD-----------------------------------
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------------------------------------------------------------
-----------------------------------PNELG--------
>gi++|161502796|ref|YP_001569908.1| hypothetical protein SARI_00847 [Salmonella
enterica subsp. arizonae serovar 62:z4,z23:--]
-------------MRSKRFEALAKRPVNQDGFVKEWIEEGFIAMESPNDPKPS-IKIVNG
AVTELDGKPVSDFDLIDHFIARYGINLARAEEVMAMDSVKLANMLCDPNVKRSDIVPLTT
AMTPAKIVEVVSQMNVVEMMMAMQKMRARRTPSQQAHVTNVKDNPVQIAADAAEGAWRGF
DEQETTVAVARYAPFNAIALLVGSQVGRPGVLTQCSLEEATELKLGMLGHTCYAETISVY
GTEPVFTDGDDTPWSKGFLASSYASRGLKMRFTSGSGSEVQMGYAEGKSMLYLEARCIYI
TKAAGVQGLQNGSVSCIGVPSAVPSGIRAVLAENLICSSLDLECASSNDQTFTHSDMRRT
ARLLMQFLPGTDFISSGYSAVPNYDNMFAGSNEDAEDFDDYNVIQRDLKVDGGLRPVREE
DVIAIRNKAARALQAVFAGMGLPPITDEEVEAATYAHGSKDMPERNIVEDIKFAQDIINK
NRNGLEVVKALAKGGFPDVAQDMLNIQKAKLTGDYLHTSAIIVGSGQVLSAVNDVNDYAG
PATGYRLQGER--WEEIKNIPGALD-----------------------------------
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------------------------------------------------------------
-----------------------------------PNELG--------
>gi++|157157290|ref|YP_001463342.1| propanediol utilization dehydratase, large
subunit [Escherichia coli E24377A]
-------------MRSKRFEALAKRPVNQDGFVKEWIEEGFIAMESPNDPKPS-IKIVNG
VVTELDGKPASQFDLIDHFIARYGINLARAEEVIAMDSVKLANMLCDPNVKRSDIVPLTT
AMTPAKIVEVVSQMNVVEMMMAMQKMRARRTPSQQAHVTNVKDNPVQIAADAAEGAWRGF
DEQETTVAVARYAPFNAIALLVGSQVGRPGVLTQCSLEEATELKLGMLGHTCYAETISVY
GTEPVFTDGDDTPWSKGFLASSYASRGLKMRFTSGSGSEVQMGYAEGKSMLYLEARCIYI
TKAAGVQGLQNGSVSCIGVPSAVPSGIRAVLAENLICSSLDLECASSNDQTFTHSDMRRT
ARFLMQFLPGTDFISSGFSAVPNYDNMFAGSNEDAEDFDDYNVIQRDLKVDGGLRPVREE
DVIAIRNKAARALQAVFAGMGLPPITDEEVEAATYAHGSKDMPERNIVEDIKFAQEIINK
NRNSLEVVKALAQGGFTDVAQDMLNMQKAKLTGDYLHTSAIIVDDGQVLSAVNDVNDYAG
PATGYRLQGER--WEEIKNIPGALD-----------------------------------
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------------------------------------------------------------
-----------------------------------PNEID--------
>gi++|74312532|ref|YP_310951.1| putative propanediol utilization protein: glycerol
dehydratase large subunit [Shigella sonnei Ss046]
-------------MRSKRFEALAKRPVNQDGFVKEWIEEGFIAMESPNDPKPS-IKIVNG
VVTELDGKPASQFDLIDHFIARYGINLARAEEVIAMDSVKLANMLCDPNVKRSDIVPLTT
AMTPAKIVEVVSQMNVVEMMMAMQKMRARRTPSQQAHVTNVKDNPVQIAADAAEGAWRGF
DEQETTVAVARYAPFNAIALLVGSQVGRPGVLTQCSLEEATELKLGMLGHTCYAETISVY
GTEPVFTDGDDTPWSKGFLASSYASRGLKMRFTSGSGSEVQMGYAEGKSMLYLEARCIYI
TKAAGVQGLQNGSVSCIGVPSAVPSGIRAVLAENLICSSLDLECASSNDQTFTHSDMRRT
ARFLMQFLPGTDFISSGFSAVPNYDNMFAGSNEDAEDFDDYNVIQRDLKVDGGLRPVREE
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DVIAIRNKAARALQAVFAGMGLPPITDEEVEAATYAHGSKDMPERNIVEDIKFAQEIINK
NRNSLEVVKALAQGSFTDVAQDMLNMQKAKLTGDYLHTSAIIVDDGQVLSAVNDVNDYAG
PATGYRLQGER--WEEIKNIPGALD-----------------------------------
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------------------------------------------------------------
-----------------------------------PNEID--------
>gi++|62180618|ref|YP_217035.1| propanediol utilization: dehydratase, large subunit
[Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
-------------MRSKRFEALAKRPVNQDGFVKEWIEEGFIAMESPNDPKPS-IKIVNG
AVTELDGKPVSEFDLIDHFIARYGINLNRAEEVMAMDSIKLANMLCDPNVKRSEIVPLTT
AMTPAKIVEVVSHMNVVEMMMAMQKMRARRTPSQQAHVTNVKDNPVQIAADAAEGAWRGF
DEQETTVAVARYAPFNAIALLVGSQVGRPGVLTQCSLEEATELKLGMLGHTCYTETISVY
GTEPVFTDGDDTPWSKGFLASSYASRGLKMRFTSGSGSEVQMGYAEGKSMLYLEARCIYI
TKAAGVQGLQNGSVSCIGVPSAVPSGIRAVLAENLICSSLDLECASSNDQTFTHSDMRRT
ARLLMQFLPGTDFISSGYSAVPNYDNMFAGSNEDAEDFDDYNVIQRDLKVDGGLRPVREE
DVIAIRNKAARALQAVFAGMGLPPITDEEVEAATYAHGSKDMPERNIVEDIKFAQEIINK
NRNGLEVVKALAQGGFTDVAQDMLNIQKAKLTGDYLHTSAIIVGDGQVLSAVNDVNDYAG
PATGYRLQGER--WEEIKNIPGALD-----------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------PNEID--------
>gi++|16765370|ref|NP_460985.1| propanediol dehydratase large subunit [Salmonella
typhimurium LT2]
-------------MRSKRFEALAKRPVNQDGFVKEWIEEGFIAMESPNDPKPS-IKIVNG
AVTELDGKPVSEFDLIDHFIARYGINLNRAEEVMAMDSVKLANMLCDPNVKRSEIVPLTT
AMTPAKIVEVVSHMNVVEMMMAMQKMRARRTPSQQAHVTNVKDNPVQIAADAAEGAWRGF
DEQETTVAVARYAPFNAIALLVGSQVGRPGVLTQCSLEEATELKLGMLGHTCYAETISVY
GTEPVFTDGDDTPWSKGFLASSYASRGLKMRFTSGSGSEVQMGYAEGKSMLYLEARCIYI
TKAAGVQGLQNGSVSCIGVPSAVPSGIRAVLAENLICSSLDLECASSNDQTFTHSDMRRT
ARLLMQFLPGTDFISSGYSAVPNYDNMFAGSNEDAEDFDDYNVIQRDLKVDGGLRPVREE
DVIAIRNKAARALQAVFAGMGLPPITDEEVEAATYAHGSKDMPERNIVEDIKFAQEIINK
NRNGLEVVKALAQGGFTDVAQDMLNIQKAKLTGDYLHTSAIIVGDGQVLSAVNDVNDYAG
PATGYRLQGER--WEEIKNIPGALD-----------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------PNEID--------
>gi++|16760973|ref|NP_456590.1| glycerol dehydratase large subunit [Salmonella
enterica subsp. enterica serovar Typhi str. CT18]
-------------MRSKRFEALAKRPVNQDGFVKEWIEEGFIAMESPNDPKPS-IKIVNG
AVTELDGKPVSEFDLIDHFIARYGINLNRAEEVMAMDSVKLANMLCDPNVKRSEIVPLTT
AMTPAKIVEVVSHMNVVEMMMAMQKMRARRTPSQQAHVTNVKDNPVQIAADAAEGAWRGF
DEQETTVAVARYAPFNAIALLVGSQVGRPGVLTQCSLEEATELKLGMLGHTCYAETISVY
GTEPVFTDGDDTPWSKGFLASSYASRGLKMRFTSGSGSEVQMGYAEGKSMLYLEARCIYI
TKAAGVQGLQNGSVSCIGVPSAVPSGIRAVLAENLICSSLDLECSSSNDQTFTHSDMRRT
ARLLMQFLPGTDFISSGYSAVPNYDNMFAGSNEDAEDFDDYNVIQRDLKVDGGLRPVREE
DVIAIRNKAARALQAVFAGMGLPPITDEEVEAATYAHGSKDMPERNIVEDIKFAQEIINK
NRNGLEVVKALAQGGFTDVAQDMLNIQKAKLTGDYLHTSAIIVGDGQVLSAVNDVNDYAG
PATGYRLQGER--WEEIKNIPGALD-----------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------PNEID--------
>gi++|167040582|ref|YP_001663567.1| glycerol dehydratase [Thermoanaerobacter sp.
X514]
-------------MRSKRFEVLAKRPVNQDGIIAEWPEVGLIAVNSPNDPKPS-IKIENG
KIVEMDGKKREEFDMIEQFIADYAINIEMAEKAMGMDSLEIARMLVDINVPREEIVKIVS
GLTPAKVVEVVNHLNVVEIMMAIQKMRARKRPGNQAHVTNLRDNPVLIAADAAEAALRGF
DELETTVGITRYAPFNALALLVGSQTGRGGVLTQDALEESFELTIGMRGFTSYAETISVY
GTEQVFVDGDDTPWSKAFLASAYASRGLKMRFTSGTGSECQMGFAEGKSMLYLEARCVMI
AKGAGVQGLQNGSISCIGVPGAVPGGIRAVAAENLITMMEDLEVASGNDQTFSHSDIRRT
ARTLLLMLPGTDLIFSGYSAVPNYDNMFAGSNFDAEDFDDYLMLQRDLMVEGGVSPVTED
EVIAVRNKAARALQSVFKKLNLPPITDEEVEAATYAHGSKDMPPRDVNADLKAATELMEK
GLTGLDVVKALAESGFTDVAENVLNMLKQRIAGDYLQTSAVLDKDFNIDSAVNNSNDYKG
PGTGFRLSKER--WERIKNVPQALK-----------------------------------
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-----------------------------------PEDLA--------
>gi++|153953477|ref|YP_001394242.1| DhaA [Clostridium kluyveri DSM 555]
------------MRRSERFEILEQRSIHKDGFVEEWPEIGLAAIESPNNPIPS-VKVEDG
KIIEMDGKSREEFDFIDIFLAEHSINVRNTEKAMAMDSLDIARMLVDINISRDEIMNIAN
SLTAAKLVEIISNLNVVEMMMALQKMKARRTPANQACVTNLRDNPVQIAADSAEGALRGF
AEMETRAGMLRYTLFNAISILIGSQTGRPGVLTQCLLGDATEIKLSMLGFASYVETISVY
GTESAFVEGDDTPWSDSFLASAYTSRGFKMRFSSSIGSEVQMGYSEGKSMLYLEARCIMM
AKGTGVQGLQNGLVNGVGISAAVPEGMRAILGRSLIIEMLGLEVVSGNEQVLTNSEIRKT
SKAMLQFLPGVDFVSPGYNSTPSYDNMFTHSNWNAEDYDDWLILQRDLRIDGGLKPVKEE
KVIAVRNKAARAIQALFKELGLPSITDEEVEAATYAHGSRDMPARNVEEDLKSIEKLLNK
GITVLDIVKGLYSGGFADVAENILNMFKQRLIGDYLHQSSIFDEQYNVISAINDRNDYMG
PGTGYRVEAKK--WDELKNVNFALE-----------------------------------
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------------------------------------------------------------
-----------------------------------PHKI---------
>gi++|206575748|ref|YP_002236782.1| propanediol utilization dehydratase, large
subunit [Klebsiella pneumoniae 342]
-------------MRSKRFEALAKRPVNQDGFVKEWIEEGFIAMESPNDPKPS-IRIVNG
AVTELDGKPVEQFDLIDHFIARYGINLARAEEVMAMDSVKLANMLCDPNVKRSDIVPLTT
AMTPAKIVEVVSHMNVVEMMMAMQKMRARRTPSQQAHVTNIKDNPVQIAADAAEGAWRGF
DEQETTVAVARYAPFNAIALLVGSQVGRPGVLTQCSLEEATELKLGMLGHTCYAETISVY
GTEPVFTDGDDTPWSKGFLASSYASRGLKMRFTSGSGSEVQMGYAEGKSMLYLEARCIYI
TKAAGVQGLQNGSVSCIGVPSAVPSGIRAVLAENLICSALDLECASSNDQTFTHSDMRRT
ARLLMQFLPGTDFISSGYSAVPNYDNMFAGSNEDAEDFDDYNVIQRDLKVDGGLRPVREE
DVIAIRNKAARALQAVFAGMGLPPITDEEVEAATYAHGSKDMPERNIVEDIKFAQEIINK
NRNGLEVVKALAKGGFPDVAQDMLNIQKAKLTGDYLHTSAIIVGEGQVLSAVNDVNDYAG
PATGYRLQGER--WEEIKNIPGALD-----------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------PNELG--------
>gi++|148544953|ref|YP_001272323.1| glycerol dehydratase [Lactobacillus reuteri DSM
20016]
------------MKRQKRFEELEKRPIHQDTFVKEWPEEGFVAMMGPNDPKPS-VKVENG
KIVEMDGKKLEDFDLIDLYIAKYGINIDNVEKVMNMDSTKIARMLVDPNVSRDEIIEITS
ALTPAKAEEIISKLDFGEMIMAVKKMRPRRKPDNQCHVTNTVDNPVQIAADAADAALRGF
PEQETTTAVARYAPFNAISILIGAQTGRPGVLTQCSVEEATELQLGMRGFTAYAETISVY
GTDRVFTDGDDTPWSKGFLASCYASRGLKMRFTSGAGSEVLMGYPEGKSMLYLEARCILL
TKASGVQGLQNGAVSCIEIPGAVPNGIREVLGENLLCMMCDIECASGCDQAYSHSDMRRT
ERFIGQFIAGTDYINSGYSSTPNYDNTFAGSNTDAMDYDDMYVMERDLGQYYGIHPVKEE
TIIKARNKAAKALQAVFEDLGLPKITDEEVEAATYANTHDDMPKRDMVADMKAAQDMMDR
GITAIDIIKALYNHGFKDVAEAILNLQKQKVVGDYLQTSSIFDKDWNVTSAVNDGNDYQG
PGTGYRLYEDKEEWDRIKDLPFALD-----------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------PEHLEL-------
>gi++|116872527|ref|YP_849308.1| glycerol dehydratase large subunit [Listeria
welshimeri serovar 6b str. SLCC5334]
-------------MKSKRFEELAKRPVNQDGFVKEWIEEGLIAMESPNDPKPS-IKIENG
KVVEMDSKKLADFDLIDHFIAKYGVDLSRAEEVMQMDSVKLANMLCDPNVPREKIVLLTT
AMTPAKIVEVVSQMNVVEMMMSMQKMRSRRTPTTQAHVTNLRDNPVQIAADAAEAAIRGF
DEQETTVAVVRYAPFNALSLLVGSQTGRGGVLTQCSLEEATELELGMRGLTCYAETISVY
GTEPVFTDGDDTPWSKGILASAYASRGLKMRFTSGTGSEVQMGYAEGKSMLYLESRCIFI
TKAAGVQGLQNGSISCIGIPGAVPSGIRAVLAENLIAVMLDLEVASGNDQTFSHSDIRRT
ARLLMQFLPGTDYISSGYSATPNYDNMFAGSNFDADDFDDYNILQRDLKVDGGLTPVTEE
EVVAVRNKAARVIQVVFEKLGLPTVTDEEVEAATYARGSNDMPERNMVEDIKAAAEMMDR
GVTGLDVVKALSAGGFDDVAESVLNMLKQRVSGDFLHTSAIIDKDWNVISSVNDLNDYAG
PGTGYRLEGER--WEKLKNIAVAVD-----------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------ANELD--------
>gi++|116334196|ref|YP_795723.1| propanediol dehydratase, large subunit
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[Lactobacillus brevis ATCC 367]
------------MKRQKRFEELEKRPIHLDGFVKEWPEEGFVAMMGPNDPKPS-IKIENG
KVTEMDSKPAADFDLIDLYIAKYGIKLENAEKVMAMDSTKIANMLCDPNVPRKDIIEITT
AMTPAKAEEVISKLNFAEMIMATQKMRPRRTPATQCHVTNIRDNPVQIAADAADAALRGF
PEQETTTAVARYAPLNAISLMVGAQTGRPGVITQCSVEEAEELSLGMRGFTGYAETISVY
GTDKVFTDGDDTPWSKGFLASCYASRGLKMRFTSGSGSEVMMGYTEGKSMLYLESRCIFI
TKASGVQGLQNGGVSCIGIPGSVPSGIRSVLGENLLCMMLDLECASANDQAFSHSDMRRT
ERLLGQFIAGTDYISSGYSSTPNYDNTFAGSNTDGLDYDDYYVMERDLAINGGIHPVDEQ
TIIKARNKAARALQGVFEDLGLPKITDEEVEAATYANTSKDMPERNMVEDMKAAQDLMDR
GITGVDIVKALFNHGFKDVAQAVLDLQKQKVCGDFLQTSAIFDSKWHVISAVNDANDYQG
PGTGYRLEEDTEEWERIKNLPFAID-----------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------PQNMQL-------
>gi++|16800186|ref|NP_470454.1| hypothetical protein lin1117 [Listeria innocua
Clip11262]
-------------MKSKRFEELAKRPVNQDGFVKEWIEEGLIAMESPNDPKPS-IKIENG
KVVEMDSKKLADFDLIDHFIAKYGVDLSRAEEVMKMDSVKLANMLCDPNVPREKIVLLTT
AMTPAKIVEVVSQMNVVEMMMSMQKMRSRRTPTTQAHVTNLRDNPVQIAADAAEAAIRGF
DEQETTVAVVRYAPFNALSLLVGSQTGRGGVLTQCSLEEATELELGMRGLTCYAETISVY
GTEPVFTDGDDTPWSKGILASAYASRGLKMRFTSGTGSEVQMGYAEGKSMLYLESRCIFI
TKAAGVQGLQNGSISCIGIPGAVPSGIRAVLAENLIAVMLDLEVASGNDQTFSHSDIRRT
ARLLMQFLPGTDYISSGYSATPNYDNMFAGSNFDADDFDDYNILQRDLKVDGGLTPVTEE
EVVAVRNKAARVIQVVFDKLGLPAVTDEEVEAATYARGSNDMPERNMVEDIKAAAEMMDR
GVTGLDVVKALAAGGFDDVAESVLNMLKQRVSGDFLHTSAIIDKDWNVISSVNDLNDYAG
PGTGYRLEGER--WEKLKDIAVAVD-----------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------ANELD--------
>gi++|46907371|ref|YP_013760.1| glycerol dehydratase large subunit [Listeria
monocytogenes str. 4b F2365]
-------------MKSKRFEELAKRPVNQDGFVKEWIEEGLIAMESPNDPKPS-IKIENG
KVVEMDSKKLADFDLIDHFIAKYGVDLSRAEEVMQMDSVKLANMLCDPNVPREKIVLLTT
AMTPAKIVEVVSQMNVVEMMMSMQKMRSRRTPTTQAHVTNLRDNPVQIAADAAEAAIRGF
DEQETTVAVVRYAPFNALSLLVGSQTGRGGVLTQCSLEEATELELGMRGLTCYAETISVY
GTEPVFTDGDDTPWSKGILASAYASRGLKMRFTSGTGSEVQMGYAEGKSMLYLESRCIFI
TKAAGVQGLQNGSISCIGIPGAVPSGIRAVLAENLIAVMLDLEVASGNDQTFSHSDIRRT
ARLLMQFLPGTDYISSGYSATPNYDNMFAGSNFDADDFDDYNILQRDLKVDGGLTPVTEE
EVVAVRNKAARVIQAVFDKLGLPEVTDAEVEAATYARGSKDMPERNMVEDIKAAAEMMDR
GVTGLDVVKALSAGGFDDVAESVLNMLKQRVSGDFLHTSAIIDKDWNVISSVNDLNDYAG
PGTGYRLEGER--WEKLKDIAVAVD-----------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------ANELE--------
>gi++|16803193|ref|NP_464678.1| hypothetical protein lmo1153 [Listeria monocytogenes
EGD-e]
-------------MKSKRFEELAKRPVNQDGFVKEWIEEGLIAMESPNDPKPS-IKIENG
KVVEMDSKKLADFDLIDHFIAKYGVDLSRAEEVMQMDSVKLANMLCDPNVPREKIVLLTT
AMTPAKIVEVVSQMNVVEMMMSMQKMRSRRTPTTQAHVTNLRDNPVQIAADAAEAAIRGF
DEQETTVAVVRYAPFNALSLLVGSQTGRGGVLTQCSLEEATELELGMRGLTCYAETISVY
GTEPVFTDGDDTPWSKGILASAYASRGLKMRFTSGTGSEVQMGYAEGKSMLYLESRCIFI
TKAAGVQGLQNGSISCIGIPGAVPSGIRAVLAENLIAVMLDLEVASGNDQTFSHSDIRRT
ARLLMQFLPGTDYISSGYSATPNYDNMFAGSNFDADDFDDYNILQRDLKVDGGLTPVTEE
EVVAVRNKAARVIQAVFDKLGLPEVTDAEVEAATYARGSKDMPERNMVEDIKAAAEMMDR
GVTGLDVVKALSAGGFDDVAESVLNMLKQRVSGDFLHTSAIIDKDWNVISSVNDLNDYAG
PGTGYRLEGER--WEKLKDIAVAVD-----------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------ANELD--------
>gi|187932789|ref|YP_001886294.1| glycerol dehydratase large subunit [Clostridium
botulinum B str. Eklund 17B]
-------------MKSKRFQVLAKRPVNQDGLIGEWPEEGLVAMNSANDPKSS-IKIENG
KVVELDNKKREDFDMIDRFIADYAINLENAEKAMSLDSVEIAKKLVDINVSRDEIVNITT
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SITPAKVVEVVSHMNVVEMMMALQKMRARKTPSNQCHVTNLKDNPVQIAADAAEAGIRGF
SEQETTVGIVRYAPFNALAILIGSQVGRGGVLTQCSVEEATELDLGMRGLTSYAETVSVY
GTEAVFTDGDDTPWSKAFLASAYASRGLKMRYTSGTGSEALMGYSEGKSMLYLESRCIYI
TKGAGVQGLQNGAVSCIGMTGAVPSGIRAVLAENLIAAMLDIEVASANDQTFSHSDIRRT
ARTLMQMLPGTDFIFSGYSAVPNYDNMFAGSNFDAEDFDDYNVLQRDLMVDGGLRPVSEE
ETIAIRNKAAKSIQAVFRELGFPAITDEEVEAATYAHGSKDMPERNIVEDLKAAEEMLKK
RINGLDIVKALSTSGFDDVASNILNMLKQRVTGDYLQTSAILDNDFDVISAVNDKNDYMG
PGTGYRISPER--WEEIKNIPNVIK-----------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------PEDID--------
>gi|188587878|ref|YP_001921323.1| coenzyme B12-dependent glycerol dehydratase, large
subunit [Clostridium botulinum E3 str. Alaska E43]
-------------MKSKRFQVLAKRPVNQDGLIGEWPEEGLVAMNSANDPKSS-IKIENG
TVVELDNKKREDFDMIDRFIADYAINLKNAQKAMSLDSVEIARKLVDINVSRDEIVDITT
SITPAKVVEVVSHMNVVEMMMALQKMRARKTPSNQCHVTNLKDNPVQIAADAAEAGIRGF
SEQETTVGIVRYAPFNALAILIGSQVGRGGVLTQCSVEEATELDLGMRGLTSYAETVSVY
GTEAVFTDGDDTPWSKAFLASAYASRGLKMRYTSGTGSEALMGYSEGKSMLYLESRCIYI
TKGAGVQGLQNGAVSCIGMTGAVPSGIRAVLAENLIAAMLDIEVASANDQTFSHSDIRRT
ARTLMQMLPGTDFIFSGYSAVPNYDNMFAGSNFDAEDFDDYNVLQRDLMVDGGLRPVSEE
ETIAIRNKAAKAIQAVFRELDFPAITDEEVEAATYAHGSKDMPERNIVEDLKAAEEMLKK
RVSGLDIVKALSTGGFDDVAGNILNMLKQRVTGDYLQTSAILDNDFDVISAVNDKNDYMG
PGTGYRISPER--WEEIKNIPNVIK-----------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------PEDIE--------
>gi|18309911|ref|NP_561845.1| coenzyme B12-dependent glycerol dehydrogenase large
subunit [Clostridium perfringens str. 13]
-------------MKSKRFQVLSERPVNQDGLIGEWADEGLIALDSPNDPKSS-IKIENG
IITELDGRSRDEFDMIDKFIAEYAINIEDAEASMKLSSKEIARRLVDINVSRDEIVKITT
SITPMKAVEVIQEMNVVEMMMALQKMRARRTPANQCHVTNVKDNPVQIAADAAEAALRGF
AEQETTVGIVRYAPFNALAILVGSQVGRGGVLTQCAVEEATELDLGMRGLTSYAETVSVY
GTESVFTDGDDTPWSKAFLASAYASRGLKMRFTSGSGSEALMGYSEGRSMLYLESRCIYI
TKGAGVQGLQNGAVSCIGMTGAVPSGIRAVLGENLIAAMLDIEVASANDQTFSHSDIRRT
ARMLMQMLPGTDFIFSGYSAVPNYDNMFAGSNFDAEDFDDYNILQRDLKVDGGLRPVTEE
ETIKVRNKAAKCIQIIFRELGFPEVTDEEVEAATYCHGSKEMPNRNVVEDLKAAEEMLER
RITGLDIIKALSKNGMEDIANNLLNMLKQRVTGDYLQTSAILDKDFNVISAVNDVNDYMG
PGTGYRLDGQR--WEEIKKVPTVMR-----------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------PEDIE--------
>gi|152972005|ref|YP_001337151.1| glycerol dehydratase [Klebsiella pneumoniae subsp.
pneumoniae MGH 78578]
------------MKRSKRFAVLAQRPVNQDGLIGEWPEEGLIAMDSPFDPVSS-VKVDNG
LIVELDGKRRDQFDMIDRFIADYAINVERTEQAMRLEAVEIARMLVDIHVSREEIIAITT
AITPAKAVEVMAQMNVVEMMMALQKMRARRTPSNQCHVTNLKDNPVQIAADAAEAGIRGF
SEQETTVGIARYAPFNALALLVGSQCGRPGVLTQCSVEEATELELGMRGLTSYAETVSVY
GTEAVFTDGDDTPWSKAFLASAYASRGLKMRYTSGTGSEALMGYSESKSMLYLESRCIFI
TKGAGVQGLQNGAVSCIGMTGAVPSGIRAVLAENLIASMLDLEVASANDQTFSHSDIRRT
ARTLMQMLPGTDFIFSGYSAVPNYDNMFAGSNFDAEDFDDYNILQRDLMVDGGLRPVTEA
ETIAIRQKAARAIQAVFRELGLPPIADEEVEAATYAHGSNEMPPRNVVEDLSAVEEMMKR
NITGLDIVGALSRSGFEDIASNILNMLRQRVTGDYLQTSAILDRQFEVVSAVNDINDYQG
PGTGYRISAER--WAEIKNIPGVVQ-----------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------PDTIE--------
>gi|206579582|ref|YP_002236501.1| glycerol dehydratase, large subunit [Klebsiella
pneumoniae 342]
------------MKRSKRFAVLAQRPVNQDGLIGEWPEEGLIAMDSPFDPVSS-VKVDNG
LIVELDGKRRDQFDMIDRFIADYAINVERTEQAMRLEAVEIARMLVDIHVSREEIIAITT
AITPAKAVEVMAQMNVVEMMMALQKMRARRTPSNQCHVTNLKDNPVQIAADAAEAGIRGF
SEQETTVGIARYAPFNALALLVGSQCGRPGVLTQCSVEEATELELGMRGLTSYAETVSVY
GTEAVFTDGDDTPWSKAFLASAYASRGLKMRYTSGTGSEALMGYSESKSMLYLESRCIFI
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TKGAGVQGLQNGAVSCIGMTGAVPSGIRAVLAENLIASMLDLEVASANDQTFSHSDIRRT
ARTLMQMLPGTDFIFSGYSAVPNYDNMFAGSNFDAEDFDDYNILQRDLMVDGGLRPVTEA
ETIAIRLKAARAIQAVFRELGLPPIADEEVEAATYAHGSNEMPPRNVVEDLSAVEEMMKR
NITGLDIVGALSRSGFEDIASNILNMLRQRVTGDYLQTSAILDRQFEVVSAVNDINDYQG
PGTGYRISAER--WAEIKSIPGVVQ-----------------------------------
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------------------------------------------------------------
-----------------------------------PDTIE--------
>gi|118472362|ref|YP_885929.1| glycerol dehydratase large subunit [Mycobacterium
smegmatis str. MC2 155]
-MTTARNLGTEAKRQSERTKLLEERPVNLDGFVQEWPEVGMVAMDSAFDPEPS-VRVENG
VIVEMDGRARADFDFIDQFIADHAIDVATTEQSMALPAVEIARMLVDPRVTRDEVIAVTG
GLTPAKLLEVAKNLNIVEIMMGIQKMRARRTPANQAHCTSARDNPLQVACEAAEASLRGF
SEVETTLGVVRYAPLVAMALQIGSQVGSGGLLTQCALEEATELELGMRGITAYAETISVY
GTESVFVDGDDTPWSKAFLAAAYASRGIKMRFTSGTGSEVQMGNAEGRSMLYLEIRCILV
AKGAGVQGLQNGSISCIGVPGAVPAGIRAVAAENLIASAVDLECASGNDQSFSHSPMRRT
ARLLPQMLPGTDFVCSGYSAVPNYDNMFAGSNLDAEDFDDFNTIQRDLQVDGGLRHVNEA
EIVAARRRAAQALQAVFRYLDLPAITDAEIEAAVYAHGSRELIPRDVLEDLKGAQQVMDR
NVTGLDLVKALESTGFADIAENLLAVLRQRVSGDLLQTSAIMTRDLKPLSAVNDRNDYAG
PGTGYRPSGAR--WEEMKRLRHVTS-----------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------AENPELEVE----
>gi|118472557|ref|YP_890539.1| glycerol dehydratase large subunit [Mycobacterium
smegmatis str. MC2 155]
MVAVTESGDPGQSPELGRMRILDAKPVNLDGFSVPDPDLGLAAMSSPHDPQPS-LVIRDG
RVVEMDGKAAEDFDVIDEFIARYGLDLDVAPEAMAMSDIDLARMAVDINVPRAEVVRLIA
GTTPAKLAKVIAVLTPVEMQAAMAKMRARRTPSNQAHVTNQLDDPLLIAADAASAVAYGF
REVETTVPVLADAPSNAVALLIGSQVGVPGAMAQCSIEEALELRLGLRGLTSYAETISIY
GTEQVFVDGDDTPFSKAILTSAYASRGLKMRVTSGGGAEVLMGAAEKCSILYLESRCVSL
ARALGSQGVQNGGIDGVGVVASVPDGMKELLAENLMVMMRDLESCAGNDNLISESDIRRS
AHTLPVLLAGADFIFSGFGSIPRYDNAFALSNFNSDDMDDFLVLQRDWGADGGLRTVPAD
QLAAVRRRAARAVQAVYRDLGLADFDDQHIENVVAANGSRDLPPGDPKAVLEAANAIEAK
QLTVFDVVASLKRTGFDPEAEAIMRLTAERMRGDQLQTSAIFDEQFRVLSKITDPNDYAG
PGTGYTLSEQR--RAEIDNIRQQRSAAELTADQAEH----AGHITVTEIEPARQGSDPRE
VCIGLSPALGRSVWLSLCGLPIGEVIRQISAGLEEEGCVPRFVRVRSTIDVGLIGLTAAK
LAGSGIGIGLQGKGTALIHRRDLAPLANLELFSVAPLLTARNYRELGRNAARHAKGMAPV
PILTGGTDESISARYHARAVALVALERQASEPGEAPVTVEVRRP----
>gi|126437898|ref|YP_001073589.1| glycerol dehydratase [Mycobacterium sp. JLS]
------------------MRILDAKPVNLDGFSVTDPALGLVAMHSPHDPQPS-LVVRDG
RVVELDGRPAADFDVIDEFIARYGIDLTVAEEAMALDDAVLARMAVDVNVPRAEVVRLIG
GTTPAKLARVMAVMTPVEMQMAMHKMRARRTPSNQAHVTNQLDDPLLIAADAASAVAYGF
REVETTVPVFGDAPSNAIALLIGSQVGVPGAMAQCSIEEAMELRLGLRGLTSYAETISIY
GTEQVFVDGDDTPFSKAILTAAYASRGLKMRVTSGGGAEVLMGAAEKCSILYLESRCVSL
ARALGSQGVQNGGIDGVGVVASVPEGMKELLAENLMVMMRDLESCAGNDNLISESDIRRS
AHTLPVLLAGADFIFSGFGSIPRYDNAFALSNFNADDMDDFLVLQRDWGADGGLRTVSRE
HLARVRRRAATAVQAVYRDLGLADFDDTRIDAVVVANDSRDLPAGDPKAVAEAATAIEAR
QLTVFDVVAALHRTGYAPEAEAIMRLTRERLRGDQLQTSAIFDDQFQVLSKITDPNDYAG
PGSGYTPTEKR--RAEIDGIRQARTSAELTADQAEH----RGHVVFSDVEPARQGSDPRE
VCIGLSPALGRSVWLTLCGLTVGEVLRQLSAGLEEEGCVPRLVRVRSTIDVGLIGLTAAR
LSGSGIGIGLQGKGTALIHRRDLAPLANLELFSVAPLLTAKMYRELGRNAARHAKGMAPL
PILAGGTDESISARYHARAVALVALERQACEPGQAPITVEAKRV----
>gi|108801917|ref|YP_642114.1| glycerol dehydratase [Mycobacterium sp. MCS]
------------------MRILDAKPVNLDGFSVTDPALGLVAMHSPHDPQPS-LVVRDG
RVVELDGRPAADFDVIDEFIARYGIDLTVAEEAMALDDAVLARMAVDVNVPRAEVVRLIG
GTTPAKLARVMAVMTPVEMQMAMHKMRARRTPSNQAHVTNQLDDPLLIAADAASAVAYGF
REVETTVPVFGDAPSNAIALLIGSQVGVPGAMAQCSIEEAMELRLGLRGLTSYAETISIY
GTEQVFVDGDDTPFSKAILTAAYASRGLKMRVTSGGGAEVLMGAAEKCSILYLESRCVSL
ARALGSQGVQNGGIDGVGVVASVPEGMKELLAENLMVMMRDLESCAGNDNLISESDIRRS
AHTLPVLLAGADFIFSGFGSIPRYDNAFALSNFNADDMDDFLVLQRDWGADGGLRTVSRE
HLARVRRRAATAVQAVYRDLGLADFDDTRIDAVVVANDSRDLPAGDPKAVAEAATAIEAR
QLTVFDVVAALHRTGYAPEAEAIMRLTRERLRGDQLQTSAIFDDQFQVLSKITDPNDYAG
PGSGYTPTEKR--RAEIDGIRQARTSAELTADQAEH----RGHVVFSDVEPAHQGSDPRE
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VCIGLSPALGRSVWLTLCGLTVGEVLRQLSAGLEEEGCVPRLVRVRSTIDVGLIGLTAAR
LSGSGIGIGLQGKGTALIHRRDLAPLANLELFSVAPLLTAKMYRELGRNAARHAKGMAPL
PILAGGTDESISARYHARAVALVALERQACEPGQAPITVEAKRV----
>gi|13475607|ref|NP_107174.1| glycerol dehydratase large subunit [Mesorhizobium loti
MAFF303099]
--------MTPKLNRWKRFADWDERPLRLDKFAAEDPANGFSAFSSPADPKPG-IGIKDG
RVISLDGVLEHDYDMIDRFIARHHIDPEVAPEAMALDSATVARWLVDMNVPRETLVRLAH
GMTPAKLAEVVSQLNALEIAFAYSKMRARKTPGNQAHVTNAKDDPLQLAADAATAVAFGF
DEIETTMRVSRNAWSNAVACAVGGAVGRWGTLFQCSSEEAEELRIAMAGFTSYAETVSVY
GTEKSFTDGDDTPWSKAFLAAAYASRGVKMRCTSGAGSELLMGFHEAKSLLYLEARCLCL
QRGMGVQGTQNGGIDGAPLTATIPGGVRELMAENLIAVWLDLECASGNDARSTESEIRVG
AKILPYLIAGSDLICSGMGSILKYDNSFNPSLINGEELEDYLVLQRDFEADGGLTPLPES
RAIELRERAVEAIAAVFEELGLSSPTEDMKSSVVYASGSDDTRSLMPRDVSFISEAIKER
GITVIDVVKALAKRGFREEAENLLDVVKLRLSGDYLQTSAMI-RNGRIVSAVNDPNDYLG
PGSGYRVSEER--RLQLNDIRDVLDQKEVLRSEALHEKDEARHIRYRNLGPAANGSAKDD
VVIGISPAFGLKLYRTTAGHRLSEVLGAMLDAIHARGLKARVVRFRHTADTSFLGLSAAR
LAGSGIGIGIQAKGTAVIHQRDRQPHNNLELFSNAPITRLEHYRALGANAAAYALGEMPE
PVVVPQRGEAMGSRYHARVALIYAIETGLTEAGAAPEEVDVILTGVKS
>gi|118470012|ref|YP_884909.1| glycerol dehydratase large subunit [Mycobacterium
smegmatis str. MC2 155]
----MHLNSTEVDSRLGRIRLLDRQRVNLDGFADVDAELGMISHLSPNDPEPSWVVADDG
TVLEMDSKPAEDFDTIDEFIVKYAIDHEQAPRSMAMTDLDLARMIVDPGRPREEILRVCS
GLTPAKMARVVASLQPVEIQMAMMKMRARRTPANQAHVTNRLDDPLLIAADAATAVVYGF
RELEATVPVLDDAPAVAVGLLIGSQVPAPGALTQCSVEEARELELGVRGLVSYAETVSVY
GTEQVFTDGDDTPWSKAFLTSCYASRGIKMRLSSGAGSEVLMGQAEGKSMNYLEARCVAL
ARGIGAQGVQNGGVDGAAITASVPGGVKELHAENLMVMLRGLESCSGNDSLMSESTMRRT
SRTLPTLLSGSDFIFSGFGSVVSYDNMFGPSNFNAADLDDYLVLQRDWGVDGGLRSVDPT
TLESMRREAAEATRAVFEYLGLADFDDDHVEAVVGAEGSKDLPQDDGVKVLSAARMIDQS
GLTVLDIVSALAETGFTHIADRVLGMARARVTGDYLQTAAIFDEEMNVLSALHDPNDYRG
PGTGYRPTPER--QAQIDAVRQARSVADLVKEQATS----AQPDRLRVLGAATVGEDPRE
VVIGVSPAFGTKLFRTLSGMTIYDVLEQILAGLEEEHCVPRLVRITDSIDLGAIGKSAAQ
LSGSGIGVGLQAKGTTLIHRRDLPPLANLELLSVAPLITPEMYRLIGINAGRHAKGATPS
PMRNAYTDEAITARYHTKVVSMVAIEREESERRE-TGNVELEITR---
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%%  PduD [targeting tail implicated]

>gi++|16765371|ref|NP_460986.1| propanediol dehydratase medium subunit [Salmonella
typhimurium LT2]
--MEINEKLLRQIIEDVLRDMK-GSDKPVSFNAPAASTAPQT----AAPAGD--------
GFLTEVGEARQGTQQDEVIIAVGPAFGLAQTVNIVGLPHKSILREVIAGIEEEGIKARVI
RCFKSSDVAFVAVEGNRLSGSGISIGIQSKGTTVIHQQGLPPLSNLELFPQAPLLTLETY
RQIGKNAARYAKRESPQPVPTLNDQMARPKYQAKSAILHIKETKYVVTGKNPQELRVAL-
---------
>gi++|62180619|ref|YP_217036.1| propanediol utilization: dehydratase, medium subunit
[Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
--MEINEKLLRQIIEDVLRDMK-GSDKPVSFNAPAASTAPQT----AAPAGD--------
GFLTEVGEARQGTQQDEVIIAVGPAFGLAQTVNIVGLPHKSILREVIAGIEEEGIRARVI
RCFKSSDVAFVAVEGNRLSGSGISIGIQSKGTTVIHQQGLPPLSNLELFPQAPLLTLETY
RQIGKNAARYAKRESPQPVPTLNDQMARPKYQAKSAILHIKETKYVVTGKNPQELRVAL-
---------
>gi++|56413057|ref|YP_150132.1| diol dehydratase medium subunit [Salmonella enterica
subsp. enterica serovar Paratyphi A str. ATCC 9150]
--MEINEKLLRQIIEDVLRDMK-GSDKPVSFNTPAASTAPQT----AAPAGD--------
GFLTEVGEARQGTQQDEVIIAVGPAFGLAQTVNIVGLPHKSILREVIAGIEEEGIRARVI
RCFKSSDVAFVAVEGNRLSGSGISIGIQSKGTTVIHQQGLPPLSNLELFPQAPLLTLETY
RQIDKNAARYAKRESPQPVPTLNDQMARPKYQAKSAILHIKETKYVVTGKNPQELRVAL-
---------
>gi++|16760974|ref|NP_456591.1| diol dehydratase medium subunit [Salmonella enterica
subsp. enterica serovar Typhi str. CT18]
--MEINEKLLRQIIEDVLRDMK-GSDKPVSFNTPAASTAP----QTAAPAGD--------
GFLTEVGEARQGTQQDEVIIAVGPAFGLAQTVNIVGLPHKSILREVIAGIEEEGIRARVI
RCFKSSDVAFVAVEGNRLSGSGISIGIQSKDTTVIHQQGLPPLSNLELFPQAPLLTLETY
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RQIGKNAARYAKRESPQPVPTLNDQMARPKYQAKSAILHIKETKYVVTGKNPQELRVTL-
---------
>gi++|161502795|ref|YP_001569907.1| hypothetical protein SARI_00846 [Salmonella
enterica subsp. arizonae serovar 62:z4,z23:--]
--MEINEKLLRQIIEDVLSEMQ-TSDTPVSFHAPSATAVA----QKAAPGGE--------
SFLTEIGEAKQGTQQDEVVIAVGPAFGLSQTVNIVGLPHKSILREVIAGIEEEGIKARVI
RCFKSSDVAFVAVEGNRLSGSGISIGIQSKGTTVIHQQGLPPLSNLELFPQAPLLTLETY
RQIGKNAARYAKRESPQPVPTLNDQMARPKYQAKSAILHIKETKYVVTGKNPQELRVAL-
---------
>gi++|218549344|ref|YP_002383135.1| Propanediol utilization: diol dehydratase,
medium subunit [Escherichia fergusonii ATCC 35469]
--MEINEKLLRQIIEQVLCEMQ-TSDKPVSFQASTATA--------APAASD--------
SFLTEIGEARQGTQQDEVIIAVGPAFGLSQTVNIVGLSHKSILREVIAGIEEEGIKARVI
RCFKSSDVAFVAVEGNRLSGSGISIGIQSKGTTVIHQQGLPPLSNLELFPQAPLLTLETY
RQIGKNAARYAKRESPQPVPTLNDQMARPKYQAKSAILHIKETKYVVTGKNPQELRVAL-
---------
>gi++|152971725|ref|YP_001336834.1| propanediol utilization: dehydratase, medium
subunit [Klebsiella pneumoniae subsp. pneumoniae MGH 78578]
--MEINETLLRQIIEEVLSEMKSGADKPVSFSAPAASVASAAPVAVAPVSGD--------
SFLTEIGEAKPGTQQDEVIIAVGPAFGLAQTANIVGIPHKNILREVIAGIEEEGIKARVI
RCFKSSDVAFVAVEGNRLSGSGISIGIQSKGTTVIHQRGLPPLSNLELFPQAPLLTLETY
RQIGKNAARYAKRESPQPVPTLNDQMARPKYQAKSAILHIKETKYVVTGKNPQELRVAL-
---------
>gi++|218705534|ref|YP_002413053.1| Propanediol utilization: diol dehydratase,
medium subunit [Escherichia coli UMN026]
--MEINEKLLRQIIEDVLAEMQ-TSDKPVSFRAPVSATAS------SAPDTG--------
NFLTEIGEAQQGTQQDEVIIAVGPAFGLAQTVNIIGIPHKNILREVIAGIEEEGIKARVI
RCFKSSDVAFVAVEGDRLSGSGIAIGIQSKGTTVIHQQGLPPLSNLELFPQAPLLTLDTY
RQIGKNAARYAKRESPQPVPTLNDQMARPKYQAKSAILHIKETKYVVTGKKPQELRVTF-
---------
>gi++|206580874|ref|YP_002236781.1| propanediol utilization dehydratase, medium
subunit [Klebsiella pneumoniae 342]
--MEINETLLRQIIEEVLSEMKSGADKPVSFSAPAASVASAAV---APVSSE--------
SFLTEIGEAKPGTQQDEVIIAVGPAFGLAQTANIVGIPHKNILREVIAGIEEEGIKARVI
RCFKSSDVAFVAVEGNRLSGSGISIGIQSKGTTVIHQRGLPPLSNLELFPQAPLLTLETY
RQIGKNAARYAKRESPQPVPTLNDQMARPKYQAKSAILHIKETKYVVTGKNPQELRMAL-
---------
>gi++|215487214|ref|YP_002329645.1| propanediol dehydratase, medium subunit,
AdoCbl-dependent [Escherichia coli O127:H6 str. E2348/69]
--MEINEKLLRQIIEDVLAEMQ-TSDKSVSFRAPVSATVS------SVPDTE--------
NFLTEIGEAQQGTQQDEVIIAVGPAFGLAQTVNIIGIPHKNILREVIAGIEEEGIKARVI
RCFKSSDVAFVAVEGDRLSGSGIAIGIQSKGTTVIHQQGLPPLSNLELFPQAPLLTLDTY
RQIGKNAARYAKRESPQPVPTLNDQMARPKYQAKSAILHIKETKYVVTGKKPQELRVTF-
---------
>gi++|74312533|ref|YP_310952.1| putative propanediol utilization protein: diol
dehydratase medium subunit [Shigella sonnei Ss046]
--MEINEKLLRQIIEDVLAEMQ-PSDKSVSFRAPVSATVP------SAPDTG--------
NFLTEIGEAQQGTQQDEVIIAVGPAFGLAQTVNIIGIPHKNILREVIAGIEEEGIKARVI
RCFKSSDVAFVAVEGDRLSGSGIAIGIQSKGTTVIHQQGLPPLSNLELFPQAPLLTLDTY
RQIGKNAARYAKRESPQPVPTLNDQMARPKYQAKSAILHIKETKYVVTGKKPQELRVTF-
---------
>gi++|157155485|ref|YP_001463343.1| propanediol utilization dehydratase, medium
subunit [Escherichia coli E24377A]
--MEINEKLLRQIIEDVLAEMQ-PSDKSVSFRAPVSATVS------SAPDTG--------
NFLTEIGEAQQGTQQDEVIIAVGPAFGLAQTVNIIGIPHKNILREVIAGIEEEGIKARVI
RCFKSSDVAFVAVEGDRLSGSGIAIGIQSKGTTVIHQQGLPPLSNLELFPQAPLLTLDTY
RQIGKNAARYAKRESPQPVPTLNDQMARPKYQAKSAILHIKETKYVVTGKKPQELRVTF-
---------
>gi++|123442947|ref|YP_001006922.1| putative propanediol utilization protein:
dehydratase, medium subunit [Yersinia enterocolitica subsp. enterocolitica 8081]
-MVDINEKLLRQIIEGVLQEMQ-GDSNTVSFKQETQPTAT------AAVASG--------
DFLTEVGEARPGTHQDEVIIAVGPAFGLSQTANIVGIPHKNILRELIAGIEEEGIKARVI
RCFKSSDVAFVAVEGNRLSGSGISIGIQSKGTTVIHQQGLPPLSNLELFPQAPLLTLETY
```

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RLIGKNAARYAKRESPQPVPTLNDQMARPKYQAKSAILHIKETKYVVTGKNPQELRVAL-
---------
>gi++|116872528|ref|YP_849309.1| propanediol utilization dehydratase, medium subunit
[Listeria welshimeri serovar 6b str. SLCC5334]
-MVEINEKVLRGIISEVLDELQ-LKEDKVSFQKEPSNPVVSDE-----------------
SFLTEVGDAKPGRQKDEVVIAVAPAFGKYQTKNIVGVPHKQILREVIAGIEEEGLKARVV
RVFRSSDVAFVAVEGDRLSGSGICIGIQSRGTALIHQKDLQPLSNLELFPQAPLITLETY
RAIGKNAAKYAKGESPNPVPMVNDQMARPKFQAKAALLHIKETKHVVQGKNAVELQVN--
---------
>gi++|16800187|ref|NP_470455.1| hypothetical protein lin1118 [Listeria innocua
Clip11262]
-MVEINEKVLRGIISEVLDELQ-LKEDKVSFQKEQPSVAVSDE-----------------
SFLTEVGDAKPGRQKDEVVIAVAPAFGKYQTKNIVGVPHKQILREVIAGIEEEGLKARVV
RVFRSSDVAFVAVEGDKLSGSGICIGIQSRGTALIHQKDLQPLSNLELFPQAPLITLETY
RAIGKNAAKYAKGESPNPVPMVNDQMARPKFQAKAALLHIKETKHVVQGKNAVELQVN--
---------
>gi++|46907372|ref|YP_013761.1| propanediol utilization: dehydratase, medium subunit
[Listeria monocytogenes str. 4b F2365]
-MVEINEKVLRGIISEVLDELQ-LKEDKVSFQKEQPSVAVSDE-----------------
SFLTEVGDAEPGRQKDEVVIAVAPAFGKYQTKNIVGVPHKQILREVIAGIEEEGLKARVV
RVFRSSDVAFVAVEGDKLSGSGICIGIQSRGTALIHQKDLQPLSNLELFPQAPLITLETY
RAIGKNAAKYAKGESPNPVPMVNDQMARPKFQAKAALLHIKETKHVVQGKNAVELQVN--
---------
>gi++|16803194|ref|NP_464679.1| hypothetical protein lmo1154 [Listeria monocytogenes
EGD-e]
-MVEINEKVLRGIISEVLDELQ-LKEDKVSFQKEQPSVAVSDE-----------------
SFLTEVGDAEPGRQKDEVVIAVAPAFGKYQTKNIVGVPHKQILRELIAGIEEEGLKARVV
RVFRSSDVAFVAVEGDKLSGSGICIGIQSRGTALIHQKDLQPLSNLELFPQAPLITLETY
RAIGKNAAKYAKGESPNPVPMVNDQMARPKFQAKAALLHIKETKHVVQGKNAVELQVN--
---------
>gi++|125717398|ref|YP_001034531.1| propanediol utilization: dehydratase, medium
subunit, putative [Streptococcus sanguinis SK36]
-MTEINETLLRSIIAEVMKEMSANTKETAAETSEKPVTKP-------VSNEK--------
AVIRTVGVAKPSQSTDEVVIAVGPAFGEQQVKTMVDIPHTEVLRQLVAGIEEEGLKARIV
KVYRSSDVAFVAVEGDHLSGSGISIGVQSKGTTVIHQRDLPPLSNLELFPQAPLLTPETY
RLIGKNAAKYAKGETPNPVPTLNDQMARPKYQAYSALLHIKETKLVKRGKPADECQVI--
---------
>gi++|148544952|ref|YP_001272322.1| dehydratase, medium subunit [Lactobacillus
reuteri DSM 20016]
-MADIDENLLRKIVKEVLSETN-QIDTKIDFDKSNDSTATATQEVQQPNSKA--VPEKKL
DWFQPVGEAKPGYSKDEVVIAVGPAFATVLDKTETGIPHKEVLRQVIAGIEEEGLKARVV
KVYRSSDVAFCAVQGDHLSGSGIAIGIQSKGTTVIHQKDQDPLGNLELFPQAPVLTPETY
RAIGKNAAMYAKGESPEPVPAKNDQLARIHYQAISAIMHIRETHQVVVGKPEEEIKVTFD
---------
>gi++|116334195|ref|YP_795722.1| diol dehydratase medium subunit [Lactobacillus
brevis ATCC 367]
MAQEIDENLLRNIIRDVIAETQ-TGDTPISFKADAPAASSATTATAAPVNGDGPEPEKPV
DWFKHVGVAKPGYSRDEVVIAVAPAFAEVMDHNLTGISHKEILRQMVAGIEEEGLKARIV
KVYRTSDVSFCGAEGDHLSGSGIAIAIQSKGTTIIHQKDQEPLSNLELFPQAPVLDGDTY
RAIGKNAAEYAKGMSPSPVPTVNDQMARVQYQALSALMHIKETKQVVMGKPAEQIEVNFN
---------
>gi++|167040581|ref|YP_001663566.1| dehydratase, medium subunit [Thermoanaerobacter
sp. X514]
--MVKTESLVEQIVKEVLKKLE-NVEIAAPATQSSDDANQEWE-----------------
MIIEEIGEAKQGVNVDEVVIGVSPGFYIKFKKNIIGIPLGNILREIISGITEQGLKARIV
RVKHTADVGFIAHTAAKLSGSGIGIGIQSRGTVVIHQKDLQPLNNLELFPQCPVLTLETY
RAIGRNAALYAKGESPTPVPVQNDQMARPKYQAIAAVMHNFETKYVQTGAKPVELKVSFA
RKGGNKSDR
>gi++|218782819|ref|YP_002434137.1| dehydratase medium subunit [Desulfatibacillum
alkenivorans AK-01]
--MKLTEEMLRQIITEVVGQMAGGAAAPAPAAVDTDKP-----------------------
LNFIEKGPAQAGSNPKEVVVAVPPGFGVTPTKTIIDIPHSVVLAEVAAGIEEEGLTARFV
RNYQTADVAFLAHSAAQLSGSGVGIGILSRGTSVIHQKDLAPLQNLELFPQAPLVEAETF
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RAIGKNAAKYAKGENPNPVPVKNDPMARPRYQGLAALLHNKEVQFLDPQKKILEVVQG--
---------
>gi|188590348|ref|YP_001921322.1| propanediol utilization: dehydratase, medium
subunit [Clostridium botulinum E3 str. Alaska E43]
-MENTTNQ-------YVIPKLQ--------------------------------------
--LTEVGEAKVGTKVDEVVIGLAPAFLKFQSKTLVNVSHSDILTEIIAGIEEEGLKARVV
RVIRTSDVSFISNDAAKLSGSGIGIGIQSKGTTVIHQKDLLPLNNLELFPQAPLLTLETY
RLIGKNAAKYAKGESPTPVPTKNDQMVRPKFMAIAALFHIKETKHVEIGAKPIEIEVKF-
---------
>gi|187933731|ref|YP_001886293.1| propanediol utilization: dehydratase, medium
subunit [Clostridium botulinum B str. Eklund 17B]
-MENTTNQ-------YVMPKLQ--------------------------------------
--LTEVGEAKVGTKVDEVVIGLAPAFLKFQSKTLVNVSHSDILTEIIAGIEEEGLKARVV
RVIRTSDVSFISNDAAKLSGSGIGIGIQSKGTTVIHQKDLLPLNNLELFPQAPLLTLDTY
RLIGKNAAKYAKGESPTPVPTKNDQMVRPKFMAIAALFHIKETKHVEIGAKPIEIEVKF-
---------
>gi|152972004|ref|YP_001337150.1| glycerol dehydratase [Klebsiella pneumoniae subsp.
pneumoniae MGH 78578]
----------MQQTTQIQPSFT--------------------------------------
LKTREGGVASADERADEVVIGVGPAFDKHQHHTLIDMPHGAILKELIAGVEEEGLHARVV
RILRTSDVSFMAWDAANLSGSGIGIGIQSKGTTVIHQRDLLPLSNLELFSQAPLLTLETY
RQIGKNAARYARKESPSPVPVVNDQMVRPKFMAKAALFHIKETKHVVQDAEPVTLHVDLV
RE-------
>gi|18309912|ref|NP_561846.1| coenzyme B12-dependent glycerol dehydrogenase medium
subunit [Clostridium perfringens str. 13]
--MTMEER-------TFIPEIT--------------------------------------
--VEEVGEAKVGLRSDEVVIGLAPAFLKYQNKTIVDVPHTETLLEIIAGIEEEGLHARVV
RILRTSDVSFIAHDAACLSGSGIGIGIQSKGTTVIHQKDLLPLNNLELFSQAPLLTTETY
RLIGKNAAKYAKGESPTPVPVKNDQMVRPKFMAKAALLHIKETKHVEPGKKPVQLEVKF-
---------
>gi|110802305|ref|YP_698328.1| glycerol dehydratase, beta subunit [Clostridium
perfringens SM101]
----MEER-------TFIPEIT--------------------------------------
--VEEVGEAKVGLRSDEVVIGLAPAFLKYQNKTIVDVPHTETLLEIIAGIEEEGLHARVV
RVLRTSDVSFIAHDAACLSGSGIGIGIQSKGTTVIHQKDLLPLNNLELFSQAPLLTPETY
RLIGKNAAKYAKGESPTPVPVKNDQMVRPKFMAKAALLHIKETKHVEPGKKPVQLEVKF-
---------
>gi|110800527|ref|YP_695620.1| coenzyme B12-dependent glycerol dehydratase, medium
subunit [Clostridium perfringens ATCC 13124]
----MEER-------TFIPEIT--------------------------------------
--VEEVGEAKVGLRSDEVVIGLAPAFLKYQNKTIVDVPHTETLLEIIAGIEEEGLHARVV
RILRTSDVSFIAHDAACLSGSGIGIGIQSKGTTVIHQKDLLPLNNLELFSQAPLLTPETY
RLIGKNAAKYAKGESPTPVPVKNDQMVRPKFMAKAALLHIKETKHVEPGKKPVQLEVKF-
---------
>gi|118467606|ref|YP_885930.1| propanediol utilization: dehydratase, medium subunit
[Mycobacterium smegmatis str. MC2 155]
-------MIMSAQSTQAQRTLE--------------------------------------
--LVGDSPAEPGKRSDEVVLAVSPAFADFFSQTIIGLSHADVIREILAGIEEQEVHARCI
RVRHSSDLAVLAHTAAKLSGSGIGIGILSRGTSMIHQRDLPRLSSLELFPQSPLMTLETY
RSIGSNAAQYAKGESPEPVPTLNDQMARPRWQAKAALLHLKETEQVVKQAKPVEVVPQFG
VAEALGT--
========================================

%%  PduE [targeting tail implicated]

>gi++|16765372|ref|NP_460987.1| propanediol dehydratase small subunit [Salmonella
typhimurium LT2]
-------------------MNTDAIESMVRDVLSRMNSLQGDAPAAAPAAGGTSRSAKV-
---SDYPLANKHPEWVKTATNKTLDDFTLENVLSNKVTAQDMRITPETLRLQASIAKDAG
RDRLAMNFERAAELTAVPDDRILEIYNALRPYRS-TKEELLAIADDLENRYQAKICAAFV
REAAGLYVERKKLKGDD
>gi++|194446555|ref|YP_002041309.1| propanediol dehydratase small subunit
[Salmonella enterica subsp. enterica serovar Newport str. SL254]
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-------------------MNTDAIESMVRDVLSRMNSLQGDAPAAASAAGGTSRSAKV-
---SDYPLANKHPEWVKTATNKTLDDFTLENVLSNKVTAQDMRITPETLRLQASIAKDAG
RDRLAMNFERAAELTAVPDDRILEIYNALRPYRS-TKEELMAIADDLENRYQAKICAAFV
REAAGLYVERKKLKGDD
>gi++|161613351|ref|YP_001587316.1| hypothetical protein SPAB_01062 [Salmonella
enterica subsp. enterica serovar Paratyphi B str. SPB7]
-------------------MNTDAIESMVRDVLSRMNSLQGDAPAAAPAAGGTSRSAKV-
---SDYPLANKHPEWVKTATNKTLDDFTLENVLSNKVTAQDMRITPETLRLQASIAKDAG
RDRLAMNFERAAELTAVPDDRILEIYNALRPYRS-TKEELMAIADDLENRYQAKICAAFV
REAAGLYVERKKLKGDD
>gi++|205353187|ref|YP_002226988.1| diol dehydratase small subunit [Salmonella
enterica subsp. enterica serovar Gallinarum str. 287/91]
-------------------MNTEAIESMVRDVLSRMNSLQGDAPAAAPAAGGTSRSAKV-
---SDYPLANKHPEWVKTATNKTLDDFTLENVLSNKVTAQDMRITPETLRLQASIAKDAG
RDRLAMNFERAAELTAVPDDRILEIYNALRPYRS-TKEELLAIADDLENRYQAKICAAFV
REAAGLYVERKKLKGDD
>gi++|16760975|ref|NP_456592.1| diol dehydratase small subunit [Salmonella enterica
subsp. enterica serovar Typhi str. CT18]
-------------------MNTDAIESMVRDVLSRMNSLQGDAPAAAPAAGGTSRSAKV-
---SDYPLANKHPEWVKTATNKTLDDFTLENVLSNKVTAQDMRITPKTLRLQASIAKDAG
RDRLAMNFERAAELTAVPDDRILEIYNALRPYRS-TKEELLAIADDLENRYQAKICAAFV
REAAGLYVERKKLKGDD
>gi++|56413056|ref|YP_150131.1| diol dehydratase small subunit [Salmonella enterica
subsp. enterica serovar Paratyphi A str. ATCC 9150]
-------------------MNIDAIESMVRDVLSRMNSLQGDAPAAAPAAGGTSRSAKV-
---SDYPLANKHPEWVKTATNKTLDDFTLENVLSNKVTAQDMRITPETLRLQASIAKDAG
RDRLAMNFERAAELTAVPDDRILEIYNALRPYRS-TKEELLAIADDLENRYQAKICAAFV
REAAGLYVERKKLKGDD
>gi++|62180620|ref|YP_217037.1| propanediol utilization: dehydratase, small subunit
[Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
-------------------MNTDAIESMVRDVLSRMNSLQGDAPAAASAAGGTSRSAKV-
---SDYPLANKHPEWVKTATNKTLDDFTLENVLSNKVTAQDMRITPETLRLQASIAKDAG
RDRLAMNFERAAELTAVPDDRILEIYNALRPYRS-TKEELMAIADDLENRYQAKICAAFV
REAATLYVERKKLKGDD
>gi++|161502794|ref|YP_001569906.1| hypothetical protein SARI_00845 [Salmonella
enterica subsp. arizonae serovar 62:z4,z23:--]
-------------------MNTEAIESMVRDVLSRMNSLQGQTSVSAAVGTSTHTAKV--
---SDYPLANKHPEWVKTATNKTLDDFTLENVLSDNVTAQDMRITPETLRIQAAIAKDAG
RDRLAMNFERAAELTAVPDDRILEIYNALRPYRS-TKEELMAIADDLESRYQAKICAAFV
REAATLYVERKKLKGDD
>gi++|218705535|ref|YP_002413054.1| Propanediol utilization diol dehydratase, small
subunit [Escherichia coli UMN026]
-------------------MNTDAIESMVRDVLNRMNSLQDAAPVSAVPSASIQSAKV--
---TDYPLANKHPEWVKTATNKTLDDFTLENVLSDNVTAQDMRITPETLRIQAAIARDAG
RDRLAMNFERAAELTSVPDDRILEIYNALRPYRS-TKQELIAIADDLERRYQAKICAAFV
REAAELYVERKKLKGDD
>gi++|215487215|ref|YP_002329646.1| propanediol dehydratase, small subunit,
AdoCbl-dependent [Escherichia coli O127:H6 str. E2348/69]
-------------------MNTDAIESMVRDVLNRMNSLQDAAPVSAVPSASIQSAKV--
---TDYPLANKHPEWVKTATNKTLDDFTLENVLSDNVTAQDMRITPETLRIQAAIARDAG
RDRLAMNFERAAELTSVPDDRILEIYNALRPYRS-TKQELIAIADDLERRYQAQICAAFV
REAAELYVERKKLKGDD
>gi++|218549345|ref|YP_002383136.1| Propanediol utilization diol dehydratase, small
subunit [Escherichia fergusonii ATCC 35469]
-------------------MNTDAIESMVRDVLSRMNSLEGAAPAPAPVTTRGSAHHAKV
---SDYPLATKHPEWVKTATNKSLDDLTLENVLSDKITAQDMRITPETLRMQAAIAKDAG
RDRLAMNFERAAELTAVPDDRILEIYNALRPYRS-TKEELLAIADDLERRYQAVICAAFV
REAAALYLERKKLKGDD
>gi++|206579980|ref|YP_002236780.1| propanediol utilization dehydratase, small
subunit [Klebsiella pneumoniae 342]
-------------------MNTDAIESMVRDVLSRMNSLQDGATPAPAAPTNDTARQPKV
---SDYPLATRHPEWVKTATNKTLDDLTLENVLSDRVTAQDMRITPETLRMQAAIAQDAG
RDRLAMNFERAAELTAVPDDRILEIYNALRPYRS-TQAELLAIADDLEHRYQARLCAAFV
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REAAGLYVERKKLKGDD
>gi++|74312534|ref|YP_310953.1| putative propanediol utilization protein: diol
dehydratase small subunit [Shigella sonnei Ss046]
-------------------MNTDAIESMVRDVLNRMNSLQDAAPVSAVPNASILSAKV--
---TDYPLANKHPEWVKTATNKTLDDFTLENVLSDNVTALDMRITPETLRIQAAIARDAG
RDRLAMNFERAAELTSVPDDRILEIYNALRPYRS-TKQELIAIADDLEQRYQAKICAAFV
REAAELYVERKKLKGDD
>gi++|152971726|ref|YP_001336835.1| propanediol utilization: dehydratase, small
subunit [Klebsiella pneumoniae subsp. pneumoniae MGH 78578]
-------------------MNTDAIESMVRDVLSRMNSLQDGITPAPAAPTNDTVRQPKV
---SDYPLATRHPEWVKTATNKTLDDLTLENVLSDRVTAQDMRITPETLRMQAAIAQDAG
RDRLAMNFERAAELTAVPDDRILEIYNALRPYRS-TQAELLAIADDLEHRYQARLCAAFV
REAAGLYIERKKLKGDD
>gi++|157156054|ref|YP_001463344.1| propanediol utilization dehydratase, small
subunit [Escherichia coli E24377A]
-------------------MNTDAIESMVRDVLNRMNSLQDAAPVSAVPNASILSAKV--
---TDYPLANKHPEWVKTATNKTLDDFTLENVLSDNVTALDMRITPETLRIQAAIARDAG
CDRLAMNFERAAELTSVPDDRILEIYNALRPYRS-TKQELIAIADDLEQRYQAKICAAFV
REAAELYVERKKLKGDD
>gi++|123442948|ref|YP_001006923.1| putative propanediol utilization protein:
dehydratase, small subunit [Yersinia enterocolitica subsp. enterocolitica 8081]
-------------------MNSEAIESMVRDVLSKMNSLQGQTPTTACAPAASSRSDAKV
---SDYPLANKHPDWVKTATNKTLDDLTLANVLNGSVTSQDLRITPEILRIQASIAKDAG
RPLLAMNFERAAELTAVPDDKVLDIYNALRPFRS-SKEELNAIADDLEQTYKATICAAFV
REAAVLYVQRKKLKGDD
>gi++|16800188|ref|NP_470456.1| hypothetical protein lin1119 [Listeria innocua
Clip11262]
-------------------MNQEALENMVRNILQEVNS--GAVTTTTSQKASGDSLTV--
---RDYPLGTKRPELVKTASSKSLDDITLKSVLDGTIKPEDVRVTAETLKMQAQVARDAG
RATLANNFERAAELTVVPDERILEIYNAMRPYRS-SREELLAIADELENVYQATICSNYV
REAAQLYQERKKLKGDN
>gi++|116872529|ref|YP_849310.1| propanediol utilization dehydratase, small subunit
[Listeria welshimeri serovar 6b str. SLCC5334]
-------------------MNQEALENMVRNILQEVNS--GAVSTTTSQKVSGDTLTV--
---RDYPLGKKRPELVKTSTSKSLDDITLKSVLDGTIKPEDVRVTAETLKMQAQVARDAG
RATLANNFERAAELTIVPDERILEIYNAMRPYRS-SKEELLAIADELESVYHATICSNYV
REAAQLYQERKKLKGDN
>gi++|46907373|ref|YP_013762.1| propanediol utilization: dehydratase, small subunit
[Listeria monocytogenes str. 4b F2365]
-------------------MNQEALENMVRNILQEVNS--GAVSTTTSQKVSGDTLTV--
---RDYPLGTKRPELVKTSTSKSLDDITLKSVLDGTIKPEDVRVTAETLKMQAQVARDAG
RATLANNFERAAELTIVPDERILEIYNAMRPYRS-SREELLAIADELESVYHATICSNYV
REAAQLYQERKKLKGDN
>gi++|16803195|ref|NP_464680.1| hypothetical protein lmo1155 [Listeria monocytogenes
EGD-e]
-------------------MNQEALENMVRNILQEVNS--GGVSTTTSQKVSGDTLTV--
---RDYPLGTKRPELVKTSTSKSLDDITLKSVLDGTIKPEDVRVTAETLKMQAQVARDAG
RATLANNFERAAELTIVPDERILEIYNAMRPYRS-SREELLAIADELESVYHATICSNYV
REAAQLYQERKKLKGDN
>gi++|125717399|ref|YP_001034532.1| B12-dependent diol dehydratase small subunit,
putative [Streptococcus sanguinis SK36]
--------------------MSESVETLVKQILAELSDSGSASQGAVNRPVSSDEATA--
---ADYPISKKHPDWIKVGQDKKFEDITLENILSGYVKAEDLRIKPEILIKQGEIAKNAG
REAIQYNFSRAAELTKVPDARVLEIYNALRPYRS-SKQELLDIANELENQYGAVICAGFV
REAAENYERRKKLKGDN
>gi++|167040580|ref|YP_001663565.1| dehydratase, small subunit [Thermoanaerobacter
sp. X514]
-----------------MIDEKTLEIIVREVLTNLTSDKGTQNQQKTASSSLPKLDPK-
---RDYPLAKNKPELAKSITGKTINEITLQAVREGKVLPDDLKISPETLLAQAEIAEAAG
RKQLANNFRRAAELTKVPDKRILEIYNALRPYRS-TKEELLAIADELDNAYGAKVCAAFV
REAAEVYERRGRLKGME
>gi++|116334194|ref|YP_795721.1| propanediol dehydratase, small subunit
[Lactobacillus brevis ATCC 367]
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---------------------MSEIDDLVAKIVQQIGGTEAADQTTATPTSTATQTQHAA
LSKQDYPLYSKHPELVHSPSGKALNDITLDNVLNDDIKANDLRITPDTLRMQGEVANDAG
RDAVQRNFQRASELTSIPDDRLLEMYNALRPYRS-TKAELLAISAELKDKYHAPVNAGWF
AEAADYYESRKKLKGDN
>gi++|219854100|ref|YP_002471222.1| hypothetical protein CKR_0757 [Clostridium
kluyveri NBRC 12016]
------------MNRGEAMSSNDLIEQIVKEVLKSMESIQNDEQKYESEEIHGSGRACEI
VSKKDYPLGKKRPELIKTSTGKSIDDISLENVLSGKITLDDVKINKKTLLYQAQIAESVG
NIQLAANFRRAAELTVVPDARVLEIYNALKPHKS-TKQQLIEIAEELESKYKAKLNAELV
REAAESYEKRNMIKV--
>gi++|153953478|ref|YP_001394243.1| DhaC [Clostridium kluyveri DSM 555]
------------------MSSNDLIEQIVKEVLKSMESIQNDEQKYESEEIHGSGRACEI
VSKKDYPLGKKRPELIKTSTGKSIDDISLENVLSGKITLDDVKINKKTLLYQAQIAESVG
NIQLAANFRRAAELTVVPDARVLEIYNALKPHKS-TKQQLIEIAEELESKYKAKLNAELV
REAAESYEKRNMIKV--
>gi++|184154288|ref|YP_001842629.1| glycerol dehydratase small subunit PduE
[Lactobacillus reuteri JCM 1112]
---------------------MSEVDDLVAKIMAQMGNSSSANSSTGTSTASTSKEMTA-
---DDYPLYQKHRDLVKTPKGHNLDDINLQKVVNNQVDPKELRITPEALKLQGEIAANAG
RPAIQKNLQRAAELTRVPDERVLEMYDALRPFRS-TKQELLNIAKELRDKYDANVCAAWF
EEAADYYESRKKLKGDN
>gi++|148544951|ref|YP_001272321.1| dehydratase, small subunit [Lactobacillus
reuteri DSM 20016]
--------------------MMSEVDDLVAKIMAQMGNSSSANSSTGTSTASTSKEMTA-
---DDYPLYQKHRDLVKTPKGHNLDDINLQKVVNNQVDPKELRITPEALKLQGEIAANAG
RPAIQKNLQRAAELTRVPDERVLEMYDALRPFRS-TKQELLNIAKELRDKYDANVCAAWF
EEAADYYESRKKLKGDN
>gi++|218782818|ref|YP_002434136.1| dehydratase small subunit [Desulfatibacillum
alkenivorans AK-01]
MVSFTKDQIADIIRKVGDGTSPEALESAVRNVLAKLQS-----EGLSAPASQGGKLDA--
---SSYPLGIKRKDLVKSATGLGLDDITIEKVVSGEIQFDDIKTRPETLAYQNEIAKSVN
RPNLANNLARAGEMTRIPDARLLEMYNFLRPYRA-AKQEMISMAEELEQKYQAPACAKLV
REAADVYEKNNRLKGDR
>gi|187933430|ref|YP_001886292.1| coenzyme B12-dependent glycerol dehydratase, small
subunit [Clostridium botulinum B str. Eklund 17B]
--------------------------------------------------MEQRKMNP--
---QDYPLATKRPESIKTPTGKNLQDITLENVLKGDIKAEDVRISPETLEMQAQIAEGMK
RDAIARNFRRAAELIKVPDDRILEIYNALRPYRS-TKEDLLAIAEELETVYGAKVNADFV
REAIEVYEARQKLRQE-
>gi|188590615|ref|YP_001921321.1| coenzyme B12-dependent glycerol dehydratase, small
subunit [Clostridium botulinum E3 str. Alaska E43]
--------------------------------------------------MEQRKMNP--
---QDYPLATKRPESIKTPTGKNLQDITLENVLKGDIKAEDVRISPETLEMQAQIAEGMK
RDAIARNFRRAAELIKVPDDRILEIYNALRPNRS-TKEELFAIADELETVYGAKVNADFV
REAIEVYEARQKLRQE-
>gi|110802854|ref|YP_698329.1| glycerol dehydrase, gamma subunit [Clostridium
perfringens SM101]
--------------------------------------------------MENKRMTA--
---ADYPLTSKRKGDIKTPTGKALEDITLEKVLSGEINADDIRISPETLEMQAQIAESMN
RDAIARNFRRAAELIRVPDDRILEMYNALRPYRS-TKEDLFKIADELETKYDAKVNANFV
REAAEVYETRNKLRIEE
>gi|18309913|ref|NP_561847.1| coenzyme B12-dependent glycerol dehydrogenase small
subunit [Clostridium perfringens str. 13]
--------------------------------------------------MENKRMTA--
---ADYPLTSKRKGDIKTPTGKALEDITLEKVLSGEINADDIRISPETLEMQAQIAESMN
RDAIARNFRRAAELIRVPDDRILEMYNALRPYRS-TKEDLFKIADELETKYDAKVNADFV
REAAEVYETRNKLRIEE
>gi|152972003|ref|YP_001337149.1| glycerol dehydratase [Klebsiella pneumoniae subsp.
pneumoniae MGH 78578]
--------------------------------------------------MSEKTMRV--
---QDYPLATRCPEHILTPTGKPLTDITLEKVLSGEVGPQDVRISRQTLEYQAQIAEQMQ
RHAVARNFRRAAELIAIPDERILAIYNALRPFRS-SQAELLAIADELEHTWHATVNAAFV
RESAEVYQQRHKLRKGS
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>gi|118472086|ref|YP_885928.1| coenzyme B12-dependent glycerol dehydrogenase small
subunit [Mycobacterium smegmatis str. MC2 155]
--------------------------------------------------MSEPVLDPA-
---VDYPLSLNRKDLLTTPNGKPIDAITMDAVMSGEVSASDLRITPETLRLQAQIAEGVG
RKQLGANLRRAAEMTAISDERVLQIYNALRPNAS-TKAELDAIAEELETQYGATMLAGLV
REAADVYERRDILATSE
>gi|13475606|ref|NP_107173.1| glycerol dehydratase small subunit [Mesorhizobium loti
MAFF303099]
--------------------------------------------------MTHTR-----
---ADYPLAETQPGAVKGKRGKSLAEITLDSVLAGDVTMEDLRITPQALQAQADVARDVG
RPTLALNFERGAELVEVPQDFIMQVYELLRPGRAKSKEELLQAATTMRDTYQAERIARFI
EEAAETYAARGLFTFRF
>gi|118469461|ref|YP_890538.1| diol dehydrase gamma subunit [Mycobacterium smegmatis
str. MC2 155]
------------------------------------------------------------
------------------MNDKFTDKYTVAAAVDGKLDLSDLRMDPAVLAHQAVIAEENG
NPQLAENFLRAAELATIDDEDVMRLYEALRPYRS-SAEDLDALQASLESR-GAARCAELV
RQAAEAYARRGLLR---
>gi|118468095|ref|YP_884908.1| coenzyme B12-dependent glycerol dehydrogenase small
subunit [Mycobacterium smegmatis str. MC2 155]
------------------------------------------------------------
-------------MTITSHSGRSIDEVTVEAARGGDLTLDDIRISRDTLISQAEAAERTG
SEQLGLNLRRAAELTALSSDDMLAAYEALRPGRS-TFSELEALAQRLAAQ-EAHTCAQLV
REAAAAYRRRGLLR---
>gi|126437897|ref|YP_001073588.1| dehydratase, small subunit [Mycobacterium sp. JLS]
------------------------------------------------------------
----------------------MTEKFTVAAAVDGKLTLSDLRMDPATLAYQAVVAEQDG
NPQLAENFLRAAELAVIDDEAVMKLYEALRPHRS-TAAELEELRVSLETG-GASRCAELV
RQAAEVYARRGLLR---
>gi|108801916|ref|YP_642113.1| propanediol utilization: dehydratase, small subunit
[Mycobacterium sp. MCS]
------------------------------------------------------------
----------------------MTEKFTVAAAVDGKLTLSDLRMDPATLAYQAVVAEQDG
NPQLAENFLRAAELAVIDDEAVMKFYEALRPHRS-TAAELEELRVSLETG-GASRCAELV
RQAAEVYARRGLLR---
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%%  PduG [targeting tail not implicated]

>gi++|16765373|ref|NP_460988.1| propanediol dehydratase reactivation protein
[Salmonella typhimurium LT2]
----MRYIAGIDIGNSSTEVALARQDETGALTITHSALAETTGIKGTLRNVFGIQEALAL
VAKRAGINVRDISLIRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGAGLGVGIT
ITPEELLTR-PADSS------YILVVSSAFDFADIANVINASMRAGYQITGVILQRDDGV
LVSNRLEKSLPIVDEVLYIDRIPLGMLAAIEVAVPGKVIETLSNPYGIATVFNLNADETK
NIVPMARALIGNRSAVVVKTPSGDVKARAIPAGNLELQAQGRTVRVDVAAGAEAIMKAVD
GCGKLDNVTGEAGTNIGGMLEHVRQTMAELTNKPSSEIFIQDLLAVDTSVPVSVTGGLAG
EFSLEQAVGIASMVKSDRLQMAMIAREIEQKLNIDVQIGGAEAEAAILGALTTPGTTRPL
AILDLGAGSTDASIINPKGEIIATHLAGAGDMVTMIIARELGLEDRYLAEEIKKYPLAKV
ESLFHLRHEDGSVQFFPTPLPPAVFARVCVVKP-DELVPL-PGDLALEKVRAIRRSAKER
VFVTNALRALRQVSPTGNIRDIPFVVLVGGSSLDFEVPQLVTDALAHYRLVAGRGNIRGS
EGPRNAVATGLILS-----WHKE----FAHGQ-
>gi++|207857478|ref|YP_002244129.1| propanediol utilization protein [Salmonella
enterica subsp. enterica serovar Enteritidis str. P125109]
----MRYIAGIDIGNSSTEVALARQDETGALTITHSALAETTGIKGTLRNVFGIQEALAL
VAKRAGINVSDISLIRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGAGLGVGIT
ITPEELLTR-PADSS------YILVVSSAFDFADIANVINASMRAGYQITGVILQRDDGV
LVSNRLEKSLPIVDEVLYIDRIPLGMLAAIEVAVPGKVIETLSNPYGIATVFNLNADETK
NIVPMARALIGNRSAVVVKTPSGDVKARAIPAGNLELQAQGRTVRVDVAAGAEAIMKAVD
GCGKLDNVTGEAGTNIGGMLEHVRQTMAELTNKPSSEIFIQDLLAVDTSVPVSVTGGLAG
EFSLEQAVGIASMVKSDRLQMAMIAREIEQKLNIDVQIGGAEAEAAILGALTTPGTTRPL
AILDLGAGSTDASIINPKGEIIATHLAGAGDMVTMIIARELGLEDRYLAEEIKKYPLAKV
ESLFHLRHEDGSVQFFPTPLPPAVFARVCVVKP-DELVPL-PGDLALEKVRAIRRSAKER
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VFVTNALRALRQVSPTGNIRDIPFVVLVGGSSLDFEVPQLVTDALAHYRLVAGRGNIRGS
EGPRNAVATGLILS-----WHKE----FAHGQ-
>gi++|198242248|ref|YP_002216128.1| glycerol dehydratase reactivation factor large
subunit [Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853]
----MRYIAGIDIGNSSTEVALARQDETGALTITHSALAETTGIKGTLRNVFGIQEALAL
VAKRAGINVSDISLIRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGAGLGVGIT
IRPEELLTR-PADSS------YILVVSSAFDFADIANVINASMRAGYQITGVILQRDDGV
LVSNRLEKSLPIVDEVLYIDRIPLGMLAAIEVAVPGKVIETLSNPYGIATVFNLNADETK
NIVPMARALIGNRSAVVVKTPSGDVKARAIPAGNLELQAQGRTVRVDVAAGAEAIMKAVD
GCGKLDNVTGEAGTNIGGMLEHVRQTMAELTNKPSSEIFIQDLLAVDTSVPVSVTGGLAG
EFSLEQAVGIASMVKSDRLQMAMIAREIEQKLNIDVQIGGAEAEAAILGALTTPGTTRPL
AILDLGAGSTDASIINPKGEIIATHLAGAGDMVTMIIARELGLEDRYLAEEIKKYPLAKV
ESLFHLRHEDGSVQFFPTPLPPAVFARVCVVKP-DELVPL-PGDLALEKVRAIRRSAKER
VFVTNALRALRQVSPTGNIRDIPFMVLVGGSSLDFEVPQLVTDALAHYRLVAGRGNIRGS
EGPRNAVATGLILS-----WHKE----FAHGQ-
>gi++|197247884|ref|YP_002147000.1| glycerol dehydratase reactivation factor large
subunit [Salmonella enterica subsp. enterica serovar Agona str. SL483]
----MRYIAGIDIGNSSTEVALARQDEAGALTITHSALAETTGIKGTLRNVFGIQEALAL
VAKRAGINVSDISLIRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGAGLGVGIT
ITPEELLTR-PADSS------YILVVSSAFDFADIANVINASMRAGYQITGVILQRDDGV
LVSNRLEKSLPIVDEVLYIDRIPLGMLAAIEVAVPGKVIETLSNPYGIATVFNLNADETK
NIVPMARALIGNRSAVVVKTPSGDVKARAIPAGNLELQAQGRTVRVDVAAGAEAIMKAVD
GCGKLDNVTGEAGTNIGGMLEHVRQTMAELTNKPSSEVFIQDLLAVDTSVPVSVTGGLAG
EFSLEQAVGIASMVKSDRLQMAMIAREIEQKLNIDVQIGGAEAEAAILGALTTPGTTRPL
AILDLGAGSTDASIINPKGKIIATHLAGAGDMVTMIIARELGLEDRYLAEEIKKYPLAKV
ESLFHLRHEDGSVQFFPTPLPPAVFARVCVVKP-DELVPL-PGDLALEKVRAIRRSAKER
VFVTNALRALRQVSPTGNIRDIPFVVLVGGSSLDFEVPQLVTDALAHYRLVAGRGNIRGS
EGPRNAVATGLILS-----WHKE----FAHGQ-
>gi++|62180621|ref|YP_217038.1| propanediol utilization: diol dehydratase
reactivation [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
----MRYIAGIDIGNSSTEVALARQDETGALTITHSALAETTGIKGTLRNVFGIQEALAL
VAKRAGINVSDISLIRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGVGLGVGIT
ITPEELLTR-PADSS------YILVVSSAFDFADIANVINASMRAGYQITGVILQRDDGV
LVSNRLEKSLPIVDEVLYIDRIPLGMLAAIEVAVPGKVIETLSNPYGIATVFNLNADETK
NIVPMARALIGNRSAVVVKTPSGDVKARAIPAGNLELQAQGRTVRVDVAAGAEAIMKAVD
GCGKLDNVTGEAGTNIGGMLEHVRQTMAELTNKPSSEIFIQDLLAVDTSVPVSVTGGLAG
EFSLEQAVGIASMVKSDRLQMAIIAREIEQKLNIDVQIGGAEAEAAILGALTTPGTTRPL
AILDLGAGSTDASIINPKGEIIATHLAGAGDMVTMIIARELGLEDRYLAEEIKKYPLAKV
ESLFHLRHEDGSVQFFPTPLPPAVFARVCVVKP-DELVPL-PGDLALEKVRAIRRSAKER
VFVTNALRALRQVSPTGNIRDIPFVVLVGGSSLDFEVPQLVTDALAHYRLVAGRGNIRGS
EGPRNAVATGLILS-----WHKE----FAYGQ-
>gi++|56413055|ref|YP_150130.1| PduG protein [Salmonella enterica subsp. enterica
serovar Paratyphi A str. ATCC 9150]
----MRYIAGIDIGNSSTEVALARQDETGALTITHSALAETTGIKGTLRNVFGIQEALAL
VAKRAGINVSDISLIRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGAGLGVGIT
ITPEELLTR-PADSS------YILVVSSAFDFADIANVINASMRAGYQITGVILQRDDGV
LVSNRLEKSLPIVDEVLYIDRIPLGMLAAIEVAVPGKVIETLSNPYGIATVFNLNADETK
NIVPMARALIGNRSAVVVKTPSGDVKARAIPAGNLELQAQGRTVRVDVAAGAEAIMKAVD
GYGKLDNVNGEAGTNIGGMLEHVRQTMAELTNKPSSEIFIQDLLAVDTSVPVSVTGGLAG
EFSLEQAVGIASMVKSDRLQMAMIAREIEQKLNIDVQIGGAEAEAAILGALTTPGTTRPL
AILDLGAGSTDASIINPKGEIIATHLAGAGDMVTMIIARELGLEDRYLAEEIKKYPLAKV
ESLFHLCHEDGSVQFFPTPLPPAVFARVCVVKP-DELVPL-PGDLALEKVRAIRRSAKER
VFVTNALRALRQVSPTGNIRDIPFVVLVGGSSLDFEVPQLVTDALAHYRLVAGRGNIRGS
EGPRNAVATGLILS-----WHKE----FAHGQ-
>gi++|16760976|ref|NP_456593.1| PduG protein [Salmonella enterica subsp. enterica
serovar Typhi str. CT18]
----MRYIAGIDIGNSSTEVALARQDETGALTITHSALAENTGIKGTLRNVFGIQEALAL
VAKRAGINVSDISLIRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGAGLGVGIT
ITPEELLTR-PADSS------YILVVSSAFDFADIANVINASMRAGYQITGVILQRDDGV
LVSNRLEKSLPIVDEVLYIDCIPLGMLAAIEVAVPGKVIETLSNPYGIATVFNLNADETK
NIVPMARALIGNRSAVVVKTPSGDVKARAIPAGNLELQAQGRTVRVDVAAGAEAIMKAVD
GYGKLDNVNGEAGTNIGGMLEHVRQTMAELTNKPSSEIFIQDLLAVDTSVPVSVTGGLAG
EFSLEQAVGIASMVKSDRLQMAMIAREIEQKLNIDVQIGGAEAEAAILGALTTPGTTRPL
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AILDLGAGSTDASIINPKGEIIATHLAGAGDMVTMIIARELGLEDRYLAEEIKKYPLAKV
ESLFHLRHEDGSVQFFPTPLPPAVFARVCVVKP-DELVPL-PGDLALEKVRAIRRSAKER
VFVTNALRALRQVSPTGNIRDIPFVVLVGGSSLDFEVPQLVTDALAHYRLVAGRGNIRGS
EGPRNAVATGLILS-----WHKE----FAYGQ-
>gi++|161613350|ref|YP_001587315.1| hypothetical protein SPAB_01061 [Salmonella
enterica subsp. enterica serovar Paratyphi B str. SPB7]
----MRYIAGIDIGNSSTEVALATLNEAGALTITHSALAETTGIKGTLRNVFGIQEALAL
VAKRAGINVSDISLIRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGVGLGVGIT
ITPEELLTR-PADSS------YILVVSSAFDFADIANVINASMRAGYQITGVILQRDDGV
LVSNRLEKSLPIVDEVLYIDRIPLGMLAAIEVAVPGKVIETLSNPYGIATVFNLNADETK
NIVPMARALIGNRSAVVVKTPSGDVKARAIPAGNLELQAQGRTVRVDVAAGAEAIMKAVD
GFGKLDNVTGEAGTNIGGMLEHVRQTMAELTNKPSSEIFIQDLLAVDTSVPVSVTGGLAG
EFSLEQAVGIASMVKSDRLQMAMIAREIEQKLNIDVQIGGAEAEAAILGALTTPGTTRPL
AILDLGAGSTDASIINPKGEIIATHLAGAGDMVTMIIARELGLEDRYLAEEIKKYPLAKV
ESLFHLRHEDGSVQFFPTPLPPAVFARVCVVKP-DELVPL-PGDLALEKVRAIRRSAKER
VFVTNALRALRQVSPTGNIRDIPFVVLVGGSSLDFEVPQLVTDALAHYRLVAGRGNIRGS
EGPRNAVATGLILS-----WHKE----FAYGQ-
>gi++|161502793|ref|YP_001569905.1| hypothetical protein SARI_00844 [Salmonella
enterica subsp. arizonae serovar 62:z4,z23:--]
----MQYIAGIDIGNSSTEVALAALSDSGELIIKSSALAETTGIKGTLRNVFGIQEALAL
AAKNAGINVSDISLIRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGVGLGIGVT
ITPQELLTC-PADKP------YILVVSSAFDFADVATMINAAVRAGYQLTGAILQQDDGV
LVSNRLEKPLPVVDEVRYIDRIPLGMLAAIEVAVPGKVIETLSNPYGIATVFNLNSEETK
NIVPMARALIGNRSAVVVKTPSGDVKARAIPAGNIELLSQGRTLRIDVAAGADAIMKAVS
NCPQLDNVTGEAGTNIGGMLEHVRQTMAELTNKPSAEIFIQDLLAVDTSVPVSVTGGLAG
EFSLEQAVGIASMVKSDRLQMAMIAREIEQKLSIDVQVGGAEAEAAILGALTTPGTTRPL
AILDLGAGSTDASIINPKGEIIATHLAGAGDMVTMIIARELGLNDRYLAEEIKKYPLAKV
ESLFHLRHEDGSVQFFPAPLPPEVFARVCVVKP-DELVPL-PGDIALEKVRAIRRSAKER
VFVTNALRALRQVSPTGNIRDIPFVVLVGGSALDFEVPQLVTDALAHYRLVAGRGNIRGT
EGPRNAVATGLILS-----WHKA----FAHGK-
>gi++|157156561|ref|YP_001463345.1| propanediol utilization diol dehydratase
reactivation protein [Escherichia coli E24377A]
----MRYIAGIDIGNSSTEVALATLSATGELSFVSSALAETTGIKGTLRNVHGIQEALAQ
ATKKVGINVSDISLIRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGVGLGVGLT
ITPQELLTR-PADTP------YILVVSSAFDFADIATMINASVRAGYQLTGVILQRDDGV
LVNNRLEIPLPIVDEVLYIDRIPLGMLAAIEVAVPGKVIETLSNPYGIATVFALNAEETK
NIVPVARALIGNRSAVVVKTPSGDVKARSIPAGNIELLSAGRTTRVDVAAGADAIMKAVG
ECPKLENVTGEPGTNIGGMLEHVRQTMAELTNKPSNEIFIQDLLAIDTSVPVSVTGGLAG
EFSLEQAVGIASMVKSDRLQMAMIASEIKQKLHVDVQVGGAEAEAAIQGALTTPGTTRPL
AILDLGAGSTDASIINQSGEIVATHLAGAGDMVTMIIARELGLNDRYLAEEIKKYPLAKV
ESLFHLRHEDGSVQFFPTPLSPHVFARVCVVKP-DELVPI-PGDLTQEKVRAVRRSAKER
VFVTNALRALRQVSPGGNIRDIPFVVLVGGSSLDFEVPQLVTDALAHYRLVAGRGNIRGS
EGPRNAVATGLLIS-----WHRE----LAHGK-
>gi++|74312535|ref|YP_310954.1| putative propanediol utilization protein: diol
dehydratase reactivation [Shigella sonnei Ss046]
----MRYIAGIDIGNSSTEVALATLSATGELSFVSSALEETTGIKGTLRNVHGIQEALAQ
ATKKVGINVSDISLIRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGVGLGVGFT
ITPQELLTR-PADTP------YILVVSSAFDFADIATMINASVRAGYQLTGVILQRDDGV
LVNNRLEIPLPIVDEVLYIDRIPLGMLAAIEVAVPGKVIETLSNPYGIATVFALNAEETK
NIVPVARALIGNRSAVVVKTPSGDVKARSIPAGNIELLSAGRTTRVDVAAGADAIMKAVG
ECPKLENVTGEPGTNIGGMLEHVRQTMAELTNKPSNEIFIQDLLAIDTSVPVSVTGGLAG
EFSLEQAVGIASMVKSDRLQMAMIASEIKQKLHVDVQVGGAEAEAAIQGALTTPGTTRPL
AILDLGAGSTDASIINQSGEIVATHLAGAGDMVTMIIARELGLNDRYLAEEIKKYPLAKV
ESLFHLRHEDGSVQFFPTPLSPHVFARVCVVKP-DELVPI-PGDLTLEKVRAVRRSAKER
VFVTNALRALRQVSPAGNIRDIPFVVLVGGSSLDFEVPQLVTDALAHYRLVAGRGNIRGS
EGPRNAVATGLLIA-----WHKE----SIHGK-
>gi++|215487216|ref|YP_002329647.1| propanediol dehydratase reactivation protein
PduG [Escherichia coli O127:H6 str. E2348/69]
----MRYIAGIDIGNSSTEVALATLSATGELSLVSSALAETTGIKGTLRNVHGIQEALAQ
ATKKVGINVSDISLIRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGVGLGVGLT
ITPQELLTC-PADTP------YILVVSSAFDFADIATMINASVRAGYQLTGVILQRDDGV
LVNNRLEIPLPIVDEVLYIDRIPLGMLAAIEVAVPGKVIETLSNPYGIATVFALNAEETK
NIVPVARALIGNRSAVVVKTPSGDVKARSIPAGNIELLSAGRTTRVDVAAGADAIMKAVG
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ECPKLENVTGEPGSNIGGMLEHVRQTMAELTNKPSNEIFIQDLLAIDTSVPVNVTGGLAG
EFSLEQAVGIASMVKSDRLQMAMIASEIKQKLHVDVQVGGAEAEAAIQGALTTPGTTRPL
AILDLGAGSTDASIINQKGEIVATHLAGAGDMVTMIIARELGLNDRYLAEEIKKYPLAKV
ESLFHLRHEDGSVQFFPTPLSPHVFARVCVVKP-DELVPI-PGDLTLEKVRAVRRSAKER
VFVTNALRALRQVSPAGNIRDIPFVVLVGGSSLDFEVPQLVTDALAHYRLVAGRGNIRGS
EGPRNAVATGLLIA-----WHKE----SIHGK-
>gi++|218705536|ref|YP_002413055.1| putative Propanediol utilization: diol
dehydratase reactivation PduG [Escherichia coli UMN026]
----MRYIAGIDIGNSSTEIALATLSATGELSFVSSALAETTGIKGTLRNVHGIQEALAQ
ATKKVGINVSDISLIRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGVGLGVGLT
ITPQELLTR-PADTP------YILVVSSAFDFADIATMINASVRAGYQLTGVILQGDDGV
LVSNRLEIAVPIVDEVLYIDRIPLGMLAAIEVAVPGKVIETLSNPYGIATVFALNAEETK
NIVPVARALIGNRSAVVVKTPSGDVKARSIPAGNIELLSAGRTTRVDVAAGADAIMKVVG
ECPKLENVTGEPGTNIGGMLEHVRQTMAELTNKPSNEIFIQDLLAIDTSVPVSVTGGLAG
EFSLEQAVGIASMVKSDRLQMAMIASEIKQKLHVDVQVGGAEAEAAIQGALTTPGTTRPL
AILDLGAGSTDASIINQKGEIVATHLAGAGDMVTMIIARELGLNDRYLAEEIKKYPLAKV
ESLFHLRHEDGSVQFFPTPLSPHVFARVCVVKP-DELVPI-PGDLTLEKVRAVRRSAKER
VFVTNALRALRQVSPAGNIRDIPFVVLVGGSSLDFEVPQLVTDALAHYRLVAGRGNIRGS
EGPRNAVATGLLIA-----LHKE----SIHGK-
>gi++|218549346|ref|YP_002383137.1| putative Propanediol utilization: diol
dehydratase reactivation PduG [Escherichia fergusonii ATCC 35469]
----MRYIAGIDIGNSSTEVALAKVSEEGHLTILTSSLAETTGIKGTLRNVFGIEEALSR
AATQAGISVSDISLIRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGVGLGVGVT
ITPEHLLTC-LADVP------YILVVSSAFDFADVAAMVNACVRAGYQITGIILQRDDGV
LVSNRLDHPVPVVDEVLYIDRIPQGMLAAIEVAIPGKVIETLSNPYGIATVFHLDAQETK
NIVPMARALIGNRSAVVVKTPSGDVKARSIPAGNIELLSQGLTRRVDVAAGAETIMKAVG
DCPRLDNVIGEAGTNIGGMLEHVRQTMAELTNKPTGEIFIQDLLAVDTAVPVTVSGGLAG
EFSLEQAVGIASMVKSDRLQMAMIAHEIKQKINAEVQVGGAEAEAAILGALTTPGTTRPL
AILDLGAGSTDASIINPQGEIIATHLAGAGDMVTMIIARELGLDDRYLAEEIKKYPLAKV
ESLFHLRHEDGSVQFFPQPLPPAVFARVCVVKP-DELVPL-PGDLALEKVRAIRRSAKER
VFVTNALRALRQVSPTGNIRDIPFVVLVGGSSLDFEIPQLVTDALAHYRLVAGRGNIRGT
EGPRNAVATGLLLS-----WQKE----LADGR-
>gi++|152971727|ref|YP_001336836.1| propanediol utilization: diol dehydratase
reactivation [Klebsiella pneumoniae subsp. pneumoniae MGH 78578]
----MRYIAGIDIGNSSTEVALATVDDAGVLNIRHSALAETTGIKGTLRNVFGIQEALTQ
AAKAAGIQLSDISLIRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGVGLGVGIT
ITPEALLSC-SADTP------YILVVSSAFDFADVAAMVNAATAAGYQITGIILQQDDGV
LVNNRLQQPLPVIDEVQHIDRIPLGMLAAVEVALPGKIIETLSNPYGIATVFDLNAEETK
NIVPMARALIGNRSAVVVKTPSGDVKARAIPAGNLLLIAQGRSVQVDVAAGAEAIMKAVD
GCGKLDNVAGEAGTNIGGMLEHVRQTMAELTNKPAQEIRIQDLLAVDTAVPVSVTGGLAG
EFSLEQAVGIASMVKSDRLQMALIAREIEHKLQIAVQVGGAEAEAAILGALTTPGTTRPL
AILDLGAGSTDASIINAQGEISATHLAGAGDMVTMIIARELGLEDRYLAEEIKKYPLAKV
ESLFHLRHEDGSVQFFPSALPPAVFARVCVVKP-DELVPL-PGDLPLEKVRAIRRSAKSR
VFVTNALRALRQVSPTGNIRDIPFVVLVGGSSLDFEIPQLVTDALAHYRLVAGRGNIRGC
EGPRNAVASGLLLS-----WQKG----GTHGE-
>gi++|206579698|ref|YP_002236779.1| propanediol utilization diol dehydratase
reactivation protein [Klebsiella pneumoniae 342]
----MRYIAGIDIGNSSTEVALATVDDAGVLNIRHSALAETTGIKGTLRNVFGIQEALTQ
AAKAAGIQVSDISLIRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGVGLGVGIT
ITPEALLSC-AADAP------YILVVSSAFDFADVAAMVNAATAAGYQISGIILQQDDGV
LVNNRLQQPLPVIDEVQHIDRIPLGMLAAVEVALPGKIIETLSNPYGIATVFNLNAEETK
NIVPMARALIGNRSAVVVKTPSGDVKARTIPAGNLLLIAQGRSVQVDVAAGAEAIMKAVD
GCGKLDNVAGEAGTNIGGMLEHVRQTMAELTNKPAQEIPIQDLLAVDTAVPVSVTGGLAG
EFSLEQAVGIASMVKSDRLQMALIAREIEHKLQIAVQVGGAEAEAAILGALTTPGTTRPL
AILDLGAGSTDASIINAQGEISATHLAGAGDMVTMIIARELGLEDRYLAEEIKKYPLAKV
ESLFHLRHEDGSVQFFPSALPPAVFARVCVVKP-DELVPL-PGDLPLEKVRAIRRSAKSR
VFVTNALRALRQVSPTGNIRDIPFVVLVVGSSLDFEIPQLVTDALAHYRLVAGRGNIRGS
EGPRNAVASGLLLA-----WQKG----GTHGE-
>gi++|123442949|ref|YP_001006924.1| putative propanediol utilization protein: diol
dehydratase reactivation [Yersinia enterocolitica subsp. enterocolitica 8081]
----MDYIVGVDIGNSSTEVALAQCMTDGQLHFVTSTLTETTGIKGTQRNIFGITKALNM
LVEKAGIALSDINLIRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGLGLGVGLT
ITIDELVTR-DPNQP------YILVVPSAVDFADVAAVVNAANGAGYRITAIILQRDDGV
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LVNNRLTHPLPIVDEVLHIDRIPMGMLAAVEVAMPGQVIETLSNPYGIATVFGLSAEETK
NIVPVARALIGTRSAVVVKTPEGDVKARAIPAGHLELFANGRTVRVDVATGAETIMTAVN
SFRHLDNVSGEAGTNIGGMLEHVRQTMAELTNKPTNEIFIQDLLAVDTAVPVNVIGGLAG
EFSLEQAVGIASMVKSDRLQMAHIASEIEKTLNIDVQVGGAEAEAAILGALTTPGTRRPL
AILDLGAGSTDASIINAQGQIVATHLAGAGDMVTMIIASELDLQDRYLAEDIKKYPLAKV
ESLFHLRHEDGSVQFFPQPLPPEVFARLVVVKP-EGLVPL-PGDYALEKVRNIRRSAKER
VFVTNALRALRQVSPTGNIRDIPFVVLVGGSSLDFEIPQLVTDALSHYKLVAGRGNIRAS
EGPRNAVATGLILS-----WQRE----NHV---
>gi++|116872530|ref|YP_849311.1| propanediol utilization diol dehydratase
reactivation protein [Listeria welshimeri serovar 6b str. SLCC5334]
----MKYIAGIDIGNSTTEVALAIKDATNKAEFVASAITDTTGIKGTKQNLHGIFKALKL
ALEKVNATTADLMEIRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGLGMGSGIT
VFLDEVTTK-PKDTD------YIVIIPKTVDFEDAAKLINEYTQSGYQITAAILQADDGV
LVHNRLNNKIPIVDEVGFIDKVPVDMLAVVEVAAPGKVIETISNPYGIATVFHLSSDETK
NIIPVARALIGNRSAVVIKTPEGDVKARTIPAGHIELQSGSRTQRVNVAEGSEKIMQAIT
SLPKLDNASGEPGTNIGGMLEKVRQTMAGLTDKLPADIFIQDLLAVDTFVPVDVQGGLAG
EFSMEQAVGIASMVKSDHLQMAAIASEIEQELNVTVKIGGAEAEAAILGALTTPGTNTPL
AILDLGAGSTDASIINGKGEIIATHLAGAGDMVTMIVQSEIGLEDRYLAEDIKKYPLAKV
ESIFHIRHEDGTVQFFDTPLSPSVFAKVVIVKP-DGFVPI-PGDVSIEKIKLIRRSAKER
VFVTNTIRALKYVSPTGNIRDIPFVVIVGGSALDFEIPQLITDALSHYSLVAGRGNIRGE
EGPRNAVATGLILS-----GGAE----A-----
>gi++|16800189|ref|NP_470457.1| hypothetical protein lin1120 [Listeria innocua
Clip11262]
----MKYIAGIDIGNSTTEVALAILDSVNNAEFVASAITDTTGIKGTKQNLHGIFKALKL
ALEKVNATTADLAEIRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGLGMGSGIT
VHLDEVASK-SKDTD------YIVIIPKTVDFEDAAQQINDYTELGYQITAAILQADDGV
LVHNRLNHKIPIVDEVGFIDKVPVDMLAAVEVAAPGKVIETISNPYGIATVFRLSSDETK
NIIPVARALIGNRSAVVIKTPEGDVKARTIPAGHIELQSGTRTQRVNVAEGSEKIMQAIM
SLPKLDNASGEPGTNIGGMLEKVRQTMAGLTDKLPADIFIQDLLAVDTFVPVDVQGGLAG
EFSMEQAVGIASMVKSDHLQMAAIASEIEQELNVTVKIGGAEAEAAILGALTTPGTNTPL
AILDLGAGSTDASIINGKGEIIATHLAGAGDMVTMIIQSEIGLEDRYLAEDIKKYPLAKV
ESIFHIRHEDGTVQFFDTPLSPSVFAKVVIVKP-DGFVPI-PGDVSIEKIKLIRRSAKER
VFVTNTIRALKYVSPTGNIRDIPFVVIVGGSALDFEIPQLITDALSHYSLVAGRGNIRGQ
EGPRNAVATGLILS-----GGAN----V-----
>gi++|16803196|ref|NP_464681.1| hypothetical protein lmo1156 [Listeria monocytogenes
EGD-e]
----MKYIAGIDIGNSTTEVALAMANSSKEAAFVASAITDTTGIKGTKQNLHGIFKALRL
ALEKVNATTEDLAEIRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGLGMGSGVT
VLLDDVTSK-SKDAD------YIVIIPKTVDFEDAAKQINTYVENGYQITAAILQADDGV
LVHNRLNHKIPIVDEVGFIDKVPVDMLAAVEVAAPGKVIETISNPYGIATVFHLNSDETK
NIIPVARALIGNRSAVVIKTPEGDVKARTIPAGHIELQSGSRTQRVNVAEGSEKIMQAIM
SLPKLDNASGEPGTNIGGMLEKVRQTMAGLTDKLPADIFIQDLLAVDTFVPVDVQGGLAG
EFSMEQAVGIASMVKSDHLQMAAIASEIEQELQVSVKIGGAEAEAAILGALTTPGTNTPL
AILDLGAGSTDASIINGKGEIIATHLAGAGDMVTMIIQSEIGLEDRYLAEDIKKYPLAKV
ESIFHIRHEDGTVQFFDTPLSPTVFAKVVIVKP-DGFVPI-PGDVSIEKIKLIRRSAKER
VFVTNTIRALKYVSPTGNIRDIPFVVIVGGSALDFEIPQLITDALSHYSLVAGRGNIRGK
EGPRNAVATGLILA-----GGAK----A-----
>gi++|46907374|ref|YP_013763.1| propanediol utilization: diol dehydratase
reactivation [Listeria monocytogenes str. 4b F2365]
----MKYIAGIDIGNSTTEVALAMANYSKEVAFVASAITDTTGIKGTKQNLHGIFKALRI
ALEKVNATTENLAEIRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGLGMGSGVT
VLLDDVTSK-SKDED------YIVIIPKTVDFEDAAKQINTYVENGYQITAAILQADDGV
LVHNRLNHKIPIVDEVGFIDKVPVDMLAAVEVAAPGKVIETISNPYGIATVFHLNSDETK
NIIPVARALIGNRSAVVIKTPEGDVKARTIPAGHIELQSGSRTQRVNVAEGSEKIMQAIM
SLPKLDNASGEPGTNIGGMLEKVRQTMAGLTDKLPADIFIQDLLAVDTFVPVDVQGGLAG
EFSMEQAVGIASMVKSDHLQMAAIASEIEQELQVSVKIGGAEAEAAILGALTTPGTNTPL
AILDLGAGSTDASIINGKGEIIATHLAGAGDMVTMIIQSEIGLEDRYLAEDIKKYPLAKV
ESIFHIRHEDGTVQFFDTPLSPTVFAKVVIVKP-DGFVPI-PGDVSIEKIKLIRRSAKER
VFVTNTIRALKYVSPTGNIRDIPFVVIVGGSALDFEIPQLITDALSHYSLVAGRGNIRGK
EGPRNAVATGLILA-----GGAK----A-----
>gi++|116334193|ref|YP_795720.1| propanediol utilization ATPase [Lactobacillus
brevis ATCC 367]
----MQKVIGVDIGNSSTEVALADISDQGAVDFINSDIAETTGIKGTKQNLIGIKKAITQ
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VLNKSHLALSDIDLIRINEATPVIGDVAMETITETVITESTMIGHNPNTPGGVGIGSGYT
VSLLQLLQETDKTRP------YIVLVPAEVDFEDAAKLINLYQQSGYQINAAILQNDDGV
LIDNRLEHKIPIVDEVARIDKVPMGMMAGVEVAGKGQVISQLSNPYGIATLFDLTADETK
NIVPVSRALIGNRSAVVIKTPKGDVKARVIPAGSIQIEGDRDSDKVNVAAGAEAIMKKVN
QFDRIQDITGEAGTNVGGMLEKVRQTMADLTNKQNRDIAIQDLLAVNTAVPVKVQGGLAG
EFSTEQAVGIAAMVKSDHLQMQQIADLIQDELHISVEIGGAEAEAAILGALTTPGTTKPI
AILDLGAGSTDASIINQQDDIVAIHLAGAGDMVTMIINSELGLDDVYLAEDIKKYPLARV
ENLFQIRHEDGTVQFFEDPLPADIFARTVVIKP-DGYVPL-PGNMNIEKVKQIRQTAKKR
VFVENARRALQHVSPTGNIRDIPFVVIVGGSALDFEIPQLVTDELSHYNLVAGRGNIRAV
EGPRNAVATGLILS-----YARERRDAYGQHNG
>gi++|125717400|ref|YP_001034533.1| propanediol utilization:dioldehydratase
reactivation, putative [Streptococcus sanguinis SK36]
----MKRIIGVDIGNSSTESALAEVQDDGSIHFLASAIADTTGIKGTKENVHGIYQSLRK
LMEQTSFELGQVDLIRINEATPVIGDVAMETITETVITESTMIGHNPRTPGGLGLGIGLT
VDILDLVHH-PIDEK------YIVVVPKVIDFDLVAQLINAYLAKGYQITAAILQADDGV
LVNNRISQKIPIVDEILFIDKVPLGMQAAVEVVEQGKVISQLSNPYGIATVFGLSAEETK
SIVPIARALIGNRSAVVIKTPAGDVQARTIPAGSIQIIGKEHTLKVDISKGADEIMEKIV
YAGEISNVVGEAGTNVGGMLEKVRQTMADLTEKEPSDIYIRDLLAVNTFAPISVRGGVAG
EFSMEQAVGIASMVNSDKLQMSIIAQEVERELGITVEIGGAEAEAAILGALTTPGTDRPL
AILDLGAGSTDASIIDSRGQILAVHLAGAGDMVTMLINSELGLENHHLAEDIKRYPLAKV
ESLFHIRHEDGTVQFFDKPLSGDLFARVVIVKENDEFVPIDDGDYSIEKIKLVRQSAKER
VFVTNAVRALKRVSPTQNIRDIPFVVIVGGSALDFEIPQLVTEALSQHAIVAGRGNVRGL
VGPRNAVATGLILTYVREKWGAD----YGISLY
>gi++|148544950|ref|YP_001272320.1| diol/glycerol dehydratase reactivating factor,
large subunit [Lactobacillus reuteri DSM 20016]
--MATEKVIGVDIGNSSTEVALADVSDSGQVHFINSGIAPTTGIKGTKQNLVGIRDSITQ
VLNKSNLTIDDIDLIRINEATPVIGDVAMETITETVVTESTMIGHNPNTPGGIGTGAGIT
VRLLDLLKKTDKSKN------YIVVVPKDIDFEDVAKLINAYVASGYKITAAILRNDDGV
LVDNRLNHKIPIVDEVAMIDKVPLNMLAAVEVAGPGQVISQLSNPYGIATLFGLTPEETK
NIVPVSRALIGNRSAVVIKTPAGDVKARVIPAGKIIINGDTGKEEVGVSEGADAIMKKVS
SFRHINNITGESGTNVGGMLENVRQTMADLTGKKNDEIAIQDLLAVDTQVPVEVRGGLAG
EFSNESAVGIAAMVKSDHLQMEVIAKLIEKEFNTKVEIGGAEVESAIRGALTTPGTDKPI
AILDLGAGSTDASIINKENNTVAIHLAGAGDMVTMIINSELGLNDIHLAEDIKRYPLAKV
ENLFQIRHEDGSVQFFKDPLPSSLFAKVVVIKP-DGYEPV-TGNPSIEKIKLVRQSAKKR
VFVTNALRALKYVSPTGNIRDIPFVVIVGGSALDFEIPQLVTDELAHFNLVAGRGNVRGV
EGPRNAVATGLILR-----YGEERRKRYEQR--
>gi++|167040579|ref|YP_001663564.1| hypothetical protein Teth514_1950
[Thermoanaerobacter sp. X514]
-----MIIAGVDIGNSTTEVALAKV-NGDEIRFLASGISNTTGIKGTPQNVEGVRHALED
AVRKANLTIKDIDLLRINEATPVISDIAMEAITETIITESTMIGHNPTTPGGVGLGIGIT
IPIFELEKC-KHGEE------VIVVIPKNVDYEDAAKIINNAFSKGVEVKGAIAQKDDGV
LIATRLQRRIPIVDEVKQIEKVPIGMLACVEVAEPGYTIKTLSNPYGIASVFNLTAEETK
NIVPVARALIGNRSAVVIRTPKGEVQERKIPAGTLIIKGNNRTFTVDIEEGAEAIMSAVE
STWPLVDAEGTPGTNVGGLIARIKETMADVTGQDSSNIQIQDVLAVDTLVRQKVKGGIAE
EFSSENAVALAAMVKSSKLPMEKVAQKIEQEIGIAVEIAGIEANMAIIGALTTPGTELPL
AILDLGGGSTDAALMTKNGEVKSVHMAGAGEMVNMLIKTELGIEDKYLVEDIKKYPVCRV
ESLFSIRLEDGTVRFFKEPLDPRTFARVCLLRE-DGLLPL-PPELNMEKVINVRRNAKRK
VFVTNALRALSKVAPAGNIRLIDFVVMVGGSALDFEIPEMISDTLAGYGIVAGRGNIRNV
EGPRNAVATGLVLS----RCKRK----------
>gi++|218782817|ref|YP_002434135.1| Diol/glycerol dehydratase reactivating factor
large subunit [Desulfatibacillum alkenivorans AK-01]
-----MLIAGVDIGNNSTEVAVARI--GAEVQFLSSALVRTIGLKGTLRNAMCVIDAVDK
AMAAVSMTRNDLDLILLNKATPVIGDVAMETITETVITESAMIGHNPDTPGGLGLGQGVT
VDIRDLTQT-APGAP------CIVVIDGDVDFTQAAEMINAAAAKGVKITGAIVKKDDGV
LIYNRLTSPIPIVDEVQHIDKVPLGMPAALEVARVGRSIEKLSNPYDIATLFELSPEETR
QITPIARALTGNRSGVVIKTPKGDVQERRIPAGTITLVGETAKETVDVELGADAIMEKLA
RVAPLKEIQSQPGTNAHGMFERVRTVMAELTDQPVSLIKIQDVLAVNTLQPQHVLGGLAG
EFTRGTAVGLAAMVMTQNIPMQRLAAKLKEETGVEVEIGGVEAEMAITGALTTPGAEAPL
AILDLGGGSTDASIIHRDGTVKSIHMAGAGDMVTMLINTELGLDDPDLAEDIKRYPLAKV
ETLFHMRHETGAVEFFDAHLDPSLFGRVAILGE-NGPIPI-MHDLNLNQIVNVRRKAKEK
VFVRNALRALEQVAPGGNIRLIDFVALVGGSALDFEIPEMIADALAEYGPVLGKGNIRGC
EGPRNAVATGLCLS-----RKGC----------
>gi|187934454|ref|YP_001886291.1| glycerol dehydratase reactivation factor large
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subunit [Clostridium botulinum B str. Eklund 17B]
----MKIIAGVDIGNATTEVALSKV-ENGKIKFLSSGIVPTTGIKGTEENIDGVFSSLKG
ALNKVNLELKDLNLVRINEAAPVIGDVAMETITETIITESTMIGHNPSTPGGVGLGIGKT
IYIEELDNL-EVDKI--EENQFIPLILSRVNFLEAAARINAATQRGINITSAVVQRDDGV
LINNRLEKKIPIVDEVMLLEKVPLGMKAAVEVAAQGGVVETLSNPYGIATVFNLTSEETK
MIVPISRALIGNRSAVVIKTPKGDVQEKSIPAGKIHINGLKRKEVVDVEHGAEKIMDAVN
LCVPIQDVKGEAGTNAGGMLERVRQVMANLTKQKISDITIQDLLAVDTFIPQMVKGGLAA
EFSMENAVGIAAMVKADKLQMQMIADKLQEQLNVPVEVGGVEADMAIRGALTTPGSSTPL
AILDMGAGSTDASIINKQGEICSIHLAGAGNMVTMLIKSELGLEDFSLAEDIKKHPLAKV
ESLFHIRHEDGTVEFFQKPLDSSVFAKVVILKD-GMLVPI-DGQNSLEKIRNIRKCAKEK
VFVTNCLRALKIVSPTGNIRDIEFVVLVGGSSLDFEVPQVVTNALSQYGVVAGRGNIRGS
EGPRNAVATGLVLA-----FDGN----GESK--
>gi|188589918|ref|YP_001921320.1| glycerol dehydratase reactivation factor large
subunit [Clostridium botulinum E3 str. Alaska E43]
----MKIIAGVDIGNATTEVALSKV-ENGNVEFLSSGIVPTTGIKGTEENIDGVFSSLKG
ALKKVNLELKDLNLVRINEAAPVIGDVAMETITETIITESTMIGHNPSTPGGVGTGIGKT
IYIEDLDNL-EIDKI--EENQFIPLILSRVNFLEAAARINAATQRGINITSAIVQRDDGV
LINNRLEKKIPIVDEVTLLEKVPVGMKAAVEVAAQGDVVETLSNPYGIATVFNLTSEETK
MIVPISRALIGNRSAVVIKTPKGDVQEKSIPAGKIHINGLKRKEVVDVEHGAEKIMDAVN
LCVPIQDVKGEAGTNAGGMLERVRQVMANLTKQKISDITIQDLLAVDTFIPQMVKGGLAA
EFSMENAVGIAAMVKADKLQMQMIADKLQEQLNVPVEVGGVEADMAIRGALTTPGSSTPL
AILDMGAGSTDASIINRQGEICSIHLAGAGNMVTMLIKSELGLEDFNLAEDIKKHPLAKV
ESLFHIRHEDGTVEFFEKPLESAVFAKVVILKD-GMLVPI-DGQTSLEKIRNIRKCAKEK
VFVTNCLRALKIVSPTGNIRDIEFVVLVGGSSLDFEVPQVVTNALSQYGVVAGRGNIRGT
EGPRNAVATGLVLA-----FNGN----GEIK--
>gi|18309914|ref|NP_561848.1| glycerol dehydratase reactivation factor, large
subunit [Clostridium perfringens str. 13]
----MKIIAGIDIGNSSTETALGKV-YENNVEFLSSGIIPTTGIKGTEENISGVIASLNQ
ALKKANLTLEDLDLVRINEAAPVIGDVAMETITETIITESTMIGHNPSTPGGLGVGIGKT
IRLETLETL-NIDEIKEEDNAFIPLVLGNISFLEAVFIINQATRRGINITAAIVQKDDGV
LINNRLDKKIPIVDEVSLLEKVPVDMKAAVEVAPQGSVIRQLSNPYGIATVFDLSPEETK
MIVPVSRALIGNRSAVVIKTPQGDVKEKKIPAGKINITGMRRKESVDVEEGADKIMEAVS
LCSPIEDLRGDAGSNVGGMLEKVRQVMADLTNQSISDIKIQDLLAVDTFIPQKVKGGLAK
EFSMENAVGIAAMVKAHKLQMQIIANKLEEKLGVPVEVGGVEADMAIRGALTTPGTNTPL
AILDMGAGSTDASIINKEGKITSIHLAGAGNMVTMLIKSELGIEDFGLAEDIKKYPLAKV
ESLFHIRHEDGTVEFFEKPLDSSVFAKIVIIKE-GMLIPV-DGQNSLEKIKNVRKTAKER
VFVINCLRALKSVSPTGNIRDIEFVVLVGGSSLDFEVPELVTDALSHYGVVAGRGNIRGC
EGPRNAVATGLVLA-----FDRK----GVKEND
>gi|110803450|ref|YP_698330.1| glycerol dehydratase reactivation factor, large
subunit [Clostridium perfringens SM101]
----MKIIAGIDIGNSSTETALGKV-YENNVEFLSSGIIPTTGIKGTEENISGVIASLNQ
ALKKANLTLEDLDLVRINEAAPVIGDVAMETITETIITESTMIGHNPSTPGGLGIGIGKT
IRLETLETL-NIDEIKEEDNAFIPLVLGNISFLEAVFRINQATRRGINITAAIVQKDDGV
LINNRLDKKIPIVDEVSLLEKVPINMKAAVEVAPQGSVIRQLSNPYGIATVFDLSPEETK
MIVPVSRALIGNRSAVVIKTPQGDVKEKKIPAGKINIKGIRRKESVDVEEGADKIMEAVS
LCSPIEDLRGDAGSNVGGMLEKVRQVMADLTNQSISDIKIQDLLAVDTFIPQKVKGGLAK
EFSMENAVGIAAMVKAHKLQMQIIANKLEEKLGVPVEVGGVEADMAIRGALTTPGTNTPL
AILDMGAGSTDASIINKEGNITSIHLAGAGNMVTMLIKSELGIEDFGLAEDIKKYPLAKV
ESLFHIRHEDGTVEFFEKPLDSSVFAKIVIIKE-GMLIPV-DGQNSLEKIKNVRKTAKER
VFVINCLRALKSVSPTGNIRDIEFVVLVGGSSLDFEVPELVTDALSHYGVVAGRGNIRGC
EGPRNAVATGLVLA-----FDRK----GVKEND
>gi|110798899|ref|YP_695622.1| glycerol dehydratase reactivation factor, large
subunit [Clostridium perfringens ATCC 13124]
----MKIIAGIDIGNSSTETALGKV-YENNVEFLSSGIIPTTGIKGTEENISGVIASLNQ
ALKKANLTLEDLDLVRINEAAPVIGDVAMETITETIITESTMIGHNPSTPGGLGVGIGKT
IRLETLETL-NINEIKEEDNAFIPLVLGNISFLEAVFRINQATRRGINITAAIVQKDDGV
LINNRLDKKIPIVDEVSLLEKVPVDMKAAVEVAPQGSVIRQLSNPYGIATVFDLSPEETK
MIVPVSRALIGNRSAVVIKTPQGDVKEKKIPAGKINITGMRRKESVDVEEGADKIMEAVS
LCSPIEDLRGDAGSNVGGMLEKVRQVMADLTNQSISDIKIQDLLAVDTFIPQKVKGGLAK
EFSMENAVGIAAMVKAHKLQMQIIANKLEEKLGVPVEVGGVEADMAIRGALTTPGTNTPL
AILDMGAGSTDASIINKEGKITSIHLAGAGNMVTMLIKSELGIEDFGLAEDIKKYPLAKV
ESLFHIRHEDGTVEFFEKPLDSSVFAKIVIIKE-GMLIPV-DGQNSLEKIKNVRKTAKER
VFVINCLRALKSVSPTGNIRDIEFVVLVGGSSLDFEVPELVTDALSHYGVVAGRGNIRGC
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EGPRNAVATGLVLA-----FDRK----GVKEND
>gi|152972002|ref|YP_001337148.1| glycerol dehyrdratase activator [Klebsiella
pneumoniae subsp. pneumoniae MGH 78578]
----MPLIAGIDIGNATTEVALASD-DPQARAFVASGIVATTGMKGTRDNIAGTLAALEQ
ALAKTPWSMSDVSRIYLNEAAPVIGDVAMETITETIITESTMIGHNPQTPGGVGVGVGTT
IALGRLATL-PAAQY---AEGWIVLIDDAVDFLDAVWWLNEALDRGINVVAAILKKDDGV
LVNNRLRKTLPVVDEVTLLEQVPEGVMAAVEVAAPGQVVRILSNPYGIATFFGLSPEETQ
AIVPIARALIGNRSAVVLKTPQGDVQSRVIPAGNLYISGEKRRGEADVAEGAEAIMQAMS
ACAPVRDIRGEPGTHAGGMLERVRKVMASLTGHEMSAIYIQDLLAVDTFIPRKVQGGMAG
ECAMENAVGMAAMVKADRLQMQVIARELSARLQTEVVVGGVEANMAIAGALTTPGCAAPL
AILDLGAGSTDAAIVNAEGQITAVHLAGAGNMVSLLIKTELGLEDLSLAEAIKKYPLAKV
ESLFSIRHENGAVEFFREALSPAVFAKVVYIKE-GELVPI-DNASPLEKIRLVRRQAKEK
VFVTNCLRALRQVSPGGSIRDIAFVVLVGGSSLDFEIPQLITEALSHYGVVAGQGNIRGT
EGPRNAVATGLLLA-----GQAN----------
>gi|206577418|ref|YP_002236504.1| glycerol dehydratase reactivation factor, large
subunit [Klebsiella pneumoniae 342]
----MPLIAGIDIGNATTEVALASD-DPQARAFVASGIVATTGMKGTRDNIAGTLAALEQ
ALAKTPWSMSDVSRIYLNEAAPVIGDVAMETITETIITESTMIGHNPQTPGGVGVGVGTT
IALGRLATL-PAAQY---AEGWIVLIDDAVDFLDAVWWLNEALDRGINVVAAILKKDDGV
LVNNRLRKTLPVVDEVTLLEQVPEGVMAAVEVAAPGQVVRILSNPYGIATFFGLSPEETQ
AIVPIARALIGNRSAVVLKTPQGDVQSRVIPAGNLYISGEKRRGEADVAEGAEAIMQAMS
VCAPVRDIRGEPGTHAGGMLERVRKVMASLTGHEMSAIYIQDLLAVDTFIPRKVQGGMAG
ECAMENAVGMAAMVKADRLQMQVIARELSARLQTEVVVGGVEANMAIAGALTTPGCAAPL
AILDLGAGSTDAAIVNAEGQITAVHLAGAGNMVSLLIKTELGLEDLSLAEAIKKYPLAKV
ESLFSIRHENGAVEFFREALSPAVFAKVVYIRE-GELVPI-DNASPLEKIRLVRRQAKEK
VFVTNCLRALRQVSPGGSIRDIAFVVLVGGSSLDFEIPQLITEALSHYSVVAGQGNIRGT
EGPRNAVATGLVLA-----GQAN----------
>gi|197247887|ref|YP_002145307.1| glycerol dehydratase reactivation factor large
subunit [Salmonella enterica subsp. enterica serovar Agona str. SL483]
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--------------------MQAIASELSARLNTPVEVGGVEANMAVAGALTTPGCDAPL
AILDLGAGSTDAAIINSDGVVKAVHLAGAGNIVSLLIQTELGLSDPFLAEEIKKYPLAKV
ESLFSIRHENGAVEFFREPLSPSVFAKVVYLKE-GELIPV-DNQTSLEKIRLVRRQAKEK
VFVTNCLRALRQVSPGGSIRDITFVVLVGGSSLDFEIPQMITDALAHYGVVAGQGNIRGT
EGPRNAVATGLVLA-----GEAK----K-----
>gi|108801915|ref|YP_642112.1| hypothetical protein Mmcs_4952 [Mycobacterium sp.
MCS]
MSRDSVVVAGCDVGNHTTEIVLARVAADGVVEPLTHGQAPTRGRKGSTESLEGAAALLNR
LEVEARVRVDEVVLATIRPVDTATAPLAPAVSPRAPV--RSLRRPDASTPAGAGHGVGTH
VPLADLSGP-VHPGP------VIVSVSAATDFEVAAQAIGDGVASGWKIAGVLVAQDDAV
LIRNRIPIDVPVVDEVE-LDGLRRGALVAVEVVAEGRAYRALADPIALSAALQLGHDRLL
DVAEFTREL--------ADAPAIAVTARTEPPDPPAVDDD----YVDCRIGGEIVRYAPA
AAHTVLRLE-PPGCAVE---VRLSALPAAENGIAVDDAFFTDLASIDNGA--WLRRGVA-
----DARGTVVALLAAE--PVTDAAATLSGLTGRPARTVAGEPAAAARGAQTTPGLPPGS
VVCDIGGGTVDLI-----GQGRTVTAAGAGETITTAVSRVLGIP-RALAERVKRTPALRV
EGPHVAHEEDGRRVFLDSPASADAIGRLCTRGS-AGLVPF-SHRLAAEEWRSLRLAIKQQ
TVAANIARCLATFDEPPSA-----LVLAGGGALDDELLRTVGESLRPARVVVGRADIDGV
HGPRFAVASGLVHL-----YAED--RVGSTSPA
>gi|126437896|ref|YP_001073587.1| hypothetical protein Mjls_5333 [Mycobacterium sp.
JLS]
MSRDSVVVAGCDVGNHTTEIVLARVAADGVVEPLTHGQAPTRGRKGSTESLEGAAALLNR
LEVEARVRVDEVVLATIRPVDTATAPLAPAVSPRAPV--RSLRRPDASTPAGAGHGVGTH
VPLADLSGP-VHPGP------VIVSVSAATDFEVAAQAIGDGVASGWKIAGVLVAQDDAV
LIRNRIPIDVPVVDEVE-LDGLRRGALVAVEVVAEGRAYRALADPIALSAALQLGHDRLL
DVAEFTREL--------ADAPAIAVTARTEPPDPPAVDDD----YVDCRIGGEIVRYAPA
AAHTVLRLE-PPGCAVE---VRLSALPAAENGIAVDDAFFTDLASIDNGA--WLRRGVA-
----DARGTVVALLAAE--PVTDAAATLSGLTGRPARTVAGEPAAAARGAQTTPGLPPGS
VVCDIGGGTVDLI-----GQGRTVTAAGAGETITTAVSRVLGIP-RALAERVKRTPALRV
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EGPHVAHEEDGRRVFLDSPASADAIGRLCTRGS-AGLVPF-SHRLAAEEWRSLRLAIKQE
TVAANIARCLATFDEPPSA-----LVLAGGGALDDELLRTVGESLRPARVVVGRADIDGV
HGPRFAVASGLVHL-----YAED--RVGSTSPA
>gi|118473492|ref|YP_890537.1| putative diol dehydratase reactivation protein
[Mycobacterium smegmatis str. MC2 155]
-MIPAGLIAGIDVGNHTTEIVLARV-TDGTVHPVGHGQAPTRGRKGSRESLEGAAALLHR
LEVDLQVRAEMLVLSAIRPVDTETAPLAPATVPHAPV--RSLRRPDASTPAGSGYAVGRH
VPLAALKHD-DRHDA------VIVSVDATTDFEDAAAAITDAVGKGANVVGVLAAQDDAV
LIRNRIPIDVPVVDEVD-LDGLAPDVLVAVEVVAEGRAYRALADPIAVCAALQLGHENLR
DIAEFTREL--------ADSPAIALTPRTRPPQPPAPDDD----YVEFARDGEQVRYPPA
QAHTILRRE-PPGSVVR---IRLRSVPTADHEMAVDDAFFTDLAALDNGT--WLRRGVA-
----DASGTVVALLAAD--HVADAAATLAELTGRPARTLASEPEAAARGARTTPGLPPDS
VVCDIGGGTIDLV-----GAERTVTAAGAGETITVAVAKMLGIP-RALAERVKRTPAIRV
EGPHVAHEEDGRRLFLDAPAPAEAIGRLCTRGT-AGLVPF-SSRLAAEEWRSLRLAIKQE
TVAANIARCMKAFEKPPTA-----LVLAGGGALDDELLRTVGESLRTAGVVVGRANIDGV
HGPRFAVASGLVHL-----YAESAGERGAQEVS
>gi|161615503|ref|YP_001589468.1| hypothetical protein SPAB_03274 [Salmonella
enterica subsp. enterica serovar Paratyphi B str. SPB7]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------MASLTSHDMNAVHIQDLLAVDTFIPRAVQGGIAG
ECSMENAVGIAAMVKSDRLQMQAIASELSARLNTPVEVGGVEANMAVAGALTTHGCAVPL
AILDLGAGSTDAAIINNDGAVRRCRRAG--------------------------------
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%%  PduH [targeting tail not implicated]

>gi++|16765374|ref|NP_460989.1| propanediol dehydratase reactivation protein
[Salmonella typhimurium LT2]
------------------------------------------------------------
----------------MDSNHSAPAIVITVINDC---ASLWHEVLLGIEEEGIPFLL-QH
HPAGDIVD-SAWQAARSSPLLVGIACDRH------SLVVHYKNLPASAPLFTL--MHHQD
SQAQRNTGNNAARLVKGIPFRDLHA----------------
>gi++|16760977|ref|NP_456594.1| PduH protein [Salmonella enterica subsp. enterica
serovar Typhi str. CT18]
------------------------------------------------------------
----------------MDSNHSAPAIVITVINDC---ASLWHEVLLGIEEEGIPFLL-QH
HPAGDVVD-SAWQAARSSPLLVGIACDRH------SLVVHYKNLPASAPLFTL--MHHQD
SQAQRNTGNNAARLVKGIPFRDLNS----------------
>gi++|194442961|ref|YP_002041311.1| propanediol dehydratase reactivation protein
[Salmonella enterica subsp. enterica serovar Newport str. SL254]
------------------------------------------------------------
----------------MDSNHSAPAIVITVINDC---ASLWHEVLLGIEEEGIPFLL-QH
HPAGDVVD-SAWQAARSSPLLVGIACDRH------SLVVHYKNLPVSAPLFTL--MHHQD
SQAQRNTGNNAARLVKGIPFRDLHA----------------
>gi++|161613349|ref|YP_001587314.1| hypothetical protein SPAB_01060 [Salmonella
enterica subsp. enterica serovar Paratyphi B str. SPB7]
------------------------------------------------------------
----------------MDSNHSAPAIVITVINDC---ASLWHEVLLGIEEEGIPFLL-QH
HPAGDVVD-SAWQAARSSPLLVGIACDRH------SLVVHYKNLPASAPLFTL--MHHQD
SQAQRNAGNNAARLVKGIPFRDLHV----------------
>gi++|198244009|ref|YP_002216129.1| propanediol dehydratase reactivation protein
[Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853]
------------------------------------------------------------
----------------MDSNHSAPAIVITVINDC---ASLWHEVLLGIEEEGIPFLL-QH
HPAGDVVD-SAWQAARSSPLLVGIACDRH------TLVVHYKNLPVSAPLFTL--MHHQD
SQAQRNTGNNAARLVKGIPFRDLHA----------------
```

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>gi++|62180622|ref|YP_217039.1| propanediol utilization: diol dehydratase
reactivation [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
------------------------------------------------------------
----------------MDSNHSAPAIVITVINDC---ASLWHEVLLGIEEEGIPFLL-QR
HPAGDVVD-SAWQAARSSPLLVGIACDRH------TLVVHYKNLPASAPLFTL--MHHQD
SQAQRNTGNNAARLVKGIPFRDLHA----------------
>gi++|197247978|ref|YP_002147001.1| propanediol dehydratase reactivation protein
[Salmonella enterica subsp. enterica serovar Agona str. SL483]
------------------------------------------------------------
----------------MDSNHSAPAIVITVINDC---ASLWHEVLLGIEEEGIPFLL-QH
HPAGDVVD-SAWQAARSSPLLVGIACDRH------SLVVHYKNLPASAPLFTL--MHHQD
SLAHRNTGNNAARLVKGIPFRDLHA----------------
>gi++|215487217|ref|YP_002329648.1| propanediol dehydratase reactivation protein
PduH [Escherichia coli O127:H6 str. E2348/69]
------------------------------------------------------------
----------------MESKERAPAIVVMEIGDC---ITTWDEVLLGIEEEGIPFRI-QH
IPSGEVID-SAWLAARQSPLLVGIACDQE------KLIVHYKNLPASAPLFTL--MYQQD
NHARRSIGTNAARLVKGIPFRELHS----------------
>gi++|74312536|ref|YP_310955.1| putative propanediol utilization protein: diol
dehydratase reactivation [Shigella sonnei Ss046]
------------------------------------------------------------
----------------MESKERAPAIVVMEIGDC---ITTWDEVLLGIEEEGIPFRI-QH
IPSGEVID-SAWLAARQSPLLVGIACDRE------ELIVHYKNLPASAPLFTL--TYQQD
NHTRRSIGTNAARLVKGIPFREFHS----------------
>gi++|218705537|ref|YP_002413056.1| putative diol dehydratase reactivation pduH
[Escherichia coli UMN026]
------------------------------------------------------------
----------------MESKERAPAIVVMEIGNC---ITIWDEVLLGIEEEGIPFRI-QH
IPSGEVID-SAWLAARQSPLLVGIACDQE------KLIVHYKNLPPSAPLFTL--MYQQD
NHARRSIGTNAARLVKGIPFREFHS----------------
>gi++|206579863|ref|YP_002236778.1| propanediol utilization protein PduH [Klebsiella
pneumoniae 342]
------------------------------------------------------------
----------------MESSLVTPAIVIAVTDEC---SEQWRDVLLGIEEEGIPFVL-QP
RTGGDLVH-HAWQAAQRSPLLVGIACDRE------QLIVHYKNLPASTPLFSL--RYHQD
RLARRNTGNNAARLVKGIPFRDRNA----------------
>gi++|152971728|ref|YP_001336837.1| propanediol utilization: diol dehydratase
reactivation [Klebsiella pneumoniae subsp. pneumoniae MGH 78578]
------------------------------------------------------------
----------------MESSVVAPAIVIAVTDEC---SEQWRDVLLGIEEEGIPFVL-QP
QTGGDLIH-HAWQAAQRSPLQVGIACDRE------RLIVHYKNLPASTPLFSL--MYHQN
RLARRNTGNNAARLVKGIPFRDRHA----------------
>gi++|161502792|ref|YP_001569904.1| hypothetical protein SARI_00843 [Salmonella
enterica subsp. arizonae serovar 62:z4,z23:--]
------------------------------------------------------------
----------------MESNHNLPAIVIT-TLRC--HISDWQHVLLGIEEEGIPWVV-QE
QEAGEVIY-QAWLAASRSPLLVGIACDRE------KLIVHYKNLPPSAPLFTL--TYHQN
NCAQRCTGNNAARLVKGIPFRECDSSSTGEKQYE-------
>gi++|218549347|ref|YP_002383138.1| putative Propanediol utilization: diol
dehydratase reactivation PduH (modular protein) [Escherichia fergusonii ATCC 35469]
MHYVPYARLARPAISATFLLWCWLAVLRWTSKSHNWLLTLSPITVWLPDAAIFVAPKVHA
MLSLRVCCSPGKRSWLMDVNASTPAIVIAVSKEC---LPLWQEVLLGIEEEGIPFVI-NE
SPFDDVTK-SAWQAACHSPLLVGIACNAQ------QLIVHYKNLPPSAPLFTL--TTQHP
SHARRSTGNNAARLVKGIPFREYQA----------------
>gi++|123442950|ref|YP_001006925.1| putative propanediol utilization protein: diol
dehydratase reactivation [Yersinia enterocolitica subsp. enterocolitica 8081]
------------------------------------------------------------
----------------MNFTQDAPAIVISLTSPT--PEAVWHQVLLGIEEEGIPWQW-QQ
DDDSDAIL-RAWQAATRSPLLVGLACSAD------EVIVHFRHLPPASPLFRQ--PLAQD
EDQLRRLGNNAARLVKGLPFK--------------------
>gi++|16803197|ref|NP_464682.1| hypothetical protein lmo1157 [Listeria monocytogenes
EGD-e]
------------------------------------------------------------
```

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----------------MIPVVSKPAIYFHADVDA--NPDSIKQVLFGIEEEGIPCEL-EI
MPLKDEVQ-AAFRASASSPLLVGVTLKND------HLVIHYRNLPPDKPLFSAHRFCAST
LENQRNMGMNAARLVKGVPFK--------------------
>gi++|16800190|ref|NP_470458.1| hypothetical protein lin1121 [Listeria innocua
Clip11262]
------------------------------------------------------------
----------------MIPVVNKPAIYFHADQSA--NPDCIKQVLFGIEEEGIPCEL-EI
MPLKDEVQ-AAFRASASSPLLVGITLKND------HLVIHYRNLPPDQPLFSEYRFCAAT
LEKQRNMGMNAARLVKGVPFK--------------------
>gi++|217964774|ref|YP_002350452.1| PduH protein [Listeria monocytogenes HCC23]
------------------------------------------------------------
----------------MIPVVSKPAIYFHADVDA--NPDSIKQVLFGIEEEGIPCEL-EI
MPLKDEVQ-AAFRASASSPLLVGVTLKND------HLVIHYRNLPPDKPLFSAYRFCATT
LENQRNMGMNAARLVKGVPFK--------------------
>gi++|116872531|ref|YP_849312.1| propanediol utilization diol dehydratase-
reactivating factor small chain [Listeria welshimeri serovar 6b str. SLCC5334]
------------------------------------------------------------
----------------MIPVVSKPAIYFHADTEA--NPECIKQVLFGIEEEGIPCEL-EI
MPLKEEVQ-AAFRASASSPLLVGITLKND------HLVIHYRNLPPDQPLFSEYRFCAAT
LEKQRNMGMNAARLVKGVPFK--------------------
>gi++|46907375|ref|YP_013764.1| PduH protein [Listeria monocytogenes str. 4b F2365]
------------------------------------------------------------
----------------MIPVVSKPAIYFHADVDA--NPDSIKQVLFGIEEEGIPCEL-EI
MSLKDEVQ-AAFRASASSPLLVGVTLKND------HLVIHYRNLPPDKPLFSAYRFCATT
LENQRNMGMNAARLVKGVPFK--------------------
>gi++|116334192|ref|YP_795719.1| diol dehydratase medium subunit [Lactobacillus
brevis ATCC 367]
------------------------------------------------------------
----------------MANTMDKPAIFIAVPTAASDLPATLKPLLNGIEEEAIPVQT-KV
IAEDDVTI-RAYQAALASRLSVGIGFDDQ------HVVVHYKNLHAEQPLFTV---TRDS
ADRLRRLGANAARLVKGVPFKTLD-----------------
>gi++|125717401|ref|YP_001034534.1| PduH protein, putative [Streptococcus sanguinis
SK36]
------------------------------------------------------------
---------------MELAYTRKPTIRLIATDDA--PADKVAQIGYGIEEEGIPFSLVSP
DEVSDPVS-LAHVAATQSQLLVGIACDGR------DAVLHYRNLPLEKFIYRIKDYSAIP
DHVLRLFGSNAARLVKGVPFKKSDLLEASF-----------
>gi++|184154286|ref|YP_001842627.1| propanediol dehydratase reactivation protein
PduH [Lactobacillus reuteri JCM 1112]
------------------------------------------------------------
-------MAKKEGSVMNNDDSQRPSIVVGLENGIT-IPDSVKPLFYGIEEEQIPVSV-RK
ININDTVE-RAYQSALASRLSVGIAFEGD------HFIVHYKNLKENQPLFDM---TIND
KKQLRILGANAARLVKGIPFKEMANR---------------
>gi++|148544949|ref|YP_001272319.1| hypothetical protein Lreu_1743 [Lactobacillus
reuteri DSM 20016]
------------------------------------------------------------
---------------MNNDDSQRPSIVVGLENGIT-IPDSVKPLFYGIEEEQIPVSV-RK
ININDTVE-RAYQSALASRLSVGIAFEGD------HFIVHYKNLKENQPLFDM---TIND
KKQLRILGANAARLVKGIPFKEMANR---------------
>gi++|218782816|ref|YP_002434134.1| hypothetical protein Dalk_4995
[Desulfatibacillum alkenivorans AK-01]
------------------------------------------------------------
------------MGSPLLQVAQKPAVYLVVLGEA--PDWFVQALENGLEEEGIPCER-RD
SQENDAVL-AASQAAKASRINVGLSVKAAAGGAITGVVLHHRDLPEKRPLFHL-TWEEVS
TESLNRLGRNAARLVKGNPFIMDTADTAGPCGDSGTKDKLN
>gi++|167040578|ref|YP_001663563.1| hypothetical protein Teth514_1949
[Thermoanaerobacter sp. X514]
------------------------------------------------------------
---------------MSKDEIKKPVVLIYCDTIEG-TNIYLKKICEGLEEEGVPFQIQQV
EKVEDSVEVLAQNASRNSNLGIGIGVLKN-----GDCALLQRRLPPNLPIQTL-RGEKYD
PNLYRNIGINAARLAKNLPLVFA------------------
>gi|18309915|ref|NP_561849.1| glycerol dehydratase reactivation factor, small
subunit [Clostridium perfringens str. 13]
```

```
------------------------------------------------------------
----------------MIKDYNHPSIFVYCSLGI--NEVDIEEILWGIEEEGIPFIL-KN
KDLNDAKE-LANLAADNSKLSVGIGVNSK-----GDVSLTINKLKEEEPLFFI--NLEEG
NTCLRSLGANGARLVKGMPLKNI------------------
>gi|110802064|ref|YP_698331.1| glycerol dehydratase reactivation factor, small
subunit [Clostridium perfringens SM101]
------------------------------------------------------------
----------------MIKDYNHPSIFVYCSLGI--NEVDIEEILWGIEEEGIPFIL-KN
KDLNDAKE-LANLAADNSKLSVGIGVNSK-----GDVSLTINKLKEEEPLFFI--NLKEG
NTCLRSLGANGARLVKGMPLKNI------------------
>gi|110800791|ref|YP_695623.1| glycerol dehydratase reactivation factor, small
subunit [Clostridium perfringens ATCC 13124]
------------------------------------------------------------
----------------MIKDYNHPSIFVYCSLGI--NEVDIEEILWGIEEEGIPFIL-KN
KDLNDAKE-LANLAADNSKLSVGIGVNSK-----GDVSLTINKLKEEEPLFFI--NLEKG
NTCLRSLGANGARLVKGMPLKNI------------------
>gi|118472367|ref|YP_885931.1| PduH protein [Mycobacterium smegmatis str. MC2 155]
------------------------------------------------------------
----------------------MIQVFTALTGTSGELAAVTRDVLAGIEEEGVPYAVTTV
AEDVPVAD-LARRAAMRSPLQVGVGIGAG-----GGVCVHHDMLEDPLPELSS--ADPAD
SAAARTLGHNAARIVVGLPLKPD------------------
>gi|187935085|ref|YP_001886290.1| glycerol dehydratase reactivation factor, small
subunit [Clostridium botulinum B str. Eklund 17B]
------------------------------------------------------------
-------------MVMRHFKYDMPTICLYHSSNLE-DLTKFNEILWGLEEEGIPCNISSK
EDSLSSEE-LSHMASQDSKLAVGIGIDKS-----GKITLTLNKLKKYEPLFTV--SLNDE
DKVLRALGANAGRLVKGIAFK--------------------
>gi|206578150|ref|YP_002236498.1| glycerol dehydratase reactivation factor, small
subunit [Klebsiella pneumoniae 342]
------------------------------------------------------------
------------------MSLSPPGVRLFYDPRGH-HAGAINELCWGLEEQGVPCQTITY
DGGGDAAA-LGALAARSSPLRVGIGLSAS-----GEIALTHAQLPADAPLATG--HVTDS
DDHLRTLGANAGQLLKVLPLSERN-----------------
>gi|188588782|ref|YP_001921319.1| glycerol dehydratase reactivation factor, small
subunit [Clostridium botulinum E3 str. Alaska E43]
------------------------------------------------------------
-------------MMMRHFKYDMPTICLYHCSTLK-DLTIFNEILWGLEEEGIPCKVSSK
EDSLSSEE-LSHIASQDSRLAVGIGIDKS-----GKVTLTLNKLKKYEPLFTV--SLDDG
DKVLRALGANAGRLVKGIAFK--------------------
========================================

%%  PduO [targeting tail not implicated]

>gi++|16765380|ref|NP_460995.1| propanediol utilization protein [Salmonella
typhimurium LT2]
------------------------------------------------------------
----MAIYTRT--GDAGTTSL--FTGQRVSKTHPRV--EAYGTLDELNAALSLC-AC-AA
--------------ADEN---------HR--TLLEAIQ--QQLFWF----SAELAS--DS
-EQPSPK---------QRYISSEEISALEAAI--------------------------DR
AMARVE-PLH------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--RC--EAASR-LHFAR---------------TLARRAERRLVELAT----EVNV----
---------RQVLMRYI-------NRLS-------DC-------------LY--ALARAE
DSDAHQANIIREVS-----KRYLAACQPPHSKETTPVALSFHDLHQLTRAAVERAQQLQV
PVVVSIVDAHGTETVTWRMPDALLVSSELAPKKAWTAVAMKTATHELSDVVQPGAALYGL
ESHLQGKVVTFGGGYALWRDGILIGGLGISGGSVEQDMDIAQTAIAAINVGTHQ
>gi++|56413048|ref|YP_150123.1| hypothetical protein SPA0821 [Salmonella enterica
subsp. enterica serovar Paratyphi A str. ATCC 9150]
------------------------------------------------------------
----MAIYTRT--GDAGTTSL--FTGQRVSKTHPRV--EAYGTLDELNAALSLC-AC-AA
--------------ADEN---------HR--TLLEAIQ--QQLFWF----SAELAS--DS
-EQPSPK---------QRYISSEEISALEAAI--------------------------DR
```

```
AMARVE-PLH------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--RC--EAASR-LHFAR---------------TLARRAERRLVELAT----EVNV----
---------RQVLMRYI-------NRLS-------DC-------------LY--ALARAE
DSDAHQANIIREVS-----KRYLAASQPTRSKETTPVALSFHDLHQLTRAAVERAQQLQV
PVVVSIVDAHGTETVTWRMPDALLVSSELAPKKAWTAVAMKTATHELSDVVQPGAALYGL
ESHLQGKVVTFGGGYALWRDGILIGGIGISGGSVEQDMDIAQTAIAAINVGTHQ
>gi++|16760982|ref|NP_456599.1| hypothetical protein STY2255 [Salmonella enterica
subsp. enterica serovar Typhi str. CT18]
------------------------------------------------------------
----MAIYTRT--GDAGTTSL--FTGQRVSKTHPRV--EAYGTLDELNAALSLC-AC-AA
--------------ADEN---------HR--TLLEAIQ--QQLFWF----SAELAS--DS
-EQPSPK---------QRYISSEEISALEAAI--------------------------DR
AMARVE-PLH------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--RC--EAASR-LHFAR---------------TLARRAERRLVELAT----EVNV----
---------RQVLMRYI-------NRLS-------DC-------------LY--ALARAE
DSDAHQANIIREVS-----KRYLAASQPTRSKETTPVALSFHDLHQLTRAAVERAQQLQV
PVVVSIVDAHGTETVTWRMPDALLVSSELAPKKAWTAVAMKTATHELSDVVQPGAALYGL
ESHLQGKVVTFGGGYALWRDGILIGGLGISGGSVEQDMDIAQTAIAAINVGTHQ
>gi++|198241779|ref|YP_002216135.1| PduO [Salmonella enterica subsp. enterica
serovar Dublin str. CT_02021853]
------------------------------------------------------------
----MAIYTRT--GDAGTTSL--FTGQRVSKTHPRV--EAYGTLDELNAALSLC-AC-AA
--------------ADEN---------HR--TLLEAIQ--QQLFWF----SAELAS--DS
-EQPSPK---------QRYISSEEISALEAAI--------------------------DR
AMARVE-PLH------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--RC--EAASR-LHFAR---------------TLARRAERRLVELAT----EVNV----
---------RQVLMRYI-------NRLS-------DC-------------LY--ALARAE
DSDAHQANIIREVS-----KRYLAASQPTRSKETTPVVLSFHDLHQLTRAAVERAQQLQV
PVVVSIVDAHGTETVTWRMPDALLVSSELAPKKAWTAVAMKTATHELSDVVQPGAALYGL
ESHLQGKVVTFGGGYALWRDGILIGGLGISGGSVEQDMDIAQTAIAAINVGTHQ
>gi++|194446088|ref|YP_002041317.1| PduO [Salmonella enterica subsp. enterica
serovar Newport str. SL254]
------------------------------------------------------------
----MAIYTRT--GDAGTTSL--FTGQRVSKTHPRV--EAYGTLDELNAALSLC-AC-AA
--------------ADEN---------HR--TLLEAIQ--QQLFWF----SAELAS--DS
-EQPSPK---------QRYISSEEISALEAAI--------------------------DR
AMARVE-PLH------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--RC--EAASR-LHFAR---------------TLARRAERRLVELAT----EVNV----
---------RQVLMRYI-------NRLS-------DC-------------LY--ALARAE
DSDAHQANIIREVS-----KRYLAASQPTRSKETTPVALSFHDLHQLTRAAVERAQQLQV
PVVVSIVDAHGTETVTWRMPDALLVSSELAPKKAWTAVAMKTATHELSDVVQPGAALYGL
ESHLQGKVVTFGGGYALWRGGILIGGLGISGGSVEQDMDIAQTAIAAINVGTHQ
>gi++|62180628|ref|YP_217045.1| hypothetical protein SC2058 [Salmonella enterica
subsp. enterica serovar Choleraesuis str. SC-B67]
------------------------------------------------------------
----MAIYTRT--GDAGTTSL--FTGQRVSKTHPRV--EAYGTLDELNAALSLC-AC-AA
--------------ADEN---------HR--TLLEAIQ--QQLFWF----SAELAS--DS
-EQPSPK---------QRYISSEEISALEAAI--------------------------DR
AMARVE-PLH------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--RC--EAASR-LHFAR---------------TLARRAERRLVELAT----EVNV----
---------RQVLMRYI-------NRLS-------DC-------------LY--ALARAE
DSDAHQANIIHEVS-----KRYLAASQPTRSKETTPVALSFHDLHQLTRAAVERAQQLQV
SVVVSIVDAHGTETVTWRMPDALLVSSELAPKKAWTAVAMKTATHELSDVVQPGAALYGL
```

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ESHLQGKVVTFGGGYALWRDGILIGGLGISGGSVEQDMDIAQTAIAAINVGTHQ
>gi++|206580295|ref|YP_002236772.1| propanediol utilization protein, PduO
[Klebsiella pneumoniae 342]
------------------------------------------------------------
----MAIYTRT--GDAGSTSL--FTGQRVSKTHPRV--EAYGTLDELNAVLSLC-VC-AA
--------------AEEE---------HR--VLLEALQ--QHIFWF----SAELAS--DS
-EQPSPG---------KRYISSEEIALLEQTI--------------------------DR
EMARVP-ALH------------QFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--RC--EAASR-LHLAR---------------TVARRAERRLVELAA----EVTI----
---------RQILLRYL-------NRLS-------DC-------------LY--ALARSE
DHADHQRRLVAEIA---ARYLAASGSPASDAPKAQAGALSFHELHQLTRQAIEHARQLQV
PVVVSIVDAHGTETVTWRMPDALLVSSELAPKKAWTAVAMKTATHELATTVQPGAALYGL
ESHLQGKVVTFGGGYPLWRDGQLIAGLGISGGSVEQDMAIAQAAMAAINVRTHQ
>gi++|152971734|ref|YP_001336843.1| propanediol utilization: B12 related [Klebsiella
pneumoniae subsp. pneumoniae MGH 78578]
------------------------------------------------------------
----MAIYTRT--GDAGSTSL--FTGQRVSKTHPRV--EAYGTLDELNAMLSLC-VC-AV
--------------AEEE---------QR--TLLEALQ--QHIFWF----SAELAS--DS
-EQPSPG---------KRYISSEEIALLEQTI--------------------------DR
EMARVP-ALH------------QFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--RC--EAASR-LHLAR---------------TVARRAERRLVELAA----EVTI----
---------RQILLRYL-------NRLS-------DC-------------LY--ALARSE
DHAAHQRRLVTEIA---ARYLAASGSPAPDAPKAQAGSLSFHELHQLIRQAIEHARQLQV
PVVISIVDAHGTETVTWRMPDALLVSSELAPKKAWTAVAMKTATHELATTVQPGAALYGL
ESHLQGKVVTFGGGYPLWRDGQLIAGLGISGGSVEQDMAIAQAAMAAINVRTHQ
>gi++|161502786|ref|YP_001569898.1| hypothetical protein SARI_00837 [Salmonella
enterica subsp. arizonae serovar 62:z4,z23:--]
------------------------------------------------------------
----MAIYTRT--GDAGTTAL--FSGQRVSKTHPRV--EAYGTLDELNAALSLC-AC-TT
--------------HHPQ---------HR--RFIESIQ--QQIFWF----SAELAS--ES
-EQPNPG---------QRYISTEEIAVLEAAI--------------------------DA
AMSRVA-VVH------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--RC--EAASR-LHFAR---------------TLARRAERRLVELSA----DIAV----
---------RQVLMRYI-------NRLS-------DC-------------LY--ALARAE
DHDAHQRHIINEVT------RRYLASTYPSTIKESSMSLSFQELHQLIRSAVARAEELHV
PVVISIVDGNGTPTVTWRMPDALLVSSELAPKKAWTAVAMKSATHELASAVQPGAALYGL
DTHMQGKIVTFGGGFALWRNGVLIGGLGISGGSVEQDMDIAQAAIAAIDVRTYQ
>gi++|218705542|ref|YP_002413061.1| putative propanediol utilization B12 related
protein (pduO-like) [Escherichia coli UMN026]
------------------------------------------------------------
----MAIYTRT--GDSGSTSL--FTGQRVSKTHLRV--ETYGTLDELNATLSLC-YC-AT
--------------AIES---------HR--ILLEAIQ--QQIFWF----SAELAS--ES
-EQPSAQ---------QRYIGTEEIAALENAI--------------------------DS
AMNAVP-PVH------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--RC--EAASR-MHFAR---------------TVARRAERRLVELTT----ETTV----
---------RNVLLHYI-------NRLS-------DC-------------LY--ALARVE
DNVAHQNLMIQEIT------KRYHEANHTPALKERTMPLSFQDLHQLIRSAALRADELHI
PVVISIVDANGTESVTWRMPDALLVSSELAPKKAWTAVAMKTATHKLADTVQPGAPLYGL
ESHMQGKVVTFGGGFPLWRDGKLLGGLGISGGSVEQDMDIAQSAMAAINVGVNQ
>gi++|157158139|ref|YP_001463351.1| propanediol utilization protein, PduO
[Escherichia coli E24377A]
------------------------------------------------------------
----MAIYTRT--GDSGSTSL--FTGQRVSKTHLRV--ETYGTLDELNATLSLC-YC-AT
--------------AIES---------HR--ILLEAIQ--QQIFWF----SAELAS--ES
-EQPSAQ---------QRYIGTEEIAALENAI--------------------------DS
```

```
AMNAVP-PVH------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--RC--EAASR-MHFAR---------------TVARRAERRLVELTT----ETTV----
---------RNVLLHYI-------NRLS-------DC-------------LY--ALARVE
DNVAHQNLMIQEIT------KRYHEANHIPALKERTMPLTFQDLHQLIRSAAMRADELHI
PVVISIVDANGTESVTWRMPDALLVSSELAPKKAWTAVAMKTATHKLADTVQPGAPLYGL
ESHMQGKVVTFGGGFPLWRDGKLLGGLGISGGSVEQDMDIAQSAMAAINVGVNQ
>gi++|215487223|ref|YP_002329654.1| propanediol utilization protein PduO,
AdoCbl-dependent [Escherichia coli O127:H6 str. E2348/69]
------------------------------------------------------------
----MAIYTRT--GDSGSTSL--FTGQRVSKTHLRV--ETYGTLDELNATLSLC-YC-AT
--------------AIES---------HR--ILLEAIQ--QQIFWF----SAELAS--ES
-EQPSAQ---------QRYIGTEEIAALENAI--------------------------DS
AMNAVP-PVH------------CFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--RC--EAASR-MHFAR---------------TVARRAERRLVELTT----ETTI----
---------RNVLLHYI-------NRLS-------DC-------------LY--ALARVE
DNVAHQNLMIQEIT------KRYHEANHTPALKERTMPLTFQDLHQLIRSAAMRADELHI
PVVISIVDANGTESVTWRMPDALLVSSELAPKKAWTAVAMKTATHKLADTVQPGAPLYGL
ESHMQGKVVTFGGGFPLWRDGKLLGGLGISGGSVEQDMDIAQSAMAAINVGVNQ
>gi++|74312542|ref|YP_310961.1| putative propanediol utilization protein: B12
related [Shigella sonnei Ss046]
------------------------------------------------------------
----MAIYTRT--GDSGSTSL--FTGQRVSKTHLRV--ETYGTLDELNATLSLC-YC-AT
--------------AIES---------HR--ILLEAIQ--QQIFWF----SAELAS--ES
-EQPSAQ---------QRYIGTEEIAALENAI--------------------------DS
AMNAVP-PVH------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--RC--EAASR-MHFAR---------------TVARRAERRLVELTT----ETTV----
---------RNVLLHYI-------NRLS-------DC-------------LY--ALARVE
DNVAHQNLMIQEIT------KRYHEANHTPALKERTMPLTFQDLHQLIRSAAMRADELHI
PVVISIVDANGTESVTWRMPDALLVSSELAPKKAWTAVAMKTATHKLADTVQPDAPLYGL
ESHMQGKVVTFGGGFPLWRDGKLLGGLGISGGSVEQDMDIAQSAMAAINVGVNQ
>gi++|218549352|ref|YP_002383143.1| putative propanediol utilization protein: B12
related pduO, Bifunctional ATP:cob(I)alamin adenosyltransferase/GlcG domain
[Escherichia fergusonii ATCC 35469]
------------------------------------------------------------
----MAIYTRT--GDKGTTAL--FTGQRVSKTHPRV--ETYGTLDELNAALSLC-RC-AV
--------------ESPE---------RR--SLLEAVQ--LQIFWF----SAELAS--ES
-EQPSAQ---------QQSISAREIAELEAAI--------------------------DH
AMSRVP-PVH------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--RS--EAASR-LHFAR---------------TLARRAERRLVELSE----QFPV----
---------RNELQRYI-------NRLS-------DC-------------LY--ALARAE
DHENHQKNLIQEVT------ARYLAAVTTQTHKESAMSLSFQELHLLTRAAIARAEELHI
PVVISVVDANGTESVTWRMPDALLVSSELAPKKAWTAVAMKMATHDLAAAVQPGASLYGL
DTHMQGKVVTFGGGFPLWRDGSIVGGLGVSGGSVEQDMDIAQTAAAAINVRTMK
>gi++|123442956|ref|YP_001006931.1| putative propanediol utilization protein: B12
related [Yersinia enterocolitica subsp. enterocolitica 8081]
------------------------------------------------------------
----MSIYTKT--GDAGTTAL--FTGQRVKKSHPRV--ETYGTLDELNAALSLC-AR-VA
--------------QGEE---------NL--QLLDAIQ--HQLFYF----SAELAS--EG
IETPPCG---------RKSISEQDIQALEQAV--------------------------DR
CIAQLP-PVQ------------GFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--NT--EAGSR-LHFAR---------------TLARRCERRLIELAE----QVPV----
---------RPVLLQYL-------NRLS-------DC-------------LY--ALARDE
DQRQTLQQTAHTVV---ARYLAATTEKPVATTQPTSAGLGFSDVHQLVKLAVEAAMTLQI
```

```
TVVVALADRHGNMIMTYRMPDTLLVSSELAPKKAWTAVALKTATHQLSAAIQPGADLFQL
EASTGGKVVSFGGGYPLWRDGQLVGGLGISGGSVEQDMYIAETAISALHLRNE-
>gi++|16800197|ref|NP_470465.1| ATP:cob(I)alamin adenosyltransferase protein PduO
[Listeria innocua Clip11262]
------------------------------------------------------------
----MSIYTKT--GDKGTTAL--FDGNRVKKYDDRV--ETYGSFDELNAEISVA-EK---
--------------FVTS---------HENKTLLRNVE--RQLFYV----CAELAT--ED
ESALAS----------KIVITEDDINELEKVI--------------------------DA
YTLKLP-KVD------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--SS--KAGAF-LHSAR---------------TIARRAERLLVRFSE----QTAV----
---------RNELLKFV-------NRLS-------DF-------------LY--ILAREE
DFRQMLDKATKLIV--------AKYLEQTEQKPSTTSDLSFSFCEKLMHQVQVVSEEVGV
PVTLAIVDAHGNARFNYRMEHALLVSAELATKKAYSAVAMKTSTEKLTEAVQPGAPLYQL
ETLTNGDIVTFGGGVPIYGKDGAIIGGMGISGGSVEEDIHIAKKALSMIEKG--
>gi++|116872538|ref|YP_849319.1| ATP:cob(I)alamin adenosyltransferase protein PduO,
putative [Listeria welshimeri serovar 6b str. SLCC5334]
------------------------------------------------------------
----MSIYTKT--GDKGTTAL--FDGNRVKKYDDRV--ETYGSFDELNAEISVA-EK---
--------------FVTS---------SENKALLRNVE--RQLFYV----CAELAT--EN
ESALAS----------KIIITEEDIKELEKVI--------------------------DD
YTAKLP-KVD------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--SS--TAGAF-LHSAR---------------TIARRGERLLVRFSE----QTTV----
---------RKELLKFV-------NRLS-------DF-------------LY--ILAREE
DFRQMLDKATKLIV--------AKYLEQTGQEKSISTDLSFSFCEKLMHQVCIVSEEVGV
PVTLAIVDAHGNPRFNYRMEHALLVSAELATKKAYSAVAMKTSTENLAEAVQPGAPLYQL
ETLTNGDIVTFGGGIPIYGKDGAIIGGMGISGGSVEEDIHIAKKALSMIEKG--
>gi++|46907382|ref|YP_013771.1| PduO protein [Listeria monocytogenes str. 4b F2365]
------------------------------------------------------------
----MSIYTKT--GDKGTTAL--FDGNRVKKYDDRV--ETYGSFDELNAEISVA-EK---
--------------FVTS---------AENKTLLRNVE--RQLFYV----CAELAT--EH
EASLAS----------KIIITENDINQLEKVI--------------------------DD
YTAKLP-KVD------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--SS--TAGAF-LHSAR---------------TVARRGERLLVRLSE----QTAI----
---------RKELLKFV-------NRLS-------DF-------------LY--ILAREE
DFRQMLDKATKLIV--------AKYLEQTGQEKSVTSDLSFSFCEKLMHQVCIVSEEIGV
PVTLAIVDAHGNARFNYRMEHALLVSAELATKKAYSAVAMKTSTEKLTEAVQPGAPLYQL
ETLTNGDIVTFGGGVPIYGKDGAIIGGMGISGGSVEEDIHIAKKALSMIEKG--
>gi++|16803204|ref|NP_464689.1| ATP:cob(I)alamin adenosyltransferase protein PduO
[Listeria monocytogenes EGD-e]
------------------------------------------------------------
----MSIYTKT--GDKGTTAL--FDGNRVKKYDDRV--ETYGSFDELNAEISVA-EK---
--------------FVTS---------AENKSLLRNVE--RQLFYV----CAELAT--EH
EASLAS----------KIIITENDINQLEKVI--------------------------DD
YTAKLP-KVD------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--SS--TAGAF-LHSAR---------------TVARRGERLLVRLSE----QTDI----
---------RKELLKFV-------NRLS-------DF-------------LY--ILAREE
DFRQMLDKATKLIV--------AKYLEQTGQEKSVTSDLSFSFCEKLMHQVCIVSEEIGV
PVTLAIVDAHGNARFNYRMEHALLVSAELATKKAYSAVAMKTSTEKLTEAVQPGAPLYQL
ETLTNGDIVTFGGGVPIYGKDGAIIGGMGISGGSVEEDIHIAKKALSMIEKG--
>gi++|217964767|ref|YP_002350445.1| PduO [Listeria monocytogenes HCC23]
------------------------------------------------------------
----MSIYTKT--GDKGTTAL--FDGNRVKKYDDRV--ETYGSFDELNAEISVA-EK---
--------------FVTS---------AENKSLLRNVE--RQLFYV----CAELAT--EH
EASLAS----------KIIITENDINQLEKVI--------------------------DD
YTAKLP-KVD------------SFVL----------------------------------
```

```
------------------------------------------------------------
-----------------------------------------------------------P
G--SS--TAGAF-LHSAR---------------TVARRGERLLVRLSE----QTAI----
---------RKELLKFV-------NRLS-------DF-------------LY--ILAREE
DFRQMLDKATKLIV--------AKYLEQTGQEKSVTCDLSFSFCEKLMHQVCIVSEEIGV
PVTLAIVDAHGNARFNYRMEHALLVSAELATKKAYSAVAMKTSTEKLTEAVQPGAPLYQL
ETLTNGDIVTFGGGVPIYGKDGAIIGGMGISGGSVEEDIHIAKKALSMIEKG--
>gi++|167040572|ref|YP_001663557.1| ATP--cobalamin adenosyltransferase
[Thermoanaerobacter sp. X514]
------------------------------------------------------------
----MRIYTRV--GDKGETSL--IGGRKVEKCDQRV--ETYGTVDEAISAISLA-RS---
--------------CVKR---------EQVRGYLQKIE--EDLFIL----NSELATLEPE
KL--------------EVRLTQEEVKWVEKKI--------------------------DE
ITENIKLPRD-------------FILPGPYLSSSSLHLARTVVRRAEREAVKLKRSQNIR
EEILMYLNRLSDFLYCCALFEETEEIIKQAVTEISKSVKEKVSNEMKEEKILFKIVKDII
QKAQEKAEEIRKPMCIAVVDEYGYLIAFERMEGALLGSIELAINKAKTAVLLKMETSELH
E--LA--QPSGE-LY------------------GINNASSLNFVTFGG------------
----------GIPLRWG-------GRLI-------GG-------------IG--VSGGSV
EEDIAVATSCVKEM----------------------------------------------
----------------------------------EHILEILYK-----------------
------------------------------------------------------
>gi++|26250349|ref|NP_756389.1| hypothetical protein c4529 [Escherichia coli CFT073]
------------------------------------------------------------
---------MS--ANEASLDN--WINEAIATQLPEL--RMSLSLEDSELLAKLV-RE-MA
QS------------SNVS---------IVF-SLVDACG--QQRFFF----SMD-------
----------------NALLVSHTLAPQKAWT--------------------------AV
ALKMPTHELA------------TLVQ----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GD--------LY------------------GLEK--EKDICCFGG------------
---------GFPCWSG--------RRLL-------GG-------------IG--ISGGSV
EEDMLIARQAMAQF----------------------------------------------
------------------------------SVLRYPLTTTR-------------------
------------------------------------------------------
>gi++|117626451|ref|YP_859774.1| putative propanediol utilization protein: B12
related [Escherichia coli APEC O1]
------------------------------------------------------------
---------MS--ANEASLDN--WINEAIATQLPEL--RMSLSLEDSELLAKLV-RE-IA
QS------------SNVS---------IVF-SLVDACG--QQRFFF----SMD-------
----------------NALLVSHTLAPQKAWT--------------------------AV
ALKMPTHELA------------TLVQ----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GD--------LY------------------GLEK--EKDICCFGG------------
---------GFPCWSG--------RRLL-------GG-------------IG--ISGGSV
EEDMLIARQAMAQF----------------------------------------------
------------------------------SVLRYPLTTTR-------------------
------------------------------------------------------
>gi++|116334185|ref|YP_795712.1| glycolate and propanediol utilization protein
[Lactobacillus brevis ATCC 367]
-----------------------------------------------------------M
NEEQLSQIIRDVIAKQGGTTM--NLFDRHMMEKVID--AAVARADELKVGVTIC------
--------------------------------IMDQATVPQMLYHM------------P-
----------------NANLVSSTLAPKKAWS--------------------------AI
AMKEPTKEIS------------KDIQ----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G---------AP-LY------------------QMETMLDGKLVSFPG--GIPLVI----
---------NGTAIGAI-------GVSG-------GL-------------IE--EDQSIC
E--AAVAAFLKESK----------------------------------------------
------------------------------------------------------------
------------------------------------------------------
>gi++|90422685|ref|YP_531055.1| hypothetical protein RPC_1173 [Rhodopseudomonas
```

```
palustris BisB18]
-----------------------------------------------------------M
SAPTAEMRSITEAIHAVLANL--NGPAFALDDACRL----ARAAEHKAAEIGVP-MV---
----------------------------------------ISIADA----TGGMLL----
----------------LHRMDGALPASFDIAI--------------------------NK
AYTAAIFRMA------------THDL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------G
A--LA--QPGRS-LY------------------GVQTTNQGRVVIFGG------------
---------GYPVLRR--------TTVI-------GA-------------IG--VSGGTV
EQDMQIATFALQTF----------------------------------------------
----------------------------------EAEAKLCAEGE---------------
------------------------------------------------------
>gi++|148544942|ref|YP_001272312.1| ATP:cob(I)alamin adenosyltransferase 
[Lactobacillus reuteri DSM 20016]
----------------------------------------------------------MN
EEQISKIVENV-IKNNASKNL--FDRHKMEK--VID--AAVARANELGVGVTIA------
--------------IMKA----------------------DQVLQM----SYHMPN----
-----------------ANLVSCTLAPKKAWS--------------------------AL
AMKEPTKDIS------------KDIQ----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--AG--------LY------------------QMETMLDGKLASFAG------------
----------GIPLKIN-------DEII-------GA-------------IG--VSGGLV
EEDQSICEAAVAEF----------------------------------------------
----------------------------------LKESK---------------------
------------------------------------------------------
>gi++|116334186|ref|YP_795713.1| adenosylcobalamin-dependent diol dehydratase gamma 
subunit [Lactobacillus brevis ATCC 367]
------------------------------------------------------------
----MPIYTKG--GDKGSTSL--YDGTRVRKDSLRV--DTYGTFDELNANVSLA-DK-FC
--------------VKAE---------NK--AILQKIE--YKMFFL----QGEIAT--QT
AGKFNAN---------SRVITDDDVTMLEQVI--------------------------DR
YTAELP-KVT------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--AS--LAGAQ-LHICR---------------TVCRRAERMFVRFST----DVEV----
---------RPVLERYV-------NRLS-------DF-------------FY--IMARSE
DYEYQVNELTDQVM----------------------------------------------
--------------------------------KRYAQAVGR-------------------
------------------------------------------------------
>gi++|148544943|ref|YP_001272313.1| ATP--cobalamin adenosyltransferase 
[Lactobacillus reuteri DSM 20016]
------------------------------------------------------------
----MAIYTKG--GDKGETSL--FDGTRVPKDSLRV--ETYGTFDELNANISLA-DK---
--------------FCES---------KRNKKLLQEIE--YKMFFL----QGEIAT--EK
RQYFTDK---------SKIITDEDTRKLEKVI--------------------------DE
YTSKLP-PVH------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--SS--TAGAQ-LHICR---------------TICRRAERLFVRLSK----NVKF----
---------RPELERYI-------NRLS-------DF-------------LY--IVARDE
DYEDLLNSVTDDVLKIYKRYQEEKDVR---------------------------------
------------------------------------------------------------
------------------------------------------------------
>gi++|83592249|ref|YP_426001.1| ATP:cob(I)alamin adenosyltransferase [Rhodospirillum 
rubrum ATCC 11170]
------------------------------------------------------MNASAQ
DIDRISVAVRTVLAEIGQTPA--ALGPLGLKDAQRL--AALAAIKAAEIAVPVV------
----------------------------------------IAVADV----SGGLIL----
----------------VHRMDGTLPASIDIAI--------------------------NK
AFTAAAFRTA------------THDL----------------------------------
------------------------------------------------------------
```

```
-----------------------------------------------------------G
A--LA--QPGQP-LY------------------GIQSTNQGRVVIFGG------------
---------GFPCRCG--------GPLA-------GA-------------IG--ISGGTV
EEDMQIASYALRMF----------------------------------------------
-----------------------------LEESGFCPEGEK-------------------
------------------------------------------------------
>gi++|125717402|ref|YP_001034535.1| PduO protein, putative [Streptococcus sanguinis
SK36]
------------------------------------------------------------
---------MA--RDREKDEL----------SSPEL--SSWGGNSELQDSI----IQ---
-------------------------------KVLARCQ---TLLDK----EPLLFT--NI
YQDA------------WELVTRARRKAEELGL--------------------------AV
VITVVD-PAA------------QVVM----------------------------------
------------------------------------------------------------
-----------------------------------------------------------T
Y------RMENA-LLVSN---------------DMAYKKAYTAVGMRMQSKDLAPL----
----------TQPGQWL-------YQLE-------TMTDNKVVSLAGGIPIY--CQSEMI
GGIGVSGGSSEEDQ----------------------------------------------
------------------------------SIAEYAVGLQSSKLAN--------------
------------------------------------------------------
>gi++|218782809|ref|YP_002434127.1| protein of unknown function DUF336
[Desulfatibacillum alkenivorans AK-01]
------------------------------------------------------------
----MEIMTHI--CNDLARVL-----------------ARIARKKALEIQVPMV------
----------------------------------------IAFADA----RGELVH----
----------------FQRMDKALPVSSDIAV--------------------------NK
AFTAAALRMS------------THKV----------------------------------
------------------------------------------------------------
-----------------------------------------------------------G
R--LV--EQGQE-LA------------------GLELTNKGKMVIFGG----GLPLSLDG
EVVGSVGVSGGSVAQDMVVAQAAANALEQMEKTAQAL-------------LP--ILPKTL
EDLTDLANKIQDLG----------------------------------------------
----------------------------------RKEGADSDILEGAFYLI---------
------------------------------------------------------
>gi++|150018877|ref|YP_001311131.1| hypothetical protein Cbei_4065 [Clostridium
beijerinckii NCIMB 8052]
------------------------------------------------------------
-MINEELIKKL------SSDL--ISSIKTPKLTLKMAKEILEKAERKAESINVP-VV---
----------------------------------------IALVDD----GGNLIA----
----------------QHRMDNSILISIKVSF--------------------------NK
AYTALALKMS------------TERF----------------------------------
------------------------------------------------------------
-----------------------------------------------------------N
E--LA--LPGKP-LY------------------GLENTGHGELCILGG------------
---------GIPIVSN--------GNII-------GA-------------IG--VSGGSI
DEDIQIA--QAALK----------------------------------------------
------------------------------------------------------------
------------------------------------------------------
>gi++|218782810|ref|YP_002434128.1| ATP/cobalamin adenosyltransferase
[Desulfatibacillum alkenivorans AK-01]
------------------------------------------------------------
----MSIYTGG--GDKGKTSL--LSGERVSKADPRV--EAYGTLDELTAQLGVC-RA-QL
NQ------------FPAC---------APFAGMIVNIQ--RDLFRV----GMQLSSSPKY
WSKL------------SAPINSDDIQSLEQAI--------------------------DA
LEKAFG-LPG------------FFVS----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--RT--LAGAS-LHVAR---------------TICRRAERQAWAAAG----DVES----
---------YALILKYI-------NRLS-------DL-------------LF--SLSWTA
E--IRIL--LTEEL----------------------------------------------
----------------------------------SHGNHDAHL-----------------
------------------------------------------------------
>gi++|29376192|ref|NP_815346.1| ATP:cob(I)alamin adenosyltransferase, putative
```

```
[Enterococcus faecalis V583]
------------------------------------------------------------
----MKIYTKT--GDKGMTKL--VGSSTVAKDSDRV--ESYGTIDELNSWVGYI-IS--Q
LP------------QENQ--------EIK--EELEALQ--HLLFDA----GTDLST--PI
EAQR------------PFKLQKASVHWLEQRI--------------------------DF
YTAQSP-DID------------RFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--PAASM-VHVAR---------------TIARRAERIIVRLNW----TAKI----
---------NEEVLIFT-------NRLS-------DY-------------FY--ALARCL
N--VQAQ--RPDVF----------------------------------------------
----------------------------------YERSEMVFHKIKEDGL----------
------------------------------------------------------
>gi++|125717377|ref|YP_001034510.1| ATP:cob(I)alamin adenosyltransferase, putative
[Streptococcus sanguinis SK36]
------------------------------------------------------------
----MQLYTKT--GDKGLTKL--VGGQSVAKDAERV--NAYGTIDELNSWIGYT-IT--K
LD------------KDDK---------LR--DELLQLQ--HYLFDC----GSDLST--P-
QGVY------------PYKVDQQLIDWIEERI--------------------------DT
YAEIPS-ALE------------RFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GD--EIASM-IHVAR---------------TIARRAERHIVGAMW----TTEI----
---------NNNVLIFV-------NRLS-------DY-------------FF--ALARVI
N--FTKN--QEDIA----------------------------------------------
----------------------------------YERGAKVFHNITKADVERWASKRQ--
------------------------------------------------------
>gi++|158319833|ref|YP_001512340.1| ATP--cobalamin adenosyltransferase [Alkaliphilus
oremlandii OhILAs]
------------------------------------------------------------
----MQIYTRT--GDKGYTRI--IGGTKLAKDSERI--KAYGTIDELNSFVGYA-IT--L
IK------------NNDA---------LK--KELIQIQ--QYLFDC----GNDLAM--P-
RGKG------------TYRVTPDLTEWIEGCI--------------------------DA
HVAIPR-EVE------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--PAASI-LHICR---------------TVARRAEREIVTFQW----TNDM----
---------NEEVLIFI-------NRLS-------DY-------------FF--SVARVA
N--ANEG--IEDVL----------------------------------------------
----------------------------------YERSGKVFHMELKKEHLQ--------
------------------------------------------------------
>gi|152972008|ref|YP_001337154.1| hypothetical protein KPN_03492 [Klebsiella
pneumoniae subsp. pneumoniae MGH 78578]
------------------------------------------------------------
---MYRIYTRT--GDKGTTAL--YGGSRIEKDHIRV--EAYGTVDELISQLGVC-YA---
--------------TTRD---------AGLRESLHHIQ--QTLFVL----GAELASDARG
LTRL------------SQTVGEEEITALERLI--------------------------DR
NMAESG-PLK------------QFVI----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--RN--LASAQ-LHVAR---------------TQSRRLERLLTAMDR----AHPL----
---------RDALKRYS-------NRLS-------DA-------------LF--AMARIE
E-----------------------------------------------------------
----------------------------------TRPDACA-------------------
------------------------------------------------------
>gi|206579020|ref|YP_002236497.1| cob(I)yrinic acid a,c-diamide adenosyltransferase
[Klebsiella pneumoniae 342]
------------------------------------------------------------
---MYRIYTRT--GDKGTTAL--YGGSRIEKDHIRV--EAYGTVDELISQLGVC-YA-TT
--------------RDAG---------LR--ESLHHIQ--QTLFVL----GAELASDARG
LTRL------------SQTIGEEEITALERLI--------------------------DR
NMAESG-PLK------------QFVI----------------------------------
------------------------------------------------------------
```

```
-----------------------------------------------------------P
G--KN--LASAQ-LHVAR---------------TQSRRLERLLTATDR----VHPL----
---------RDALKRYS-------NRLS-------DA-------------LF--SMARIE
E-----------------------------------------------------------
----------------------------------TRPDACA-------------------
------------------------------------------------------
>gi|18309916|ref|NP_561850.1| hypothetical protein CPE0934 [Clostridium perfringens
str. 13]
------------------------------------------------------------
----MNIYTKT--GDKGTTSL--FGGSRVDKCDLRV--DAYGTIDELISFIGLA-YA---
--------------ELTD---------EEEKEILNKIQ--KELFML----GAELASDEKG
LELL------------KDKIQSEHIEYLEKLI--------------------------DK
YMGIAG-PLT------------AFVI----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--KN--KPSAT-LHVAR---------------TVARRGERIMTALNE----VQPL----
---------REEIKKYI-------NRLS-------DT-------------LF--ALARYY
E--EK-------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------
>gi|110802632|ref|YP_698332.1| ATP:cob(I)alamin adenosyltransferase, putative
[Clostridium perfringens SM101]
------------------------------------------------------------
----MNIYTKT--GDKGTTSL--FGGSRVDKCDLRV--DAYGTIDELISFIGLA-YA---
--------------ELTD---------EEEKEILNKIQ--KELFML----GAELASDEKG
LELL------------KDKIQLENIEYLEELI--------------------------DR
YMGIAG-PLT------------AFVI----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--KN--KPSAT-LHVAR---------------TVARRGERIMTALNE----VQPL----
---------REEIKKYI-------NRLS-------DT-------------LF--ALARYY
E--EK-------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------
>gi|187933018|ref|YP_001886289.1| ATP:cob(I)alamin adenosyltransferase [Clostridium
botulinum B str. Eklund 17B]
------------------------------------------------------------
----MKIYTKT--GDKGTTAL--YGGSRVDKDSLRV--EAYGTVDEVISFIGLA-CA---
--------------EIED---------KEEKNALEEIQ--KKLFVL----GAELASDEKG
LTYL------------KEIITDEDIEKLEVLI--------------------------DK
YMELAG-PFK------------GFVT----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--KN--KISAA-LHVAR---------------TVTRRAERRIATLCK----EENV----
---------REQVKMYV-------NRLS-------DV-------------LF--AFARYE
E--EK-------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------
>gi|110798903|ref|YP_695624.1| putative ATP:cob(I)alamin adenosyltransferase
[Clostridium perfringens ATCC 13124]
------------------------------------------------------------
----MNIYTKT--GDKGTTSL--FGGSRVDKCDLRV--DAYGTIDELISFIGLA-YA---
--------------ELTD---------EEEKEILNKIQ--KELFML----GAELASDEKG
LELL------------KDKIQLEHIEYLEKLI--------------------------DK
YMGIAG-PLT------------AFVI----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--KN--KPSAT-LHVAR---------------TVARRGERIMTALNE----VQPL----
---------REEIKKYI-------NRLS-------DT-------------LF--ALARYY
E--EK-------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------
>gi|188590374|ref|YP_001921317.1| DhaG protein [Clostridium botulinum E3 str. Alaska
```

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E43]
------------------------------------------------------------
-------MKKL--NEIKQLSL------EVVKEMAKA-------AEEKAASMNVP-VI---
----------------------------------------FAAVDA----GANLML----
----------------MHRMEDAFITSIDIAI--------------------------NK
AYTAACLKQG------------SHGI----------------------------------
------------------------------------------------------------
-----------------------------------------------------------A
E--CV--QPGQS-LY------------------GLQLTNNCRIVPFGG------------
---------GFPIIVD--------GSVV-------GA-------------VG--VSGGTV
EEDMAIAQAAVDAF----------------------------------------------
---------------------------------------NK-------------------
------------------------------------------------------
>gi|110799882|ref|YP_695625.1| hypothetical protein CPF_1179 [Clostridium
perfringens ATCC 13124]
------------------------------------------------------------
-------MKKL--NDVKELSL------EIVKEMAKA-------AEAKACEMNVP-VI---
----------------------------------------FAAVDA----GANLML----
----------------MHRMEDAFLTSIDIAI--------------------------NK
AYTAACLKQG------------SHEI----------------------------------
------------------------------------------------------------
-----------------------------------------------------------A
E--CV--QPGQS-LY------------------GLQLTNNCRIVPFGG------------
---------GFPIIV-D-------GKVV-------GA-------------VG--VSGGTV
EEDMAIAQAAVDCF----------------------------------------------
----------------------------------NNK-----------------------
------------------------------------------------------
>gi|18309917|ref|NP_561851.1| hypothetical protein CPE0935 [Clostridium perfringens
str. 13]
------------------------------------------------------------
-------MKKL--NDVKELSL------EIVKEMAKA-------AEAKACEMNVP-VI---
----------------------------------------FAAVDA----GANLML----
----------------MHRMEDAFLTSIDIAI--------------------------NK
AYTAACLKQG------------SHEI----------------------------------
------------------------------------------------------------
-----------------------------------------------------------A
E--CV--QPGQS-LY------------------GLQLTNNCRIVPFGG------------
---------GFPIIV-D-------RKVV-------GA-------------VG--VSGGTV
EEDMAIAQAAVDCF----------------------------------------------
----------------------------------NNK-----------------------
------------------------------------------------------
>gi|150009910|ref|YP_001304653.1| ATP:cob(I)alamin adenosyltransferase, putative
[Parabacteroides distasonis ATCC 8503]
------------------------------------------------------------
-MKKSIIYTRT--GDKGTTSL--VGGQRVSKAHDRI--ESYGTVDELNSFIGLL-IT-AL
--------------NDEK---------DT--DFLSFIQ--HKLFTI----GSYLAT--DQ
ATTELKI---------ESKVTPESIERIEREI--------------------------DR
LDNELP-KMH------------AFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GC--RSAAL-AHVCR---------------TVCRRAERQIYRLAE----NCPV----
---------EEPVLIFM-------NRLS-------DY-------------FF--VLARKE
C--INNN--GKEII----------------------------------------------
----------------------------------WDYTCV--------------------
------------------------------------------------------
>gi|163848992|ref|YP_001637036.1| ATP--cobalamin adenosyltransferase [Chloroflexus
aurantiacus J-10-fl]
------------------------------------------------------------
----MKIYTRT--GDAGETGL--FGGQRVRKDDLRV--QAYGTVDECNAALGVA-RA---
--------------AGPD---------PALDAVLAVVQ--NQLFVV----GADLAS--PG
ESPY------------IPRVSAELTSFLEEQI--------------------------DA
MEAELS-PLK------------QFIL----------------------------------
------------------------------------------------------------
```

```
-----------------------------------------------------------P
G--GH--PVAAH-LHLAR---------------TICRRAERVVVTLAT----EEEV----
---------RPEILTYL-------NRLS-------DF-------------LF--VAARIA
N--ARAG--VSDVP----------------------------------------------
----------------------------------WQK-----------------------
------------------------------------------------------
>gi|34540854|ref|NP_905333.1| ATP:cob(I)alamin adenosyltransferase, putative
[Porphyromonas gingivalis W83]
------------------------------------------------------------
-----MIYTRT--GDKGTTSL--VGGERVPKYHQRL--ECYGTIDELNSFIGLL-MS-ED
--------------LPEE---------DR--DFLRTIQ--HKLFTV----GSYLAT--NQ
ESRELMV---------ESRVHPETIERVEQEI--------------------------DR
LDNAIP-KMT------------AFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--RSASL-AHVCR---------------TVCRRAERHIYRLSE----EALV----
---------EEPVMRYI-------NRLS-------DY-------------FF--ALARKE
V--WRTT--GGEII----------------------------------------------
----------------------------------WDKTCD--------------------
------------------------------------------------------
>gi|188995085|ref|YP_001929337.1| probable ATP:corrinoid adenosyltransferase
[Porphyromonas gingivalis ATCC 33277]
------------------------------------------------------------
-MSKSMIYTRT--GDKGTTSL--VGGERVPKYHQRL--ECYGTIDELNSFIGLL-MS-ED
--------------LPEE---------DR--HFLRTIQ--HKLFTV----GSYLAT--NQ
ESRELMV---------ESRVHPETIERVEQEI--------------------------DR
LDNAIP-KMT------------AFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--RSASL-AHVCR---------------TVCRRAERHIYRLSE----EALV----
---------EEPVMRYI-------NRLS-------DY-------------FF--ALARKE
V--WRTT--GGEII----------------------------------------------
----------------------------------WDKTCD--------------------
------------------------------------------------------
>gi|187934031|ref|YP_001886288.1| DhaG protein [Clostridium botulinum B str. Eklund
17B]
------------------------------------------------------------
-------MKKL--NEIKQLSL------EIVKEMAKA-------AEEKAASMNVP-VI---
----------------------------------------FAAVDA----GANLML----
----------------MHRMEEAFITSIDIAI--------------------------NK
AYTAACLKQG------------SHGI----------------------------------
------------------------------------------------------------
-----------------------------------------------------------A
E--CV--QPGES-LY------------------GLQLTNNCRIVPFGG------------
---------GLPIIVD--------GKVV-------GA-------------VG--VSGGTV
EEDMAIAQAAVDAF----------------------------------------------
---------------------------------------NK-------------------
------------------------------------------------------
>gi|188589368|ref|YP_001921318.1| ATP:cob(I)alamin adenosyltransferase [Clostridium
botulinum E3 str. Alaska E43]
------------------------------------------------------------
----MKIYTKT--GDKGTTAL--YGGSRVDKDSLRV--EAYGTVDEVISFIGLA-YA---
--------------ESED---------KEEKDALQEIQ--KKLFVL----GAELASDEKG
LTYL------------KEVITDEDIEKLEVLI--------------------------DK
YMELAG-PFN------------GFVT----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--KN--KISAA-LHVAR---------------TVTRRAERIIATLSK----EEHI----
---------NEPVKMYI-------NRLS-------DV-------------LY--AFARYN
E--EK-------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------
>gi|150390664|ref|YP_001320713.1| ATP--cobalamin adenosyltransferase [Alkaliphilus
```

```
metalliredigens QYMF]
------------------------------------------------------------
----MKIYTKT--GDKGQTSL--YDGKRVDKDDIRV--ESYGTIDELNSALGFA-RT---
--------------FVED---------DEISNYIFQIQ--RELFDV----AGELAT--ED
KEKF------------PEKIEQSHTKCLEEMI--------------------------DY
FLSKME-LMD------------RFII----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--TN--RASAS-LHVAR---------------TICRRAERRILTLQK----EVYV----
---------SVNLVKYV-------NRLS-------DA-------------IY--AMARYL
E---------SDLK----------------------------------------------
----------------------------------YVEFKK--------------------
------------------------------------------------------
>gi|116872582|ref|YP_849363.1| ATP:cob(I)alamin adenosyltransferase, putative
[Listeria welshimeri serovar 6b str. SLCC5334]
------------------------------------------------------------
----MRIYTKT--GDKGMTRI--IGGSKVSKDNVRI--DAYGTLDELNSLIGFTITT---
--------------LGDE---------PEIQAELEQIQ--QQLFDA----GGDLAT--EE
GKR-------------DYKLTSEPVAWLEDRI--------------------------DI
YADEPP-EIE------------KFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--QAASL-LHMAR---------------TVTRRAEREIVGMLK----IAST----
---------NQEVLKYV-------NRLS-------DY-------------FF--AVARVV
N--YRAG--ETDIF----------------------------------------------
----------------------------------YKNSELVFRNKKK-------------
------------------------------------------------------
>gi|150024678|ref|YP_001295504.1| hypothetical protein FP0583 [Flavobacterium
psychrophilum JIP02/86]
------------------------------------------------------------
----MKVYTKT--GDKGTTAL--FGGTRVPKDHSRI--ESYGTVDELNSYIGLI-RD---
--------------QEIN---------QHYKNILIEIQ--DRLFTV----GAILAT--PP
EKEVMKNGQLRLQ---KLGIIESDIELLENEI--------------------------DT
MENSLP-QMT------------HFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GH--TTVSY-CHIAR---------------CVCRRAERLAVHLSH----NEPV----
---------ADIAIKYL-------NRLS-------DY-------------LF--VLARKL
T--SDLH--ADEVK----------------------------------------------
----------------------------------WIPRK---------------------
------------------------------------------------------
>gi|152972006|ref|YP_001337152.1| hypothetical protein KPN_03490 [Klebsiella
pneumoniae subsp. pneumoniae MGH 78578]
------------------------------------------------------------
------MMNKS--QQVQTITL---------AAAQQM--AEAVEKKAAEINVAVV------
----------------------------------------FSVVDH----GGNTLL----
----------------IQRMDEAFVSSCDISL--------------------------NK
AWSACSLKQG------------THEI----------------------------------
------------------------------------------------------------
-----------------------------------------------------------T
S--AV--QPGQS-LY------------------GLQLTNQQRIIIFGG------------
----------GLPVIFN-------EQVI-------GA-------------VG--VSGGTV
EQDQLLAQCALDCF----------------------------------------------
----------------------------------SAL-----------------------
------------------------------------------------------
>gi|206580189|ref|YP_002236500.1| hypothetical protein KPK_0625 [Klebsiella
pneumoniae 342]
------------------------------------------------------------
------MMNKS--QQVQTITL---------AAAQQM--AAAVEKKATEINVAVV------
----------------------------------------FSVVDR----GGNTLL----
----------------IQRMDEAFVSSCDISL--------------------------NK
AWSACSLKQG------------THEI----------------------------------
------------------------------------------------------------
```

```
-----------------------------------------------------------T
S--AV--QPGQS-LY------------------GLQLTNQQRIIIFGG------------
----------GLPVIFN-------EQVI-------GA-------------VG--VSGGTV
EQDQLLAQCALDCF----------------------------------------------
----------------------------------SAL-----------------------
------------------------------------------------------
>gi|53715559|ref|YP_101551.1| hypothetical protein BF4276 [Bacteroides fragilis
YCH46]
------------------------------------------------------------
-MKKSLVYTKT--GDKGTTGL--IGGTRVPKTHIRL--EAYGTVDELNSNLGLL-AT-YL
--------------MDEH---------DL--NFVQSVQ--DKLFAI----GSHLAT--DQ
EKVQLND---------VSIITPAEVEAIEREI--------------------------DA
ADEILP-PLH------------SFII----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--RGSAV-CHVCR---------------TVCRRAERRILALSE----SCTI----
---------SADLLAYI-------NRLS-------DY-------------LF--VLSRKM
N--FNEG--KDEIF----------------------------------------------
----------------------------------WNNSCK--------------------
------------------------------------------------------
>gi|46199862|ref|YP_005529.1| hypothetical protein TTC1560 [Thermus thermophilus
HB27]
------------------------------------------------------------
----MKIYTRT--GDAGETGL--YGAERVVKAHPRV--EAYGTVDEANSAIGLARSL---
--------------LPGK--------HRDLHDLLERLQ--NALFDL----GADLAT--RM
GSPYEKN---------IARMDAEDVRALEEAI--------------------------DR
YQEESP-PFQ------------GFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GH--PAAAA-LHLAR---------------TVVRRAERKAVALSR----EEPV----
---------NPEVIRYL-------NRLS-------DL-------------LF--VLARVV
N--AREG--IKEEG----------------------------------------------
----------------------------------WLVKKRR-------------------
------------------------------------------------------
>gi|158320386|ref|YP_001512893.1| ATP--cobalamin adenosyltransferase [Alkaliphilus
oremlandii OhILAs]
------------------------------------------------------------
----MKIYTKT--GDRGETSL--YDGKRVKKDDIRV--ESYGTIDELNSALGLA-RN---
--------------FIED---------QEIVEIIYGIQ--RELFNV----AGELAT--EN
TDNF------------KGKVDETQIQALEKII--------------------------DD
YLEKMP-KMD------------KFII----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--SN--KASAS-LHVAR---------------TVCRRAERRILTFSR----EEDV----
---------SPLLIKYV-------NRLS-------DT-------------IY--ALARYL
E---------SDLR----------------------------------------------
----------------------------------YVDFKK--------------------
------------------------------------------------------
>gi|83816164|ref|YP_445418.1| ATP:cob(I)alamin adenosyltransferase, putative
[Salinibacter ruber DSM 13855]
------------------------------------------------------------
--MSKRIYTRT--GDDGTTSL--FGGERVGKGNPRI--DAYGTVDETNSIVGLA-RSHLE
G-------------EPGQ---------ETLDPVLGDVQ--EELFVL----GADLAT--PM
DAKPV-----------VERIEDAHIEALEERI--------------------------DR
FEADLP-SLE------------RFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GA--PAGAS-LHSAR---------------TVCRRAERRSVEAKT----STPI----
---------NEQVIVYL-------NRLS-------DL-------------LF--VLARWA
N--RQAG--VREDT----------------------------------------------
----------------------------------WSPGSGGGDGASADPS----------
------------------------------------------------------
>gi|194364451|ref|YP_002027061.1| ATP/cobalamin adenosyltransferase
```

```
[Stenotrophomonas maltophilia R551-3]
-----------------------------------------------------------M
GHRLSRIYTRT--GDDGSTGL--GDGQRVAKDDARV--ASYGTVDEANAALGLL-LA--A
P-------------LPED---------VR--ALVVHLQ--HQLFDL----GAELCI--PG
----------------HAAIHAADVSALEQQL--------------------------DH
YNAGLP-MLK------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GG--EAAAR-CHLAR---------------TIVRRAERETVTLAR----HEAV----
---------RSEALQYL-------NRLS-------DL-------------LF--VLARVL
A--RADG--HGEAL----------------------------------------------
----------------------------------WQPQQRQR------------------
------------------------------------------------------
>gi|118472987|ref|YP_885926.1| PduO protein [Mycobacterium smegmatis str. MC2 155]
------------------------------------------------------------
---------------MGALSL--STAQKVVD-------AAIEKANEIGQPMNIA------
--------------VVDD--------------------------------GGHLVA----
----------------FARMDGAIKASIDISI--------------------------RK
ARTSILMNLP------------TSAL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------M
D--VA--QPGGE-LY------------------GLEQLSGGLVLFGGG------------
-----------LLLERD-------GEVI-------GA-------------IG--VSAGSV
EQDVKVAEAGVAAL----------------------------------------------
------------------------------------------------------------
------------------------------------------------------
>gi|146302729|ref|YP_001197320.1| ATP--cobalamin adenosyltransferase [Flavobacterium johnsoniae UW101]
------------------------------------------------------------
----MKVYTKT--GDKGTTAL--FGGTRVPKDHIRI--DSYGTVDELNSYIGLI-RD---
--------------QEID---------SHYKTILIEIQ--DRLFTV----GAILAT--PQ
EKEVLKNGELRLK---NLGIIDSDIELLENEI--------------------------DK
MEESLP-QMT------------HFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GH--PTVSH-CHIAR---------------CICRRAERLAVHLSH----NEHV----
---------PEIAIMYL-------NRLS-------DY-------------LF--VLARKL
S--SDLK--AEEVK----------------------------------------------
----------------------------------WIPRK---------------------
------------------------------------------------------
>gi|190572868|ref|YP_001970713.1| putative cobalamin adenosyltransferase
[Stenotrophomonas maltophilia K279a]
-----------------------------------------------------------M
GHRLSRIYTRT--GDDGSTGL--GDGQRVPKDDARV--ASYGTVDEANAALGLL-LA-VP
--------------LPED---------VR--ALVVHLQ--HQLFDL----GAELCI--PG
----------------HAAIHAADVSALEQQL--------------------------DH
YNADLP-MLK------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GG--EAAAR-CHLAR---------------TIVRRAERETVTLAR----HEAV----
---------RSEALQYL-------NRLS-------DL-------------LF--VLARVL
A--RADG--QGEAL----------------------------------------------
----------------------------------WQPQQRQR------------------
------------------------------------------------------
>gi|120434897|ref|YP_860583.1| cobalamin adenosyltransferase family protein
[Gramella forsetii KT0803]
------------------------------------------------------------
----MKIYTKT--GDKGTTSL--FGGTRVPKHHIRI--ESYGTVDELNSHIGLL-RD-QD
--------------TDKQ---------TK--EFLTEIQ--DRLFTI----GAILAT--DP
EKATLKNGKERLN---IPKVSDEDIEKLEKGI--------------------------DK
MNEELP-EMT------------HFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
```

```
G--GH--QSVSF-CHIAR---------------CVCRRAERLSSALYD----IETF----
---------DEKVLIYL-------NRLS-------DY-------------LF--VLARKL
S--KQLQ--AEEIQ----------------------------------------------
----------------------------------WIPKKS--------------------
------------------------------------------------------
>gi|15806642|ref|NP_295361.1| hypothetical protein DR_1638 [Deinococcus radiodurans
R1]
------------------------------------------------------------
----MKLYTRT--GDQGQTGL--YGADRVSKAHPRV--EAYGTVDELNSALGLA-RA---
--------------HSTD---------AALDTDLEYLQ--NALFDV----GADLAT--RS
GTPYEKN---------LVRIDAEDVAFLEAMI--------------------------DR
YQEAAP-PFT------------GFVH----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--PAAAA-LQLAR---------------AVARRAERDVIRLLD----VEEA----
---------NAQVQVYL-------NRVS-------DL-------------LF--IMARAV
N--ARSG--LSEEA----------------------------------------------
----------------------------------WTVKKRR-------------------
------------------------------------------------------
>gi|94984773|ref|YP_604137.1| cobalamin adenosyltransferase [Deinococcus
geothermalis DSM 11300]
------------------------------------------------------------
----MKLYTRT--GDKGTTGL--YGADRVSKAHPRV--EAYGTVDELNSVVGLA-RAHNA
RS------------HQPD---------SGLDADLEYLQ--NALFDL----GADLAT--RQ
DSPYAKN---------LSRMDAQDVAFVEAMI--------------------------DR
YQEGAP-PFT------------GFVH----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--PTAAA-LHVAR---------------TVARRAEREVIRLAQ----EEEI----
---------GEHVQVYL-------NRVS-------DL-------------LF--VMARAA
N--QAAG--ISEQA----------------------------------------------
----------------------------------WTVKKRR-------------------
------------------------------------------------------
>gi|16800241|ref|NP_470509.1| hypothetical protein lin1172 [Listeria innocua
Clip11262]
------------------------------------------------------------
----MRIYTKT--GDKGMTRI--IGGSKVSKDNIRI--NAYGTLDELNSLIGYT-IT--T
LG------------NEPE---------IQ--AELEQIQ--QQLFDA----GGDLAT--E-
EGKR------------DYKLTAEPVAWLEDRI--------------------------DI
YADEPP-EIE------------KFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--QAASL-LHMAR---------------TVARRAEREIVGMLK----IAST----
---------NQEVLKYV-------NRLS-------DY-------------FF--AVARVV
N--YRAG--ETDIF----------------------------------------------
----------------------------------YKNSELVFRNKKK-------------
------------------------------------------------------
>gi|220918720|ref|YP_002494024.1| ATP/cobalamin adenosyltransferase
[Anaeromyxobacter dehalogenans 2CP-1]
------------------------------------------------------------
----MKIYTKT--GDAGETGL--FGGPRVRKSDARV--EAYGEVDELNACLGTV-RA---
--------------VVED---------PEIDAQLARIQ--DELFCV----GAELAT--PH
GEKARSA---------IPAVEPRWAERLEAAI--------------------------DA
WEAELP-PLR------------QFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--RTAAQ-LHLAR---------------CVCRRAERRVVALAA----EAEV----
---------SPVALAYL-------NRLS-------DL-------------LF--VAARVA
N--HRAR--KPETA----------------------------------------------
----------------------------------WDPHRER-------------------
------------------------------------------------------
>gi|197123951|ref|YP_002135902.1| ATP/cobalamin adenosyltransferase
[Anaeromyxobacter sp. K]
```

```
------------------------------------------------------------
----MKIYTKT--GDAGETGL--FGGPRVRKSDARV--EAYGEVDELNACLGTV-RA---
--------------LVED---------PEIDAQLARIQ--DELFCV----GAELAT--PH
GEKARSA---------IPAVEPRWAERLEAAI--------------------------DA
WEAELP-PLR------------QFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--RTAAQ-LHLAR---------------CVCRRAERRVVALAA----EAEV----
---------SPVALAYL-------NRLS-------DL-------------LF--VAARVA
N--HRAR--KPETA----------------------------------------------
----------------------------------WDPHRER-------------------
------------------------------------------------------
>gi|16803249|ref|NP_464734.1| hypothetical protein lmo1209 [Listeria monocytogenes
EGD-e]
------------------------------------------------------------
----MRIYTKT--GDKGMTRI--IGGSKVSKDNIRI--DAYGTLDELNSLIGYTITT---
--------------LGAE---------PEIQAELEQIQ--QQLFDA----GGDLAT--EE
GKR-------------AYKLTSEPVAWLEDRI--------------------------DI
YADEPP-EIE------------KFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--QAASL-LHMAR---------------TVTRRAEREIVGMLK----IASS----
---------NEEVLKYV-------NRLS-------DY-------------FF--AVARVV
N--YRAG--ETDIF----------------------------------------------
----------------------------------YKNSELVFRNKKK-------------
------------------------------------------------------
>gi|46907428|ref|YP_013817.1| ATP:cob(I)alamin adenosyltransferase, putative
[Listeria monocytogenes str. 4b F2365]
------------------------------------------------------------
----MRIYTKT--GDKGMTRI--IGGSKVSKDNIRI--DAYGTLDELNSLIGYTITT---
--------------LGAE---------PEIQAELEQIQ--QQLFDA----GGDLAT--EE
GKR-------------AYKLTSEPVAWLEDRI--------------------------DI
YADEPP-EIE------------KFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--QAASL-LHMAR---------------TVTRRAEREIVGMLK----IASS----
---------NEEVLKYV-------NRLS-------DY-------------FF--AVARVV
N--YRAG--EKDIF----------------------------------------------
----------------------------------YKNSELVFRNKKK-------------
------------------------------------------------------
>gi|85375662|ref|YP_459724.1| hypothetical protein ELI_14175 [Erythrobacter
litoralis HTCC2594]
------------------------------------------------------------
MVRLNKIYTRT--GDDGTTGL--VDGSRRAKHDVRM--TAIGVVDEANSAIGLA-AV---
--------------SLER---------SDHAPMLFRIQ--NDLFDL----GADLAT--PG
EDFEPGEM--------TLRMVPEQVDWIEQRI--------------------------DA
LNERLE-PLA------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--EAAAR-LHVAR---------------ATTRAAERAMAALAQ----SEPV----
---------NPAALAYI-------NRLS-------DL-------------LF--VLARVA
N---DDG--KTDVN----------------------------------------------
----------------------------------WVPGANR-------------------
------------------------------------------------------
>gi|51891750|ref|YP_074441.1| putative cobalamin adenosyltransferase
[Symbiobacterium thermophilum IAM 14863]
------------------------------------------------------------
-MRPMRIYTRT--GDKGDTSL--RWGERVPKNALRV--EVYGTVDEANAHVGMA-VAMME
--------------GPAF---------AAVRDVLLRVQ--NELFYV----GADLAT--PP
NRDRGE----------QPRITQASVDALEADI--------------------------DR
LEAGLP-PLR------------NFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
```

```
G--GS--APAAA-LHVAR---------------TVVRRAERLLVSLMQ----QEPV----
---------DPALLRYL-------NRLS-------DL-------------LF--VAARAA
N--QAAG--HGDVL----------------------------------------------
--------------------------------VDWNRSS---------------------
------------------------------------------------------
>gi|150004033|ref|YP_001298777.1| hypothetical protein BVU_1468 [Bacteroides
vulgatus ATCC 8482]
------------------------------------------------------------
-MKKSMIYTKT--GDKGTTSL--VGGTRVPKTHIRL--EAYGTVDELNSYLGLL-QT-YL
--------------TDEE---------DK--QIIFRIQ--NKLFSV----GSYLAT--DQ
TQTKLRM---------ESRIEDEDIRMLEQAI--------------------------DV
IDNELP-PLN------------AFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GD--RGAAV-GHICR---------------TVCRRAERRILALAE----ECDI----
---------DARVTAFV-------NRLS-------DY-------------LF--ILTRKL
N--HLTK--TDEIF----------------------------------------------
----------------------------------WDKSCK--------------------
------------------------------------------------------
>gi|156743715|ref|YP_001433844.1| ATP--cobalamin adenosyltransferase [Roseiflexus
castenholzii DSM 13941]
------------------------------------------------------------
-MTGMKIYTRT--GDEGETGL--WGGLRVPKDAPRV--QAYGTVDECNAAIGVA-RS---
--------------AGVD---------TYLDALLARVQ--SDLFVV----GADLAT--PG
EAAN------------IPRIGADAVQALEQAI--------------------------DE
LEAQLE-PLR------------QFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GA--PSAAY-LHLAR---------------TICRRAERRVVTLSR----SEPV----
---------NPQITIYL-------NRLS-------DF-------------LF--VAARCA
N--ASAG--VPDVP----------------------------------------------
----------------------------------WESPRMRKEAKDE-------------
------------------------------------------------------
>gi|159900211|ref|YP_001546458.1| ATP--cobalamin adenosyltransferase [Herpetosiphon
aurantiacus ATCC 23779]
------------------------------------------------------------
MPRITKVYTRT--GDNGTTAL--GGGQRVPKESLRV--TAFGTVDELNSNLGVA-LA-VG
--------------VSER---------LQ--APLQAIQ--NELFHL----GSDLCM--LE
EDKQKWP---------IPQIEARHIEALEQLM--------------------------DE
LMDAVG-PLE------------NFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--QTSAH-LHVAR---------------TVCRRAERDVVALSR----EETI----
---------GSFVIKYL-------NRLS-------DA-------------LF--VMARYE
N--FVRN--VPDVI----------------------------------------------
----------------------------------WDSRA---------------------
------------------------------------------------------
>gi|160902345|ref|YP_001567926.1| ATP--cobalamin adenosyltransferase [Petrotoga
mobilis SJ95]
------------------------------------------------------------
---MVSITTKT--GDKGETSL--WSGERVSKDDLRV--EAYGTVDELNSFLSEA-SH-YL
--------------KSHE---------VK--KIINEVQ--NNLFKV----AGELAS--KS
QTY-------------KYPIQEEDALKITNYV--------------------------YE
FENRLD--LK------------GFVI----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--RT--LQSAK-LDICR---------------TIARRAERRIIALDK----KEPV----
---------SEPLKKYA-------NRLS-------DL-------------LF--VLARFE
EYIE-DK--IEFKK----------------------------------------------
----------------------------------W-------------------------
------------------------------------------------------
>gi|219847175|ref|YP_002461608.1| ATP/cobalamin adenosyltransferase [Chloroflexus
aggregans DSM 9485]
```

```
------------------------------------------------------------
----MKIYTRT--GDTGETGL--FGGPRVRKDVLRV--EAYGTADECNSAIGVA-RA---
--------------AGPD---------PMLDAVLAEVQ--NQLFVV----GADLAS--PN
DSPY------------IPRVSATMTAFLEEQI--------------------------DA
METELA-PLQ------------QFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--TVAAY-LHLAR---------------TICRRAERVVVSLAA----EEAI----
---------NPELLPYL-------NRLS-------DF-------------LF--VAARIA
N--ARAG--VDDVP----------------------------------------------
----------------------------------WRKP----------------------
------------------------------------------------------
>gi|170740251|ref|YP_001768906.1| ATP--cobalamin adenosyltransferase
[Methylobacterium sp. 4-46]
------------------------------------------------------------
MVVLNRIYTRT--GDAGTTAL--ASGERRSKADLRI--ETYGTVDETNACLGLARQH---
--------------TTGE-----------LDAMLSRAQ--NDLFDL----GADLAT--PE
SDQPLPYE--------PLRLVAAQVERVEREI--------------------------DA
LNAALT-PLR------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--PAAAA-LHLAR---------------TVCRRAERLAVALAA--TPGERV----
---------SPVAIQYL-------NRLS-------DF-------------LF--VASRVA
N---DGG--ARDVL----------------------------------------------
----------------------------------WVPGQNRA------------------
------------------------------------------------------
>gi|163939392|ref|YP_001644276.1| ATP--cobalamin adenosyltransferase [Bacillus
weihenstephanensis KBAB4]
------------------------------------------------------------
----MKLYTKT--GDKGETSV---IGGRVDKDHIRV--EAYGTIDEANSHIGYA-MS-KL
QE-------------ECF---------RNIYNELENIQ--HELFDC----GGDLAI--V-
EKKI------------PYKVTIEMVEYLERRI--------------------------DS
YTEEAP-PLE------------RFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--EISAA-LHIAR---------------TVIRRAERCIVSLQK----EGET----
---------NEIVLKYV-------NRLS-------DY-------------LF--ALARVI
N--ARLQ--VKDVE----------------------------------------------
----------------------------------YNRSALVFRNKEEKEVE---------
------------------------------------------------------
>gi|197106610|ref|YP_002131987.1| hypothetical protein PHZ_c3149 [Phenylobacterium
zucineum HLK1]
------------------------------------------------------------
MVTLNRIYTRT--GDQGTTRL--ATGEPVSKAAARV--EAYGAVDETNACLGMARVH---
--------------TAAD---------PELDTLLARLQ--NELFDL----GADLAT--PP
RPDEAEGA--------VLRVSDRQVERLEAEI--------------------------DA
LNDRLP-PLQ------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GT--PAAAA-LHLAR---------------TVCRRAEREAVRLVE---AGETV----
---------SPAALRYL-------NRLS-------DL-------------LF--VAARAA
N---DLG--RSEVF----------------------------------------------
----------------------------------WKSGATR-------------------
------------------------------------------------------
>gi|114327537|ref|YP_744694.1| protein glcG [Granulibacter bethesdensis CGDNIH1]
------------------------------------------------------------
-----------------MITL---------EDAVRI----ATAAEKHARKIGQP-MN---
----------------------------------------IAIVDG----GGNLKL----
----------------HHRMDDAWLGSIDISI--------------------------NK
AFTARAFDIS------------TKDL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------A
G--NA--QPGQQ-FY------------------GIQQSNHGRVMIFAG------------
```

```
----------GIPLRRD-------GKVV------GG--------------VG--ISGGSG
EQDQSVAEAAAAAF----------------------------------------------
----------------------------------EQTGAKPPAPKTKA------------
------------------------------------------------------
>gi|108760949|ref|YP_634078.1| putative ATP:cob(I)alamin adenosyltransferase
[Myxococcus xanthus DK 1622]
------------------------------------------------------------
----MKIYTKS--GDAGETGL--FGGGRVAKDDVRV--DAYGEVDELNATLGLV-RS---
--------------FEGP---------PDVDALLHRLQ--DQLFTV----GAVLAT--PE
GTKASAH---------IPELKAEWAEDMERAI--------------------------DG
FEAELP-PMT------------HFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--QAASA-LHLAR---------------TVCRRAERRTVPLLR----EGKI----
---------PKAVVVYL-------NRLS------DL--------------LF--VLARVV
N--HRAS--VEDVK----------------------------------------------
----------------------------------WIPAKPSK------------------
------------------------------------------------------
>gi|42780677|ref|NP_977924.1| ATP:cob(I)alamin adenosyltransferase, putative
[Bacillus cereus ATCC 10987]
------------------------------------------------------------
----MKLYTKT--GDKGTTSV---IGGRVDKDNIRV--EAYGTIDEANSHIGYAMTK---
--------------LQGG-------SFGDIYNELETIQ--HELFDC----GGDLAI--VG
EKI-------------PYKVKIEMVENLESRI--------------------------DS
YIEEAP-PLE------------RFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--ESAAA-IHIAR---------------TVVRRAERCIVSLQK----EGEI----
---------NEVVLKYV-------NRLS------DY--------------LF--AVARVI
N--ARLQ--VKDVE----------------------------------------------
----------------------------------YNRSAIVFRDKKEKEVE---------
------------------------------------------------------
>gi|212638891|ref|YP_002315411.1| ATP-binding cobalamin adenosyltransferase
[Anoxybacillus flavithermus WK1]
------------------------------------------------------------
-MIRMKLYTKT--GDKGQTSL---VGGRVDKNDVRV--EAYGTIDEANSMIGWAMTL---
--------------LQDE-------KFRDIYQELQRIQ--HELFDC----GGDLAI--VG
EKI-------------PYKVKAEMVTFLEERI--------------------------DA
YIQQAP-PLE------------RFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--PQAAA-LHMAR---------------TVTRRAERCVVALMK----QQQT----
---------NEVVLQYM-------NRLS------DY--------------LF--AVARVV
N--ARLQ--VKDVE----------------------------------------------
----------------------------------YERSAIVFRDKNEKKGESE-------
------------------------------------------------------
>gi|116250077|ref|YP_765915.1| hypothetical protein RL0309 [Rhizobium leguminosarum
bv. viciae 3841]
------------------------------------------------------------
---------MP--RTLNTLTL---------SDAKQM----LQAGEAKAANLGIP-YN---
----------------------------------------IAVVDA----GGALIA----
----------------FTRQDGALAGSIDLAI--------------------------GK
AKTARLFDKT------------TEYL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------A
E--LA--QPGAP-LF------------------GIEQSNGGNVVIFGG------------
----------GLPVKYD-------NQII------GA--------------VG--TSAGSV
EQDIAVAVAAAEAI----------------------------------------------
-----------------------------------SPNAKP-------------------
------------------------------------------------------
>gi|114797243|ref|YP_762132.1| putative ATP:cob(I)alamin adenosyltransferase
[Hyphomonas neptunium ATCC 15444]
------------------------------------------------------------
```

```
MVRIDKIYTRT--GDKGQTRL--STGEQVPKWHPRV--AAYGTVDELNAAVGVAALE---
--------------AGSD---------ML--ARIRRIQ--NDLFDL----GADLAT--PD
RGRVLEWT--------PLRIIATQVTRLEEEI--------------------------DA
MNAAIA-PLD------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--RLAAQ-LHVAR---------------TLCRRAERYMAELAS--LENEPV----
---------NAEALAFI-------NRLS-------DW-------------LF--VAGRAA
N---NDG--ADDVK----------------------------------------------
----------------------------------WVPGANR-------------------
------------------------------------------------------
>gi|110668230|ref|YP_658041.1| atp-binding cobalamin adenosyltransferase
[Haloquadratum walsbyi DSM 16790]
------------------------------------------------------------
----MKIYTKR--GDSGQTDL--RDMSRISKQHPRI--EAYGNADELNSLLGTV-RP---
-T------------GYDD---------ID--TILHSIQ--NHLHIV----QADFAN--PD
PDEDD------------PTVDMSHVEELEEWI--------------------------DT
IDEELE-PLE------------DFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GA--EAGAK-LHHAR---------------AVCRRAERRAVSFES---EVEDM----
---------NNVAVTYL-------NRLS-------DL-------------LF--TLARVT
N--QRDDVAEENPT----------------------------------------------
----------------------------------Y-------------------------
------------------------------------------------------
>gi|154687429|ref|YP_001422590.1| YvqK [Bacillus amyloliquefaciens FZB42]
----------------------------------------------------MCKSGGRR
RNTTMKLYTKT--GDKGQTSL--IGG-RTDKDSLRV--ESYGTIDELNSFIGLA-LA-EL
DD------------CENC---------GDVKAELRNIQ--HELFDC----GGDLAT--V-
TEHR------------SYTLRETSISALEDCI--------------------------DR
YTAEAP-PLE------------KFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GH--KAAAQ-LHIAR---------------TVTRRAERLVVKLGK----TEEI----
---------NDTVMRYL-------NRLS-------DY-------------FF--AAARAV
N--ARQG--VQDIE----------------------------------------------
----------------------------------YERSAAVFRDDE--------------
------------------------------------------------------
>gi|77164385|ref|YP_342910.1| cobalamin adenosyltransferase [Nitrosococcus oceani
ATCC 19707]
-----------------------------------------------------------M
GYRLSKIYTRT--GDQGTTGL--GPKQRVPKDHPRI--EAIGTIDELNALLGLL-LA--H
-S------------IPHS---------LH--QSLTPIQ--HELFDL----GGELSI--PP
----------------TLIIQASQVQALERLL--------------------------DN
LNEELP-PLK------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--IPAGI-CHLAR---------------TTCRRAERRLVSLAK----EESV----
---------NAESLKYL-------NRLS-------DL-------------LF--VMAREL
T--RTAG--AKEIL----------------------------------------------
----------------------------------WEKHR---------------------
------------------------------------------------------
>gi|66769737|ref|YP_244499.1| hypothetical protein XC_3435 [Xanthomonas campestris
pv. campestris str. 8004]
-----------------------------------------------------------M
GNRLSRIYTRT--GDDGSTGL--GDGSRTGKDALRV--NAYGTVDEANSAIGVL-LA--A
PN------------VPEP---------VA--ALLTTVQ--HQLFDL----GGELCI--PG
----------------HAAIDADDIAALERQL--------------------------DH
FNDDLP-ALK------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GG--EAAAR-CHLAR---------------TIVRRAEREAVALSR----QEPV----
---------RSEAIGYL-------NRLS-------DL-------------LF--VLARVL
```

```
A--RADG--QQEVL----------------------------------------------
----------------------------------WRHDRRRG------------------
------------------------------------------------------
>gi|52081804|ref|YP_080595.1| hypothetical protein BL00723 [Bacillus licheniformis
ATCC 14580]
------------------------------------------------------------
----MKLYTKT--GDRGKTSL--IGG-RADKDHLRV--EAYGTLDEANSFIGLA-QS--Y
LK------------AEEA-----LFHDIL--SELTAIQ--HELFDC----GSDLAH--V-
NVQE------------EGKLKAESITMLEERI--------------------------DA
YVEEAP-QLT------------KFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--EAASF-LHAAR---------------TVIRRAERKIVALAK----EEDI----
---------PPLALPYV-------NRLS-------DY-------------LF--AAARIV
N--HRLG--EVDVE----------------------------------------------
----------------------------------YERSADVFRTKKKS------------
------------------------------------------------------
>gi|21230270|ref|NP_636187.1| hypothetical protein XCC0796 [Xanthomonas campestris
pv. campestris str. ATCC 33913]
-----------------------------------------------------------M
GNRLSRIYTRT--GDDGSTGL--GDGSRTGKDALRV--NAYGTVDEANSAIGVL-LA--A
PN------------VPEP---------VA--ALLTTVQ--HQLFDL----GGELCI--PG
----------------HAAIDADDIAALERQL--------------------------DH
FNDDLP-ALK------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GG--EAAAR-CHLAR---------------TIVRRAERETVALSR----QEPV----
---------RSEAIGYL-------NRLS-------DL-------------LF--VLARVL
A--RADG--QQEVL----------------------------------------------
----------------------------------WRHDRRRG------------------
------------------------------------------------------
>gi|124263081|ref|YP_001023551.1| ATP:cob(I)alamin adenosyltransferase [Methylibium
petroleiphilum PM1]
-----------------------------------------------------------M
GKRLTSIVTRT--GDNGTTGL--GDGSRLSKTAPRV--MAMGDVDELNSAVGML-LS-LG
VN------------VDED---------LKTSTLLRTVQ--QDLFDL----GGELSI--PG
----------------YTLLKAERVVALDEWL--------------------------RQ
ANARLP-RLE------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--LAAAQ-AHVAR---------------TVCRRAERSVVALAE----QHPV----
---------NATVLQFL-------NRLS-------DL-------------LF--VLARLV
N--RVAG--GVDEQ----------------------------------------------
----------------------------------WNRSR---------------------
------------------------------------------------------
>gi|222095208|ref|YP_002529268.1| hypothetical protein BCQ_1548 [Bacillus cereus Q1]
------------------------------------------------------------
----MKLYTKT--GDKGTTSV---IGGRVDKDNIRV--EAYGTIDEANSHIGYAMTK---
--------------LQGG-------SFGDIYNELETIQ--HELFDC----GGDLAI--VG
EKI-------------PYKVKIEMVENLESRI--------------------------DS
YIEEAP-PLE------------RFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--ESAAA-IHIAR---------------TVVRRAERCIVSLQK----EGEI----
---------NAVVLKYV-------NRLS-------DY-------------LF--AVARVI
N--ARLQ--VKDVE----------------------------------------------
----------------------------------YNRSAIVFRDKKEKEVE---------
------------------------------------------------------
>gi|170749366|ref|YP_001755626.1| ATP--cobalamin adenosyltransferase
[Methylobacterium radiotolerans JCM 2831]
------------------------------------------------------------
MVKLNRIYTRT--GDKGTTAL--ADGQRRSKADLRV--ETYGTVDETNACIGMARLH---
--------------TQGP---------LD--GMLGAIQ--NDLFDL----GADLAT--PP
```

```
TPEPLPYE--------PLRIVASQVDRLERDI--------------------------DA
LNAAIP-PLK------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--PAAAA-LHLAR---------------TVCRRAERLAVSLAA--REGETV----
---------SPEALRYL-------NRLS-------DF-------------LF--VASRAA
N---ADG--ADDVL----------------------------------------------
----------------------------------WVPGANR-------------------
------------------------------------------------------
>gi|148556013|ref|YP_001263595.1| ATP:cob(I)alamin adenosyltransferase [Sphingomonas
wittichii RW1]
------------------------------------------------------------
MVRLTKIYTRT--GDRGETGL--VDGSRLPKSAPRM--AAIGDVDELNSAIGVA-LT---
------------HDLPED---------AR--AQLGRIQ--NELFDL----GADFAT--PG
PDYAPSEM--------SLRIVPSQVERLEAEI--------------------------DA
MNADLE-SLR------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GD--PGAAA-IHLAR---------------AICRRAERSAVTADA----DVGL----
---------NPTGLAYI-------NRLS-------DH-------------LF--VLARWL
N---RAG--AGDIL----------------------------------------------
----------------------------------WKPGATR-------------------
------------------------------------------------------
>gi|116619267|ref|YP_821423.1| ATP:cob(I)alamin adenosyltransferase [Solibacter
usitatus Ellin6076]
--------------------------------MFFSAVLCVSAALREKESFMTHDPFNTP
RLAINRVYTRK--GDTGETGL--VGGQRVPKDGPRI--DAYGTVDELNSFLGIA-RA-TA
NQ------------LAVQEP-----RLALLAAILLRVQ--HELFNL----GSILAT--LP
------EDVHPR----QPRVTAAEIAQLESEM--------------------------DA
MNEDLP-PLR------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--RLDAE-LHVGR---------------TVCRRAERIVVALAR----SETV----
---------PPDAIRYL-------NRLS-------DS-------------LF--VWSRWA
N--HITG--TPETL----------------------------------------------
----------------------------------WEPNQSASGRVDNG------------
------------------------------------------------------
>gi|21241640|ref|NP_641222.1| hypothetical protein XAC0870 [Xanthomonas axonopodis
pv. citri str. 306]
-----------------------------------------------------------M
GNRLSRIYTRT--GDDGSTGL--GDGSRTGKDALRV--NAYGTVDEANSAIGVL-LA--A
PG------------VPEP---------IA--ALLTTVQ--HQLFDL----GGELCI--PG
----------------HAAIDATDIQALETQL--------------------------DA
FNQTLP-ALQ------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GG--EAAAR-CHLAR---------------TIVRRAERETVALSR----QEAV----
---------RSEAIGYL-------NRLS-------DL-------------LF--VLARVL
A--RADG--RQEVL----------------------------------------------
----------------------------------WRHDRRRG------------------
------------------------------------------------------
>gi|110639212|ref|YP_679421.1| cobalamin adenosyltransferase [Cytophaga hutchinsonii
ATCC 33406]
------------------------------------------------------------
----MKIYTKG--GDKGKTSL--LGGTRVPKHHIRI--EAYGTTDELNSCIGLL-IE--E
LP------------NDSD---------QK--ALLKTVQ--YKIFEL----GASLAT--EP
DKQQLY----------APDLTEAHIQQLEEAI--------------------------DA
MQAVLP-EQK------------YFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GH--RSVAM-AHLCR---------------TVCRRAERQVVLLNE----KDPV----
---------HPVILPFL-------NRLS-------DY-------------LF--VVSRKL
A--QDFG--ADEVF----------------------------------------------
```

```
----------------------------------WIPEKA--------------------
------------------------------------------------------
>gi|218896507|ref|YP_002444918.1| putative ATP:cob(I)alamin adenosyltransferase
[Bacillus cereus G9842]
------------------------------------------------------------
----MKLYTKT--GDKGTTSV---IGGRVDKDDIRV--EAYGTIDEANSHIGYA-MT-KL
QG-------------RTY---------RDIYNELENIQ--HELFDC----GGDLAI--V-
EQKI------------PYKVTIEMVESLERKI--------------------------DL
YIEEAP-PLE------------RFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--ESAAA-IHIAR---------------TVVRRAERCIVSLQK----EGEI----
---------NEVVLKYV-------NRLS-------DY-------------LF--AVARVI
N--ARLQ--VKDVE----------------------------------------------
----------------------------------YNRSALVFRDKKEKEVE---------
------------------------------------------------------
>gi|91774978|ref|YP_544734.1| ATP:cob(I)alamin adenosyltransferase [Methylobacillus
flagellatus KT]
-----------------------------------------------------------M
GNRLSKIYTRT--GDNGTTGL--GDGSRIEKDSPRV--EAMGCVDELNAALGVL-LA--E
-T------------LPEQ---------IT--QSLTQIQ--HDLFDL----GSEISI--PG
----------------YQRLQTSRVAALEQTL--------------------------DK
LNADLE-PLK------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--RAAAL-CHQAR---------------TICRRAERVLLSLHR----EQVT----
---------SDAALPYL-------NRLS-------DL-------------LF--VMARHL
N--HTAG--RADIL----------------------------------------------
----------------------------------WQNQARILKINITID-----------
------------------------------------------------------
>gi|58583366|ref|YP_202382.1| hypothetical protein XOO3743 [Xanthomonas oryzae pv.
oryzae KACC10331]
-----------------------------------------------------------M
GNRLSRIYTRT--GDDGSTGL--GDGSRTGKDALRV--NAYGTVDEANSAIGLL-LA--A
PG------------MPEP---------IT--VLLTTVQ--HQLFDL----GGELCI--PG
----------------HAAIDAADIEALEHQL--------------------------DA
FNDTLP-ALK------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GG--EAAAR-CHLAR---------------TIVRRAERETVALSR----LEAV----
---------RSEAIGYL-------NRLS-------DL-------------LF--VLARVL
A--RADG--RQEVL----------------------------------------------
----------------------------------WRHDRRRG------------------
------------------------------------------------------
>gi|30019627|ref|NP_831258.1| putative cytoplasmic protein [Bacillus cereus ATCC
14579]
------------------------------------------------------------
----MKLYTKT--GDKGTTSV---IGGRVDKDDIRV--EAYGTIDEANSHIGYA-MT-KL
QG-------------GAF---------IDIYNELENIQ--HELFDC----GGDLAI--V-
EQKI------------PYKVTIVMVESLERKI--------------------------DL
YIEEAP-PLE------------RFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--EAAAT-IHIAR---------------TVVRRAERSIVSLQK----EVKI----
---------NEVVLKYV-------NRLS-------DY-------------LF--AIARVI
N--ARLQ--VKDVE----------------------------------------------
----------------------------------YNRSAVVFRDKKEKEVE---------
------------------------------------------------------
>gi|15599595|ref|NP_253089.1| hypothetical protein PA4399 [Pseudomonas aeruginosa
PAO1]
-----------------------------------------------------------M
GNRLSKIYTRT--GDRGETGL--AGGRRVPKSHPRI--EAIGAVDELNSQLGLL-LA---
-E------------LLEARGAHPGLEEIV--QALAPVQ--HRLFDL----GGELAM--PE
```

```
----------------YRALDETEVARLESCI--------------------------DR
WNDELG-PLK------------NFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--RPVAQ-AHVCR---------------SLARSAERRCQALDQ----EETL----
---------EGVGLRYL-------NRLS-------DL-------------LF--VAARAI
A--RRQG--VAEIL----------------------------------------------
----------------------------------WEAAAKPD------------------
------------------------------------------------------
>gi|220920503|ref|YP_002495804.1| ATP/cobalamin adenosyltransferase
[Methylobacterium nodulans ORS 2060]
------------------------------------------------------------
MVVLNRIYTRT--GDTGTTAL--ASGERRSKADLRI--ETYGTVDETNACVGLARQH---
--------------STGD---------LD--AMLSRIQ--NDLFDL----GADLAT--PE
SDTPPAYE--------PLRIVPEQVERVEREI--------------------------DA
LNAGLQ-PLR------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--AAAAA-LHLAR---------------TVCRRAERLAVALAA--TPGERV----
---------SPVAIQYL-------NRLS-------DF-------------LF--VASRVA
N---DGG--AKDVL----------------------------------------------
----------------------------------WVPGKNRG------------------
------------------------------------------------------
>gi|167645014|ref|YP_001682677.1| ATP--cobalamin adenosyltransferase [Caulobacter
sp. K31]
------------------------------------------------------------
MVTLNRIYTRT--GDKGLTRL--STGQPVSKASLRV--EAYGGVDETNAFIGVARQH---
--------------TKGD---------AELDALLERIQ--NDLFDL----GADLAT--PE
QNEKPAWE--------PLRVVDSQVERLEREI--------------------------DQ
MNSRLS-PLT------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GS--PASAA-LHVAR---------------TVCRRAERKVVELMS--VEGEIV----
---------GEAALKYL-------NRLS-------DL-------------LF--VASRRA
N---DDG--AADVL----------------------------------------------
----------------------------------WKPGATR-------------------
------------------------------------------------------
>gi|218231992|ref|YP_002366259.1| putative ATP:cob(I)alamin adenosyltransferase
[Bacillus cereus B4264]
------------------------------------------------------------
----MKLYTKT--GDKGTTSV---IGGRVDKDDIRV--EAYGTIDEANSHIGYA-MT-KL
QG-------------GAF---------IDIYNELENIQ--HELFDC----GGDLAI--V-
EQKI------------PYKVTIEMVESLEKKI--------------------------DL
YIEEAP-PLE------------RFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--EAAAT-IHIAR---------------TVVRRAERSIVSLQK----EVKI----
---------NEVVLKYV-------NRLS-------DY-------------LF--AIARVI
N--ARLQ--VKDVE----------------------------------------------
----------------------------------YNRSALVFRDKKEKEVE---------
------------------------------------------------------
>gi|56420792|ref|YP_148110.1| hypothetical protein GK2257 [Geobacillus kaustophilus
HTA426]
------------------------------------------------------------
----MKLYTRT--GDQGKTSL--VGG-RVDKDHLRV--EAYGTIDEANSFIGWA-LA-LL
AG------------DERF---------RDLCAELQKIQ--HELFDC----GGDLAI--V-
NGKL------------PYKVTEAMVTFLEERI--------------------------DA
HVQEAP-PLQ------------KFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--KAAAA-LHMAR---------------TVARRAERCIVSLQK----AEPI----
---------NDVVLKYM-------NRLS-------DY-------------LF--AAARVV
N--ARLG--VKDIE----------------------------------------------
```

```
----------------------------------YERSAIVFRDKEEKQ-----------
------------------------------------------------------
>gi|30261574|ref|NP_843951.1| ATP:cob(I)alamin adenosyltransferase, putative
[Bacillus anthracis str. Ames]
------------------------------------------------------------
----MKLYTKT--GDKGTTSV---IGGRVDKDDIRV--EAYGTIDEANSHIGYA-MT-KL
QG-------------GAF---------IDIYNELENIQ--HELFDC----GGDLAI--V-
EQKI------------PYKVTIEMVESLERKI--------------------------DL
YIEEAP-PLE------------RFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--EAAAT-IHIAR---------------TVVRRAERSIVSLQK----EVKI----
---------NEVVLKYV-------NRLS-------DY-------------LF--AIARVI
N--ARLQ--VKDVE----------------------------------------------
----------------------------------YNRSALVFRDKKEKEVE---------
------------------------------------------------------
>gi|124268957|ref|YP_001022961.1| ATP:cob(I)alamin adenosyltransferase [Methylibium
petroleiphilum PM1]
-----------------------------------------------------------M
GNRLTQIATRT--GDDGTTGL--GDGTRVAKDHLRV--QAMGDVDELNSLLGLL-LC--E
-P------------LPDA---------LR--VLLVAVQ--HELFNL----GGELSI--PG
----------------YTLLKDEAVAALDDAL--------------------------AE
HNAALP-RLK------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GT--RSASI-AHLGR---------------TVARRAERAVVALAN--AEPGAV----
---------RSAPRQYL-------NRLS-------DL-------------LF--VLARVL
NRANLDGLGGDDVY----------------------------------------------
----------------------------------WRSPRLETPD----------------
------------------------------------------------------
>gi|16124982|ref|NP_419546.1| hypothetical protein CC_0729 [Caulobacter crescentus
CB15]
------------------------------------------------------------
MVTLNRIYTRT--GDGGTTRL--ATGAPVSKASLRV--DSYGGVDETNAAIGQARQH---
--------------TAAD---------PVLDAILERIQ--NDLFDL----GADLAT--PE
QHGKPEWE--------PLRVVESQVERLEREI--------------------------DQ
LNGEMS-ALT------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--PAAAA-LHVAR---------------TVCRRAERGVVALSE--MDGEIV----
---------GTPAIKYL-------NRLS-------DL-------------LF--VAARWA
N---DKG--QADVL----------------------------------------------
----------------------------------WKPGATR-------------------
------------------------------------------------------
>gi|27381381|ref|NP_772910.1| hypothetical protein blr6270 [Bradyrhizobium japonicum
USDA 110]
------------------------------------------------------------
--MDLLSYAKT--IAERIEAE--ATRARVPMAVCII--DIHGNIILKHRMSGAPTFS-LE
--------------LSERKAYTSALVGLRTAELSPMVQPGQALFPLMGVAGGRFCSM-GG
GAPLHIDGQLVAGVGISGGSVEQDVDILEAGLREPAATDTVDMKIEVVVLPVSDVERAKR
FYADLGWRLDIDYQGPSNYRVIQFTP----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
S-SGCSVIFGSN-LTIAAPGSVKGLHLIVSDIEAACDDLRRRGITVGEPFHDPGGIFHHA
SVQDLAAGPNPQRKSYA-------SYASFSDPDGNGW-------------VFQEITARLT
G--HIED--GDES-----------------------------------------------
----------------------------------FTPELTDVVRRAEAAARASAGAGDRA
AA----------------------------------------------------
>gi|188580955|ref|YP_001924400.1| ATP--cobalamin adenosyltransferase
[Methylobacterium populi BJ001]
------------------------------------------------------------
MVKLNRIYTRT--GDQGTTGL--ANGERRSKADLRV--EAYGTVDETNACIGLARLT---
--------------AEPA---------LD--AMLARIQ--NDLFDL----GADLAT--PP
```

```
SDTPLGYE--------PLRVVAAQVQRLEAEI--------------------------DA
LNANIP-PLK------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--ATAAA-LHLAR---------------TVCRRAERLVVALSG--VESEAI----
---------SAEALQYL-------NRLS-------DF-------------LF--VASRAA
N---RDG--ADDVL----------------------------------------------
----------------------------------WVPGQNR-------------------
------------------------------------------------------
>gi|119899071|ref|YP_934284.1| hypothetical protein azo2781 [Azoarcus sp. BH72]
-----------------------------------------------------------M
GHRLSKIYTRT--GDAGTTGL--GDGKRVSKNSLRI--HSLGEVDEVNAIIGVL-LC--E
-E------------LPED---------VR--ALLTNVQ--HDLFDL----GGEVCI--PG
----------------MSMITGKQVDHLETEL--------------------------DR
LNEPLE-PLK------------DFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--RAAAL-AHHAR---------------TVCRRAERALVALAL----EEAV----
---------NDGPRQYL-------NRLS-------DL-------------LF--VLGRVL
N--RAGG--RGDVL----------------------------------------------
----------------------------------WQKRKNA-------------------
------------------------------------------------------
>gi|49481049|ref|YP_035695.1| hypothetical protein BT9727_1361 [Bacillus
thuringiensis serovar konkukian str. 97-27]
------------------------------------------------------------
----MKLYTKT--GDRGTTSV---IGGRVDKDNIRV--EAYGTIDEANSHIGYAMTK---
--------------LQGG-------AFGDIYNELETIQ--HELFDC----GGDLAI--VG
EKI-------------PYKVKIEMVENLEGRI--------------------------DS
YIEEAP-PLE------------RFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--ESAAA-IHIAR---------------TVVRRAERCIVSLQK----EGEI----
---------NAVVLKYV-------NRLS-------DY-------------LF--AVARVI
N--ARLQ--VKDVE----------------------------------------------
----------------------------------YNRSAIVFRDKKEKEVE---------
------------------------------------------------------
>gi|52143869|ref|YP_082959.1| hypothetical protein BCZK1360 [Bacillus cereus E33L]
------------------------------------------------------------
----MKLYTKT--GDKGTTSV---IGGRVDKDNIRV--EAYGTIDEANSHIGYAMTK---
--------------LQGG-------AFGDIYNELETIQ--HELFDC----GGDLAI--VG
EKI-------------PYKVKIEMVENLEGRI--------------------------DS
YIEEAP-PLE------------RFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--ESAAA-IHIAR---------------TVVRRAERCIVSLQK----EGEI----
---------NAVVLKYV-------NRLS-------DY-------------LF--AVARVI
N--ARLQ--VKDVE----------------------------------------------
----------------------------------YNRSAIVFRDKKEKEVE---------
------------------------------------------------------
>gi|77462237|ref|YP_351741.1| ATP:cob(I)alamin adenosyltransferase [Rhodobacter
sphaeroides 2.4.1]
------------------------------------------------------------
MVVLSRIYTRT--GDAGETAL--GNGARVAKHSPRV--AAYGTVDETNATVGLARLH---
--------------AQGE---------MQ--EALARIS--NDLFDL----GADLCR--PE
MERDHEADYT------PLRIIAAQVNRLEREI--------------------------DG
MNARLE-PLR------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--ALAAQ-LHLCR---------------TVSRRAERELVELAT----VESV----
---------NPEALRYL-------NRLS-------DW-------------FF--VAGRIA
N---DDG--RADVL----------------------------------------------
----------------------------------WVPGLTREA-----------------
------------------------------------------------------
```

```
>gi|218902688|ref|YP_002450522.1| putative ATP:cob(I)alamin adenosyltransferase
[Bacillus cereus AH820]
------------------------------------------------------------
----MKLYTKT--GDKGTTSV---IGGRVDKDNIRV--EAYGTIDEANSHIGYA-MT-KL
QG-------------GVF---------GDIYNELETIQ--HELFDC----GGDLAI--V-
DEKI------------PYKVKIEMVENLEGRI--------------------------DS
YIEEAP-PLE------------RFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--ESAAA-IHIAR---------------TVVRRAERCIVSLQK----EGEI----
---------NAVVLKYV-------NRLS-------DY-------------LF--AVARVI
N--ARLQ--VKDVE----------------------------------------------
----------------------------------YNRSAIVFRDKKEKEVE---------
------------------------------------------------------
>gi|118477034|ref|YP_894185.1| ATP:cob(I)alamin adenosyltransferase [Bacillus
thuringiensis str. Al Hakam]
------------------------------------------------------------
----MKLYTKT--GDKGTTSV---IGGRVDKDNIRV--EAYGTIDEANSHIGYAMTK---
--------------LQGG-------VFGDIYNELETIQ--HELFDC----GGDLAI--VG
EKI-------------PYKVKIEMVENLEGRI--------------------------DS
YIEEAP-PLE------------RFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--ESAAA-IHIAR---------------TVVRRAERCIVSLQK----EGEI----
---------NAVVLKYV-------NRLS-------DY-------------LF--AVARVI
N--ARLQ--VKDVE----------------------------------------------
----------------------------------YNRSAIVFRDKKEKEVE---------
------------------------------------------------------
>gi|89900271|ref|YP_522742.1| cobalamin adenosyltransferase [Rhodoferax
ferrireducens T118]
-----------------------------------------------------------M
GQRLTQIATRT--GDNGTTGL--GDNTRVSKDSLRV--HAMGDVDELNSNIGVL-LC--E
-A------------MPQG---------VR--TLLVEIQ--HQLFNL----GGELSI--PG
----------------FELLKPEAVLALDAAL--------------------------AE
HNEALP-RLQ------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GT--RAASL-AHVCR---------------TVARRAERAVVALEG----QESL----
---------KDTPRQYL-------NRLS-------DL-------------MF--VLARVL
NRYRTDGSVGDDVY----------------------------------------------
----------------------------------WKSEKLARASAD--------------
------------------------------------------------------
>gi|54303335|ref|YP_133328.1| hypothetical protein PBPRB1668 [Photobacterium
profundum SS9]
------------------------------------------------------------
----------------MMISL--DLAKQLTSIAIKQ-----AEQQEFNICVSVV------
--------------------------------------------DL----AGLLVH----
----------------FQRMDDAPLGAIDVAV--------------------------KK
ARTAALFQTN------------SAEL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------G
T--MA--KPGGA-IYTLE-------------------ATNGGLISFGG------------
---------GVMIRNEQ-------GKVI-------GA-------------IG--VAGATL
EADEAIAQFAVQQ-----------------------------------------------
------------------------------------------------------------
------------------------------------------------------
>gi|182411923|ref|YP_001816989.1| ATP--cobalamin adenosyltransferase [Opitutus
terrae PB90-1]
------------------------------------------------------------
----MSIATRT--GDQGMTGL--LYGQRVPKDHPQI--EAVGAFDELNAAVGLA-KA---
--------------ACPD---------TDRRAALEAIQ--HDLIAL----MGEVACAESD
LARYEASK--------FPKLGETELARIDAAV--------------------------AA
IEARKI-RFD------------GWAT----------------------------------
```

```
------------------------------------------------------------
-----------------------------------------------------------P
G--AN--TFAGA-LELAR---------------TVARRAERRLVALKS---HGRTV----
---------RPVVGQYV-------NRVA-------DL-------------LW--LMAREA
E--K--------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------
>gi|171057630|ref|YP_001789979.1| ATP--cobalamin adenosyltransferase [Leptothrix
cholodnii SP-6]
-----------------------------------------------------------M
AHRLTQISTRT--GDDGTTGL--GDGQRVPKDHLRV--QAMGDVDELNSQLGVL-LA--E
-P------------LPAD---------VR--ELLVVIQ--HELFNL----GGELSI--PG
----------------YTLLKTEAVLRLDEAL--------------------------AH
YNAQLP-RLQ------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GT--RSAAL-AHVAR---------------TVARRAERAVVALAA----AEAI----
---------NEAPRHYL-------NRLS-------DL-------------LF--VLARVL
NRANLDGLGGDDVY----------------------------------------------
----------------------------------WHSERLERAQG---------------
------------------------------------------------------
>gi|163859120|ref|YP_001633418.1| hypothetical protein Bpet4799 [Bordetella petrii
DSM 12804]
-----------------------------------------------------------M
GNRLSAVATRT--GDDGTTGL--GDGTRTGKDTPRI--AALGDVDELNSVIGLL-RT--E
-A------------LPDA---------VQ--ADLGVIQ--NDLFDL----GAELCI--PG
----------------HAALDASQLAFLDERL--------------------------AH
YNGGLA-PLR------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GC--RAAAL-AHLAR---------------TVARRAERSVVALGR----ADQV----
---------NAPVRQYL-------NRLS-------DL-------------MF--VLARHL
N--GAHG--AGDVF----------------------------------------------
----------------------------------WTSRHSRVQPQE--------------
------------------------------------------------------
>gi|113869044|ref|YP_727533.1| cobalamin adenosyltransferase [Ralstonia eutropha
H16]
-----------------------------------------------------------M
GNRLSKIATRT--GDAGTTGL--GDGSRTGKASPRI--AAIGDVDELNCHVGVL-LT--E
-A------------LPDD---------VR--AALLHIQ--HDLFDL----GGELSI--PG
----------------YTLLKPEQVAQLDTWL--------------------------AD
YNANLP-RLA------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--RAAAQ-AHVCR---------------TVCRRAERALVALGA----AEPL----
---------NEAPRQYL-------NRLS-------DL-------------MF--VLARVL
N--RAGG--GSDVL----------------------------------------------
----------------------------------WQRDRDAPGGME--------------
------------------------------------------------------
>gi|56475971|ref|YP_157560.1| hypothetical protein ebA1022 [Aromatoleum aromaticum
EbN1]
-----------------------------------------------------------M
GHRLSKIYTRT--GDAGTTGL--GDGKRVAKNSLRI--DTLGEVDELNAVVGLL-LC--E
-D------------LPDD---------VQ--ALLTDVQ--HDLFDL----GGEICI--PG
----------------MSMISQKHVDKLETEL--------------------------DR
LNEPLE-PLK------------DFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--RAAAL-AHLAR---------------TVCRRAERAIVALGQ----EEAI----
---------NDGPRQYL-------NRFS-------DL-------------LF--VLGRVL
N--RAAG--RGDVL----------------------------------------------
----------------------------------WQKGKNA-------------------
------------------------------------------------------
```

```
>gi|189349460|ref|YP_001945088.1| cob(I)alamin adenosyltransferase [Burkholderia
multivorans ATCC 17616]
-----------------------------------------------------------M
GNRLSKIATRT--GDDGTTGL--GDGRRVGKDDARI--AAIGDVDELNSNLGVL-LA--E
-T------------LPDD---------VR--TALVTIQ--HDLFDL----GGELCI--PG
----------------HTVIDDTHLARLDRWL--------------------------AD
YNATLP-PLK------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GS--RAASL-THVCR---------------TVCRRAERSIVALGR----HEAL----
---------NDAPRRYV-------NRLS-------DL-------------LF--VLARVL
N--RAAG--GADVL----------------------------------------------
----------------------------------WERGRVR-------------------
------------------------------------------------------
>gi|161525819|ref|YP_001580831.1| ATP--cobalamin adenosyltransferase [Burkholderia
multivorans ATCC 17616]
MSRRPGSRRPTVRKNGSRFDAVSAHSTLERLLRPSPRAAIIAFQRNRAASRPRTGEDIRM
GNRLSKIATRT--GDDGTTGL--GDGRRVGKDDARI--AAIGDVDELNSNLGVL-LA--E
-T------------LPDD---------VR--TALVTIQ--HDLFDL----GGELCI--PG
----------------HTVIDDTHLARLDRWL--------------------------AD
YNATLP-PLK------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GS--RAASL-THVCR---------------TVCRRAERSIVALGR----HEAL----
---------NDAPRRYV-------NRLS-------DL-------------LF--VLARVL
N--RAAG--GADVL----------------------------------------------
----------------------------------WERGRVR-------------------
------------------------------------------------------
>gi|161528366|ref|YP_001582192.1| ATP--cobalamin adenosyltransferase [Nitrosopumilus
maritimus SCM1]
------------------------------------------------------------
----MKIYTKT--GDDGNTGL--QGNLRISKSHPRI--FAYGAVDEANAALGIV-LT-NS
--------------LDED---------IF--DVLRKIQ--NDLFVV----GSDLSN--PN
LNDV------------KNRVSLEMIQELEQNI--------------------------DK
FESELP-PLT------------NFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--TPTSK-LHYAR---------------TVVRRAETLTVQLAE----KDEI----
---------NSNCIIYL-------NRLS-------DL-------------FF--VMGRLI
N--KRNG--TEDII----------------------------------------------
----------------------------------WKI-----------------------
------------------------------------------------------
>gi|152986291|ref|YP_001350306.1| hypothetical protein PSPA7_4970 [Pseudomonas
aeruginosa PA7]
-----------------------------------------------------------M
GNRLSKIYTRT--GDRGETGL--AGGRRVPKSHPRI--EAIGAVDELNSQLGLL-LA---
-E------------LLEARGAHPGLEEIV--QALAPVQ--HRLFDL----GGELAM--PE
----------------YQALDETEVARLESCI--------------------------DR
WNDELG-PLK------------NFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--RLVAL-AHVCR---------------SLARRAERRCQALDQ----EETL----
---------DGVGLRYL-------NRLS-------DL-------------LF--VAARAI
A--RRQG--VAEIL----------------------------------------------
----------------------------------WEAAAKPD------------------
------------------------------------------------------
>gi|221641192|ref|YP_002527454.1| PduO [Rhodobacter sphaeroides KD131]
------------------------------------------------------------
MVVLSRIYTRT--GDAGETAL--GNGARVAKHSPRV--AAYGSVDETNATVGLARLH---
--------------AQGE---------MQ--EALARIS--NDLFDL----GADLCR--PE
MERDHEADYT------PLRIIAAQVNRLEREI--------------------------DG
MNARLE-PLR------------SFIL----------------------------------
------------------------------------------------------------
```

```
-----------------------------------------------------------P
G--GS--ALAAQ-LHLCR---------------TVSRRAERELVELAT----VESV----
---------NPEALRYL-------NRLS-------DW-------------FF--VAGRIA
N---DDG--RADVL----------------------------------------------
----------------------------------WVPGLTREA-----------------
------------------------------------------------------
>gi|218529796|ref|YP_002420612.1| ATP/cobalamin adenosyltransferase
[Methylobacterium chloromethanicum CM4]
------------------------------------------------------------
MVKLNRIYTRT--GDQGTTGL--ANGERRSKADLRV--EAYGTVDETNACIGLARLT---
--------------AEPA---------LD--AMLARIQ--NDLFDL----GADLAT--PP
SDKPLGYE--------PLRIVPTQVQRLETEI--------------------------DA
LNANIP-PLK------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--AAAAA-LHLAR---------------TVCRRAERLVVALSG--VESEAI----
---------SGEALQYL-------NRLS-------DF-------------LF--VASRAA
N---RDG--ADDVL----------------------------------------------
----------------------------------WVPGQNR-------------------
------------------------------------------------------
>gi|163850968|ref|YP_001639011.1| ATP--cobalamin adenosyltransferase
[Methylobacterium extorquens PA1]
-----------------------------------------------------MARGRDA
VVKLNRIYTRT--GDQGTTGL--ANGERRSKADLRV--EAYGTVDETNACIGLARLT---
--------------AEPA---------LD--AMLARIQ--NDLFDL----GADLAT--PP
SDKPLGYE--------PLRIVPAQVQRLETEI--------------------------DA
LNANIP-PLK------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--AAAAA-LHLAR---------------TVCRRAERLVVALSG--VESEAI----
---------SGEALQYL-------NRLS-------DF-------------LF--VASRAA
N---RDG--ADDVL----------------------------------------------
----------------------------------WVPGQNR-------------------
------------------------------------------------------
>gi|32472259|ref|NP_865253.1| hypothetical protein RB2976 [Rhodopirellula baltica SH
1]
------------------------------------------------------------
----MKIYTRT--GDSGTTGL--FGGPRVAKDDTRI--EAYGTVDELNATLGQV-RS--A
-LKESAGEATAANDGLSE---------LD--ARIAQVQ--HELFSI----GAELAS--PH
------PDQFD-----LRVIGPVHIQRIEDWI--------------------------DD
AEQQLP-PLK------------QFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--ILASH-VHLSR---------------AVCRRAERRVISLADAVQTETPI----
---------SDTVIIYL-------NRLS-------DW-------------LF--VVSRLV
N--QILN--VPDQI----------------------------------------------
----------------------------------WEKP----------------------
------------------------------------------------------
>gi|126461099|ref|YP_001042213.1| ATP--cobalamin adenosyltransferase [Rhodobacter
sphaeroides ATCC 17029]
------------------------------------------------------------
MVVLSRIYTRT--GDAGETAL--GNGARVAKHSPRV--AAYGSVDETNATVGLARLH---
--------------AQGE---------MQ--EALARIS--NDLFDL----GADLCR--PE
MERDHEADYT------PLRIIAAQVNRLEREI--------------------------DG
MNARLE-PLR------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--ALAAQ-LHLCR---------------TVSRRAERELVELAT----AESV----
---------NPEALRYL-------NRLS-------DW-------------FF--VAGRIA
N---DDG--RADVL----------------------------------------------
----------------------------------WVPGLTREA-----------------
------------------------------------------------------
>gi|103488562|ref|YP_618123.1| cobalamin adenosyltransferase [Sphingopyxis
```

```
alaskensis RB2256]
------------------------------------------------------------
MVKLNKIYTRT--GDDGTTGL--VGGSRIAKSAPLM--AAIGDVDEANSWVGLAAVA---
--------------LDEA---------PDAAAMLTRIQ--NELFDL----GADLAT--PP
DAERGFGPHDM-----ALRIVPGQIARLEEEI--------------------------DA
MNAALD-ALK------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--EAAAR-LHLAR---------------AVTRRAERSAVAAAA----DRAL----
---------NPLALTYL-------NRLS-------DH-------------LF--VLARSI
N-----GAAGGDVL----------------------------------------------
----------------------------------WKPGATR-------------------
------------------------------------------------------
>gi|76802145|ref|YP_327153.1| hypothetical protein NP3008A [Natronomonas pharaonis
DSM 2160]
------------------------------------------------------------
----MKIYTGR--GDEGMTDL--RDMSRVSKTSARI--EAYGTVDEVNSLVGMV-RP---
-S------------GHDD---------VD--EKLAAVQ--NHLHII----QADFAN--PD
ADDPD-----------APHIEADHVERLESWM--------------------------DD
FDDELD-PLE------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--DTGAK-LHHAR---------------SVCRRAERRAVALAS----DEPV----
---------NDAAVAYL-------NRLS-------DA-------------LF--VWARVV
N--KRDGVREESPS----------------------------------------------
----------------------------------Y-------------------------
------------------------------------------------------
>gi|125717347|ref|YP_001034480.1| ATP:cobalamin adenosyl transferase, putative
[Streptococcus sanguinis SK36]
------------------------------------------------------------
----MRIYTKY--GDKGFTRL--YGGDRVSKTHIRV--EAYGTMDELCSHLGYV-VS--E
MR------------DYPV------LDDLR--LECEEIQ--QHLFDC----GSDLAT--P-
RELR------------PYKQEPANVSWLEERM--------------------------DE
YMHIPP-KID------------RFII----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GH--RIASL-LHVAR---------------TMTRRLERRMVAVIE---ADEAV----
---------NEIGLIYI-------NRLS-------DY-------------FF--VLARLV
N--DRLE--EPDTI----------------------------------------------
----------------------------------YKRSAKIFREKK--------------
------------------------------------------------------
>gi|57640980|ref|YP_183458.1| cobalamin adenosyltransferase [Thermococcus
kodakarensis KOD1]
------------------------------------------------------------
----MSITTKT--GDKGLTGL--FTGDRVAKFSPIM--EANGTIDELDSFIGEA-KH--Y
--------------VPEE---------MA--ETLERIQ--VQLYDL----MAELAS--KG
K---------------YSKVSEEDVKWLEGFI--------------------------HK
YEEEVQ--LK------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--ST--IASAK-LDVCR---------------AIARRAERRVAKLVL----DYGF----
---------GQNALVYL-------NRLS-------DL-------------LF--IMARAI
E--KREG-KLKEVK----------------------------------------------
------------------------------------------------------------
------------------------------------------------------
>gi|188995125|ref|YP_001929377.1| probable cobalamin adenosyltransferase
[Porphyromonas gingivalis ATCC 33277]
------------------------------------------------------------
-----MIYTKT--GDKGTTGI--FGGERVPKDDVRV--EAYGTMDELNAAIGMIRTF---
--------------LPEE---------DERQTVLYDIQ--MRMMAA----MSIVAT--PA
GKREQN----------PNHFPEEAAADCEAFI--------------------------DR
LLAETT-DNG------------YFIL----------------------------------
------------------------------------------------------------
```

```
-----------------------------------------------------------P
G--GT--PLSAH-LQLAR---------------TIARRAERRLWTLHR----SDEV----
---------PDAILKWM-------NRLS-------DL-------------FF--VMARHE
M--QQQG--WSEEK----------------------------------------------
----------------------------------WHRFAYKRKKK---------------
------------------------------------------------------
>gi|186477260|ref|YP_001858730.1| ATP--cobalamin adenosyltransferase [Burkholderia
phymatum STM815]
-----------------------------------------------------------M
GNRLSKISTRT--GDDGTTGL--GDGSRVRKDDARI--AAIGDVDELNSNIGVL-LC--E
-T------------LPND---------LR--VALTAIQ--HDLFDL----GGELCI--PG
----------------HSMIADAHLAQLDSWL--------------------------AE
YNATLP-PLR------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GT--RAASL-AHVCR---------------TVCRRAERSIVALGA----VDAI----
---------NDAPRRYV-------NRLS-------DL-------------LF--VLARVL
N--RVDG--GDDVL----------------------------------------------
----------------------------------WRHDRSAQKDDAQSGE----------
------------------------------------------------------
>gi|66047317|ref|YP_237158.1| hypothetical protein Psyr_4090 [Pseudomonas syringae
pv. syringae B728a]
-----------------------------------------------------------M
GFRLSKIYTRT--GDAGETGL--GDGRRVSKDHPRV--EAIGEVDTLNSQLGLL-LA---
-G------------LIDEAQRVPALNEVI--EVLAPCQ--HRLFDL----GGELAM--PT
----------------YKALNEAEVERLEAAI--------------------------DV
WNEELG-PLE------------NFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--SLIAQ-AHICR---------------SLARSAERRCQHLNA----VEPL----
---------EGAGLAYI-------NRLS-------DL-------------LF--VAARLI
A--RRQG--ISEIL----------------------------------------------
----------------------------------WQPAPKPL------------------
------------------------------------------------------
>gi|120556212|ref|YP_960563.1| hypothetical protein Maqu_3305 [Marinobacter
aquaeolei VT8]
------------------------------------------------------------
-----------------MMTI-----KRLDISDARL--LIKGAADKARD-IGVP-MC---
----------------------------------------IAVVDE----SGNLVA----
----------------FERMDGGKTTSVIIAQ--------------------------DK
AFTAAAARKA------------THDY----------------------------------
------------------------------------------------------------
-----------------------------------------------------------N
A--AN--VPGNL-AF------------------GIHTEVGGRLSTVGG------------
---------GLPVIVD--------GEVV-------GG-------------IG--LSSGTP
RQDMDCAQAGIDYF----------------------------------------------
----------------------------------LSNR----------------------
------------------------------------------------------
>gi|189500448|ref|YP_001959918.1| ATP/cobalamin adenosyltransferase [Chlorobium
phaeobacteroides BS1]
------------------------------------------------------------
----MKIYTRT--GDEGTTGL--FGGSRVDKDDIRV--ECYGTFDEVNSYIGLLRAK---
--------------LPVD---------HPWQERLQEVQ--IAFMNM----MSHLAT--PS
DAEKPN----------SVILPIDGAAFCERWI--------------------------DE
LEEMAG-PSD------------CFLL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--EISAL-CHVVR---------------TQVRRGERILVRLIK----QDNV----
---------HPSIPVYV-------NRLS-------DL-------------FF--ALARAE
M--AGAG--VEEER----------------------------------------------
----------------------------------WNSFIYKMKKST--------------
------------------------------------------------------
>gi|217979910|ref|YP_002364057.1| ATP/cobalamin adenosyltransferase [Methylocella
```

```
silvestris BL2]
------------------------------------------------------------
MVVLNRIYTRT--GDAGQTSL--GTGERRPKNDLRV--EVYGTIDEANCAIGLARVATSK
--------------DPAC---------ARVDAMLLCVQ--NDMFDL----GADLCV--PE
TEPIPQYE--------PLRIVQAQVDRLERKI--------------------------DD
LNAELP-PLM------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--SAAAS-LHLAR---------------TITRRAERLLVALAA--VPNEHV----
---------GEPALKYV-------NRLS-------DF-------------LF--VAARYV
N---RKG--DGDIL----------------------------------------------
----------------------------------WVPGQNR-------------------
------------------------------------------------------
>gi|146283484|ref|YP_001173637.1| ATP:cob(I)alamin adenosyltransferase, putative
[Pseudomonas stutzeri A1501]
-----------------------------------------------------------M
GNRLSKIYTRT--GDSGETGL--GDGRRVAKDHPRV--EAMGEVDTLNSQLGLL-LA---
-E------------LADAQVQWPALNELI--SVFGPCQ--HRLFDL----GGELAM--PD
----------------YQALQESEIERLEQAI--------------------------DR
WNQELG-PLK------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--RLIAL-AHLCR---------------SVTRTAERRCQQLNA----SETV----
---------RPMLLAYL-------NRLS-------DA-------------LF--VAARLI
A--RRQG--CGEIL----------------------------------------------
----------------------------------WQPAAAAAGADD--------------
------------------------------------------------------
>gi|187476655|ref|YP_784678.1| ATP:cob(I)alamin adenosyltransferase [Bordetella
avium 197N]
-----------------------------------------------------------M
ANRLSVITTRT--GDDGSTGL--GDGSRVPKDDPRI--MALGDVDEFNSTLGLL-RC--E
-A------------LPDE---------VS--ADLLTIQ--HDLFDM----GAELCI--PG
----------------HAALSDEQVAYLDARL--------------------------AF
YNAALP-PLR------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--RAAAL-AHLAR---------------TAARRAERSVIALAA----QAAV----
---------NAPLCQYL-------NRSS-------DL-------------MF--VLARYL
N--QSQG--QADIY----------------------------------------------
----------------------------------WSSRHSRVSGA---------------
------------------------------------------------------
>gi|116254052|ref|YP_769890.1| putative cobalamin adenosultransferase [Rhizobium
leguminosarum bv. viciae 3841]
------------------------------------------------------------
MVKLNKIYTKT--GDDGTTGL--VSGPRRLKDDLRV--EAYGTIDEANSAIGLARLH---
--------------TADL---------PELDAMLMSIQ--NDLFDL----GADLAT--PD
TGEPPAYE--------PLRIAETQVDRVERDI--------------------------DQ
LNAGLE-PLK------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--PAAAH-LHLAR---------------TIARRAERLMVALAR--TDGEIV----
---------GEPAMKYV-------NRLS-------DF-------------LF--VAARHA
N---DRG--HADVL----------------------------------------------
----------------------------------WVPGKNR-------------------
------------------------------------------------------
>gi|104783441|ref|YP_609939.1| Cob(I)yrinic acid a,c-diamide adenosyltransferase
[Pseudomonas entomophila L48]
-----------------------------------------------------------M
GYRLSKIYTRT--GDKGETGL--GDGRRVPKDHPRI--EAIGEVDSLNSQLGVL-LA---
-G------------LADA-----GLTEVF--EVLAPCQ--HRLFDL----GGELAM--PS
----------------YQALNVAEVERLEAAI--------------------------DR
WNEELG-PLK------------NFIL----------------------------------
------------------------------------------------------------
```

```
-----------------------------------------------------------P
S--GS--ALVAQ-AHVCR---------------SQARAAERRCQQLNA----VEPL----
---------EGVGLAYI-------NRLS-------DL-------------LF--VAARII
G--RRQG--VAEVL----------------------------------------------
----------------------------------WQPAGKPQA-----------------
------------------------------------------------------
>gi|87198577|ref|YP_495834.1| ATP:cob(I)alamin adenosyltransferase [Novosphingobium
aromaticivorans DSM 12444]
------------------------------------------------------------
MVKLNKIYTRT--GDDGTTGL--VDGSRRAKHDARM--QAIGDVDEANSLIGLA-AV--A
---------S-----PVA---------TA--RDLQRIQ--NDLFDL----GADLAT--PG
-ED------FAPSEMVLRVV-PSQVAWLETAI--------------------------DA
LNEALP-PLT------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--EVAAR-VHVAR---------------AVVRRAERSAVALAS----VEPV----
---------NAQALAYL-------NRLS-------DY-------------LF--VLARAT
N-------AGGDPL----------------------------------------------
----------------------------------WVPGASR-------------------
------------------------------------------------------
>gi|83719852|ref|YP_441840.1| ATP:cob(I)alamin adenosyltransferase, putative
[Burkholderia thailandensis E264]
-----------------------------------------------------------M
GNRLSKIATRT--GDDGTTGL--GDGSRVRKDDARI--AAIGDVDELNSQIGVL-LA--E
-P------------LPDD---------VR--AALSAIQ--HDLFDL----GGELCI--PG
----------------HAAITDAHLARLDGWL--------------------------AH
YNGQLP-PLE------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GA--RGAAL-AHVCR---------------TVCRRAERSIVALGA----SEPL----
---------NAAPRRYV-------NRLS-------DL-------------LF--VLARVL
N--RAAG--GADVL----------------------------------------------
----------------------------------WDRTRAH-------------------
------------------------------------------------------
>gi|46446375|ref|YP_007740.1| hypothetical protein pc0741 [Candidatus Protochlamydia
amoebophila UWE25]
------------------------------------------------------------
----MKIYTRT--GDKGTTSL--FTGKRVSKNDVFI--ETLGTVDEGNSSIGMA-IS---
-L------------LPKE----PFYQQIK--EQLEVIQ--HALFDV----GAALAT--PR
TSQHAKKLE-------KTRFDQEEIRLVEKWI--------------------------DQ
METELP-PLK------------NFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GH--SAGAA-LHLSR---------------SIIRRAERLVVPLYE----QADV----
---------VEDILIYL-------NRLS-------DY-------------LF--VVSRFV
N--FHLN--VPETA----------------------------------------------
----------------------------------WEPHKCSSLN----------------
------------------------------------------------------
>gi|117927864|ref|YP_872415.1| ATP:cob(I)alamin adenosyltransferase [Acidothermus
cellulolyticus 11B]
-----------------------------------------------------------M
AVHLTRIYTRT--GDDGTTAL--AAGGRVAKTDPRL--SAFGSCDEANTVIGVA-LALGG
--------------IPAD---------VG--ALLRDIQ--NDLFDV----GADLAT--PV
DPDPRRP---------ALRIVDADIARLEAAI--------------------------DR
YNEELP-QLA------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--PAAAL-LHQAR---------------AVVRRAERETWAAIA--AYGDAV----
---------SRLPAQYL-------NRLS-------DL-------------LF--VLARYL
N--VRLG--YGDIL----------------------------------------------
----------------------------------WQPAGSRRK-----------------
------------------------------------------------------
>gi|146278589|ref|YP_001168748.1| ATP--cobalamin adenosyltransferase [Rhodobacter
```

```
sphaeroides ATCC 17025]
------------------------------------------------------------
MVVLSRIYTRT--GDAGDTAL--GNGARVAKHSSRV--TAYGTVDETNATVGLARLH---
--------------AEGE-----------MQAALARIS--NDLFDL----GADLCR--PE
MERDHEADYT------PLRIIAAQVARLEREI--------------------------DA
MNARLE-PLR------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--ALAAQ-LHLCR---------------TVCRRAERKVVELAA----VESV----
---------NPEALRYL-------NRLS-------DW-------------FF--VVGRIA
N---DDG--RSDVL----------------------------------------------
----------------------------------WVPGLTREA-----------------
------------------------------------------------------
>gi|146343273|ref|YP_001208321.1| putative ATP:cob(I)alamin adenosyltransferase,
monofunctional PduO type [Bradyrhizobium sp. ORS278]
------------------------------------------------------------
MVILNRIYTRT--GDDGTTAL--GNGERRPKFDLRV--SAYGTVDETNAAIGVVRLH---
--------------LADA---------PEIDAMLGLIQ--NDLFDL----GADLAV--PQ
REGKAE----------RLRVVASQVDRLERDI--------------------------DT
LNDKLA-PLT------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--PAAAH-LHVAR---------------TICRRAERIMAELAS--RPDEPV----
---------SEAAIRYM-------NRLS-------DF-------------LF--VASRAA
N---RNG--AGDVL----------------------------------------------
----------------------------------WVPGQNR-------------------
------------------------------------------------------
>gi|108758160|ref|YP_630340.1| hypothetical protein MXAN_2113 [Myxococcus xanthus DK
1622]
----------------------------------------------------------MG
GGGVLRVANLT--QECSMVRL---------EDARPL----IAAAEKKAQELGQP-MN---
----------------------------------------IAVADE----GGNLVA----
----------------HVRMDGAWLGSIDISI--------------------------KK
AFTSRAFDIT------------TQEL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------A
K--NA--QPGGQ-FY------------------GIHASNDGRVMIFAG------------
----------GIPLKKN-------GKVV-------GA-------------VG--VSEGSG
DQNHADATAGASAF----------------------------------------------
------------------------------------------------------------
------------------------------------------------------
>gi|42523107|ref|NP_968487.1| cobalamin adenosyltransferase [Bdellovibrio
bacteriovorus HD100]
------------------------------------------------MTLNTRRVKSMT
NAPKAKIYTRT--GDKGSTRL--VDGSCVEKFNPRV--EAYGTVDELNSYLGVV-RS-TL
AP------------FPEM---------SELNHSLEKVQ--NELFNI----GSLLAT--EK
------DEVFKL----LPPITEEQIRYLELQI--------------------------DE
LTTTLP-ELR------------NFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GH--PTSAH-LHVAR---------------TLCRRSERRSAEIAV----KDER----
---------YSMTLQYL-------NRLS-------DY-------------LF--VAARWA
N--MKHG--VADVL----------------------------------------------
----------------------------------WKKT----------------------
------------------------------------------------------
>gi|16080368|ref|NP_391195.1| hypothetical protein BSU33150 [Bacillus subtilis
subsp. subtilis str. 168]
------------------------------------------------------------
----MKLYTKT--GDKGQTGL--VGG-RTDKDSLRV--ESYGTIDELNSFIGLA-LA-EL
SG------------QPGF---------EDLTAELLTIQ--HELFDC----GGDLAI--V-
TERK------------DYKLTEESVSFLETRI--------------------------DA
YTAEAP-ELK------------KFIL----------------------------------
------------------------------------------------------------
```

```
-----------------------------------------------------------P
G--GS--KCASL-LHIAR---------------TITRRAERRVVALMK----SEEI----
---------HETVLRYL-------NRLS-------DY-------------FF--AGARVV
N--ARSG--IGDVE----------------------------------------------
----------------------------------YERSAIVFRDRNSSES----------
------------------------------------------------------
>gi|148252709|ref|YP_001237294.1| ATP:cob(I)alamin adenosyltransferase
[Bradyrhizobium sp. BTAi1]
------------------------------------------------------------
MVVLNRIYTRT--GDDGTTAL--GNGERRPKYDLRV--SAYGTVDETNAAIGVARLH---
--------------LGEA---------PEIDAMLGLIQ--NDLFDL----GADLAV--PQ
REGKAE----------RLRVVASQVDRLERDI--------------------------DA
LNERLS-PLT------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--PAAAH-LHVAR---------------TICRRAERMIAELAG--RPDEPV----
---------SEAAIRYM-------NRLS-------DF-------------LF--VASRAA
N---RNG--AGDVL----------------------------------------------
----------------------------------WVPGQNR-------------------
------------------------------------------------------
>gi|91975409|ref|YP_568068.1| ATP [Rhodopseudomonas palustris BisB5]
------------------------------------------------------------
MVVLNRIYTRT--GDDGSTSL--GTGERRPKYDLRI--AAYGTVDETNAALGVARAH---
--------------LSGN---------PEIDAMLGRIQ--NDLFDL----GADLAV--PE
REGKAE----------RLRVLSSQVERLEREI--------------------------DQ
LNDRLA-PLT------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GK--PGAAY-LHLAR---------------TICRRAERVMVELAA--QPDETI----
---------TKAAVQYV-------NRLS-------DF-------------LF--VASRAV
N---DAG--SGDVL----------------------------------------------
----------------------------------WVPGQNR-------------------
------------------------------------------------------
>gi|220926674|ref|YP_002501976.1| protein of unknown function DUF336
[Methylobacterium nodulans ORS 2060]
------------------------------------------------------------
----MHVTIKE--AQQAIEAA------R-----AKA--EAIGT--------QMC------
----------------------------------------IAVVDS----GGNLKA----
----------------FYRMDDAWVGSIDIAQ--------------------------KK
AKTALFFGMP------------TGQI----------------------------------
------------------------------------------------------------
-----------------------------------------------------------G
A--LS--QPGGP-LY------------------GIEHSNDG-LITFPG------------
---------GIPIVDKD-------GVMS-------GA-------------IG--VSGSTV
ENDHAVAEAGARAI----------------------------------------------
-------------------------GETELPGHPWRT-----------------------
------------------------------------------------------
>gi|170744318|ref|YP_001772973.1| hypothetical protein M446_6273 [Methylobacterium
sp. 4-46]
------------------------------------------------------------
----MHVTIEE--AEKAIAAA------R-----AKA--QAIGT--------QMC------
----------------------------------------IAVVDS----GGNLKA----
----------------FSRMDDAWVGSIDIAQ--------------------------KK
ARTALFFGMP------------TGQI----------------------------------
------------------------------------------------------------
-----------------------------------------------------------G
A--LS--QPGGP-LY------------------GIEH-SNGGLITFPG------------
---------GIPIVDKD-------GVMS-------GA-------------IG--VSGSTV
EDDHAVAEAGARAV----------------------------------------------
-------------------------GATELPAHPWRT-----------------------
------------------------------------------------------
>gi|86747944|ref|YP_484440.1| cobalamin adenosyltransferase [Rhodopseudomonas
palustris HaA2]
```

```
------------------------------------------------------------
MVVLNRIYTRT--GDDGSTAL--GTGERRPKFDLRF--SAYGTIDETNAALGVARLH---
--------------MAGY---------PEIDAMLARIQ--NDLFDL----GADLAV--PE
REGKAE----------RLRVLSSQVERLEREI--------------------------DE
LNERLA-PLT------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GR--PGAAH-LHLAR---------------TICRRAERIIAELAA--KPDEIV----
---------TPAAVQYV-------NRLS-------DF-------------LF--VASRAV
N---DDG--AGDVL----------------------------------------------
----------------------------------WVPGQNR-------------------
------------------------------------------------------
>gi|159185812|ref|NP_357019.2| hypothetical protein Atu3593 [Agrobacterium
tumefaciens str. C58]
------------------------------------------------------------
MVKLNKIYTRT--GDKGTTAL--VSGPRRLKHDLRV--EAYGTVDETNSAIGIARLH---
--------------TSGL---------ETLDAMLFRIQ--NDLFDL----GADLAT--PD
NGEPLSYE--------PLRIVESQVMRLENEI--------------------------DE
LNAALE-PLT------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--AAAAN-LHMAR---------------TVCRRAERLMVELSV--TDNEIV----
---------SPAALKYA-------NRLS-------DF-------------LF--VAARFT
N---EAG--RADIL----------------------------------------------
----------------------------------WVPGKNR-------------------
------------------------------------------------------
>gi|53804097|ref|YP_114252.1| ATP:cob(I)alamin adenosyltransferase, putative
[Methylococcus capsulatus str. Bath]
-----------------------------------------------------------M
GNRLTRIYTRT--GDDGTTGL--GDGCRTGKDSLRI--EACGTVDELNSVIGLV-LT--Q
-A------------TSEE---------LR--ACLVEVQ--QTLFDL----GGELSL--PG
----------------QPSIQRRQTEWLEVWL--------------------------NH
FNARLP-PLE------------DFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--LAAAH-CHVAR---------------TVCRRAERRLVALAR----GEAV----
---------NPESLAYL-------NRLS-------DF-------------LF--VVARML
A--RMGG--HHEPI----------------------------------------------
----------------------------------WHRDREPPRPRVDSAVMP--------
------------------------------------------------------
>gi|39937809|ref|NP_950085.1| hypothetical protein RPA4751 [Rhodopseudomonas
palustris CGA009]
------------------------------------------------------------
MVVLNRIYTRT--GDDGTTAL--GSGERRPKSDPRI--AAYGTVDETNAALGVVRLH---
--------------LSEL---------PELDAMIGRIQ--NDLFDL----GADLAV--PE
REGKAE----------RLRVLSSQVERLERDI--------------------------DQ
LNEGLA-PLT------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GK--PAAAY-LHVAR---------------TICRRAERAMVELSA--KPNEKI----
---------TPAAVQYV-------NRLS-------DF-------------LF--VAARTV
N---DGG--ARDVL----------------------------------------------
----------------------------------WVPGQNR-------------------
------------------------------------------------------
>gi|116625945|ref|YP_828101.1| hypothetical protein Acid_6903 [Solibacter usitatus
Ellin6076]
------------------------------------------------------------
-----------------MITL---------ADAKRV----LAAAERKAEEIGQP-MN---
----------------------------------------IAVVDA----GGNLVA----
----------------HVRMDKAWIGSVDIAI--------------------------NK
AWTSRAFDIS------------TKEL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------A
```

```
E--LS--QSGDQ-FF------------------GIHASNHGRVMIFAG------------
----------GIPLKRG-------DQVL-------GA-------------VG--VSGGMG
KQDQAVAEAGAEAF----------------------------------------------
------------------------------------------------------------
------------------------------------------------------
>gi|190893626|ref|YP_001980168.1| putative cobalamin adenosultransferase protein
[Rhizobium etli CIAT 652]
------------------------------------------------------------
MVKLNKIYTKT--GDDGTTGL--ASGPRRRKDDLRV--EAYGTIDEANSAIGLARLY---
--------------TTDL---------ADLDAMLMSIQ--NDLFDL----GADLAT--PD
TGEPPAYE--------PLRIVETQVERIERDI--------------------------DR
LNADLN-PLT------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--PAAAH-LHLAR---------------TIARRGERLMVTLAR--MEGEIV----
---------GGAAMKYI-------NRLS-------DF-------------LF--VAARHA
N---DRG--RADVL----------------------------------------------
----------------------------------WVPGKNR-------------------
------------------------------------------------------
>gi|145296554|ref|YP_001139375.1| hypothetical protein cgR_2463 [Corynebacterium
glutamicum R]
-----------------------------------------------------------M
AVHLTKIYTRT--GDDGTTGL--SNFERVPKDDPRL--IAYADSDEANCAIGQVLAL---
--------------GSPT---------EDMATLLRTIQ--NELFDV----GADLAT--PI
EENPKYP---------PLRVLPEYIERLEKEC--------------------------DK
WNEDVP-ALD------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--PAAAL-LHTAR---------------VITRRAERAAWIAVR--EFPSTT----
---------STLPAQYL-------NRLS-------DL-------------LF--ILSRVA
N-----N--GNDVK----------------------------------------------
----------------------------------WVPGGKR-------------------
------------------------------------------------------
>gi|187922728|ref|YP_001894370.1| ATP/cobalamin adenosyltransferase [Burkholderia
phytofirmans PsJN]
-----------------------------------------------------------M
GNRLSKIATRT--GDDGTTGL--GDGSRVRKDSARI--AAIGDVDELNSNLGVL-LC--E
-T------------LPDK---------VR--VALVAIQ--HDLFDL----GGELCI--PG
----------------HTMITDRQLAQLDDWL--------------------------AD
YNAALP-PLK------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--RAASL-AHVCR---------------TVCRRAERAIVALGE----HETI----
---------NAAPRQYV-------NRLS-------DL-------------LF--VLARVL
N--RADG--GTDVL----------------------------------------------
----------------------------------WQHERNAG------------------
------------------------------------------------------
>gi|91786024|ref|YP_546976.1| ATP:cob(I)alamin adenosyltransferase [Polaromonas sp.
JS666]
-----------------------------------------------------------M
ANRLSQIATRT--GDNGTTGL--GDNTRVSKDSLRV--HAMGDVDELNSQIGVL-LC--E
-E------------MPPG---------VR--DLLVEVQ--HQLFNL----GGELSI--PG
----------------FELLKPEAVALLDAAL--------------------------AE
HNAQLP-RLA------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GS--RAAAL-AHVCR---------------TVARRAERAVVALGA----AEPL----
---------KEAPRQYL-------NRLS-------DL-------------LF--VLSRVL
N--RMNG--GDDVY----------------------------------------------
----------------------------------WKSERMARAASEE-------------
------------------------------------------------------
>gi|34540885|ref|NP_905364.1| ATP:cob(I)alamin adenosyltransferase, putative
[Porphyromonas gingivalis W83]
```

```
------------------------------------------------------------
-----MIYTKT--GDKGTTGI--FGGERVPKDDVRV--EAYGTMDELNAAIGMI-RT---
-------------FLPEE---------DERQTVLYDIQ--MRMMAA----MSIVAT--PA
GKREQN----------PNHFPEEAAANCEAFI--------------------------DR
LLAETT-DNG------------YFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--PLSAH-LQLAR---------------TIARRVERRLWTLHR----SDEV----
---------PDAILKWM-------NRLS-------DL-------------FF--VMARHE
M--QQQG--WSEEK----------------------------------------------
----------------------------------WHRFAYKRKKK---------------
------------------------------------------------------
>gi|19553756|ref|NP_601758.1| hypothetical protein NCgl2471 [Corynebacterium
glutamicum ATCC 13032]
-----------------------------------------------------------M
AVHLTKIYTRT--GDDGTTGL--SNFERVPKDDPRL--IAYADSDEANCAIGQVLAL---
--------------SSPT---------EDMATLLRTIQ--NELFDV----GADLAT--PI
EENPKYP---------PLRVLPEYIERLEKEC--------------------------DK
WNEDVP-ALD------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--PAAAL-LHTAR---------------VITRRAERAAWIAVR--EFPSTT----
---------STLPAQYL-------NRLS-------DL-------------LF--ILSRVA
N-----N--GNDVK----------------------------------------------
----------------------------------WVPGGKR-------------------
------------------------------------------------------
>gi|121998704|ref|YP_001003491.1| ATP--cobalamin adenosyltransferase [Halorhodospira
halophila SL1]
-----------------------------------------------------------M
GNRLSKIATRT--GDEGRTGL--GDGSRVDKDSHRV--EAFGEVDELNSFMGRL-LA--H
-E------------LPED---------VA--PVLAQVQ--NELFDL----GAELAV--PG
----------------HSALPLEAVERLDGAL--------------------------AY
FNDSLP-HLK------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GG--KATAD-CHIAR---------------AVCRRAERKLVALSH----HEAV----
---------RDESMAYL-------NRLS-------DL-------------LF--VVARVL
S--RYEN--GGEVL----------------------------------------------
----------------------------------WRPAGQRAADEGA-------------
------------------------------------------------------
>gi|90426352|ref|YP_534722.1| ATP [Rhodopseudomonas palustris BisB18]
------------------------------------------------------------
MVVLNRIYTRS--GDDGTTAL--ANGERRPKYDLRI--CAYGTVDETNAAIGVVRLH---
--------------LADA---------PAVDAMLGRIQ--NDLFDL----GADLAV--PQ
RQGSAE----------RLRVLASQVERLEREI--------------------------DS
LNATLA-PLE------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--PAAAH-LHVAR---------------TICRRAERAMVELAA--RADETL----
---------SPIAIQYI-------NRLS-------DF-------------LF--VASRTA
N---DNG--AGDVL----------------------------------------------
----------------------------------WVPGQNR-------------------
------------------------------------------------------
>gi|114326759|ref|YP_743916.1| cobalamin adenosyltransferase family protein
[Granulibacter bethesdensis CGDNIH1]
-----------------------------------------------------------M
SIRIDRVTTRG--GDGGMTSL--ADGSRLPKDAARI--EALGAVDELNAVLGVL-TL--H
--------------VPEA---------ER--IILHAIQ--NDLFDL----GAVLCF--PS
PENNASP---------ARGIGEDAVARLDTWS--------------------------TD
WNRSLP-PLR------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--EGAAH-AHLAR---------------TVARRAERRVMSLTR----TEAV----
```

```
---------DGEIIRYL-------NRLS-------DL-------------LF--ILARRL
N-------AGADIL----------------------------------------------
----------------------------------WQPGGQSQKTG---------------
------------------------------------------------------
>gi|86357657|ref|YP_469549.1| hypothetical protein RHE_CH02038 [Rhizobium etli CFN
42]
------------------------------------------------------------
------MFTID--------------------EARRI--IAAGEARANEIGVRVN------
----------------------------------------IAVLDA----GAHLKA----
----------------FTRMDGAVLGSIDLAM--------------------------GK
ARTAVLFQTT------------SEAV----------------------------------
------------------------------------------------------------
-----------------------------------------------------------W
D--YC--KPGAP-AH------------------GLELSNGG-LTPFAG------------
---------GISLFARD-------GTVI-------GA-------------VG--VSGGAV
PQDLEIAQAAAAAA----------------------------------------------
-----------------------------------------------A------------
------------------------------------------------------
>gi|82703769|ref|YP_413335.1| ATP protein [Nitrosospira multiformis ATCC 25196]
-----------------------------------------------------------M
RKRLSRIYTRT--GDDGTTGL--GDGTRSSKHSQRV--EAMGMVDELNSFIGLL-LA--E
-A------------LDGD---------IR--IKLEDIQ--HELFDL----GGDLCI--PG
----------------RVTINVGQANRLEAQL--------------------------DH
YNEGLP-ALG------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--RAASL-CHVAR---------------AVCRRAERRLVELYQ----AETL----
---------IPAHLQYL-------NRLS-------DF-------------LF--VLCRFL
N--RQQG--VEDVM----------------------------------------------
----------------------------------WQPGKTAV------------------
------------------------------------------------------
>gi|107021812|ref|YP_620139.1| cobalamin adenosyltransferase [Burkholderia
cenocepacia AU 1054]
-----------------------------------------------------------M
GNRLSKIATRT--GDDGTTGL--GDGRRIGKDDARI--AAIGDVDELNSNLGVL-LA--E
-T------------LPDD---------VR--TALVTIQ--HDLFDL----GGELCI--PG
----------------HAVLDDTHLARLDRWL--------------------------AD
YNATLP-PLK------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GS--RAASL-AHVCR---------------TVCRRAERSIVALGR----GDTL----
---------NDAPRRYV-------NRLS-------DL-------------LF--VLARVL
N--RADG--GTDVL----------------------------------------------
----------------------------------WERGRVR-------------------
------------------------------------------------------
>gi|162148618|ref|YP_001603079.1| hypothetical protein GDI_2845 [Gluconacetobacter
diazotrophicus PAl 5]
------------------------------------------------------------
----MEVLMTC--------SL---------EDARRV----ITAAETEALMIGQP-VN---
----------------------------------------IAVVDA----GGNLVA----
----------------HARMDGARIGAIDIAI--------------------------NK
AFTARAFDMS------------TADL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------A
E--HS--QPGGP-FF------------------GIHTSNNGRVMIFAG------------
----------GVPLRRG-------EKIV-------GA-------------IG--ISGGSG
EQDERVAQAGVQAL----------------------------------------------
------------------------------------------------------------
------------------------------------------------------
>gi|159042774|ref|YP_001531568.1| ATP--cobalamin adenosyltransferase
[Dinoroseobacter shibae DFL 12]
------------------------------------------------------------
MVVLNKIYTKT--GDAGETAL--GNGARVAKHAMRV--AAYGTVDETNATVGLARQH---
```

```
--------------ATGE---------MD--AQLAMIQ--NDLFDL----GADLCR--PD
MEKDAEAEYP------PLRMADSQVARLEAEI--------------------------DA
MNKDLE-PLR------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--ALAAQ-LHLCR---------------TVSRRAERLSVELAT----IETV----
---------NPAAVKYL-------NRLS-------DW-------------FF--VAGRVA
N---SNG--ADDVL----------------------------------------------
----------------------------------WVPGANR-------------------
------------------------------------------------------
>gi|172059713|ref|YP_001807365.1| ATP--cobalamin adenosyltransferase [Burkholderia
ambifaria MC40-6]
-----------------------------------------------------------M
GHRLSKIATRT--GDDGTTGL--GDGRRIGKDDTRI--AAIGDVDELNSTLGVL-LA--E
-P------------LPDD---------VR--TALVTIQ--HDLFDL----GGELCI--PG
----------------HGVLDDTHLARLDRWL--------------------------AD
YNATLP-PLK------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GS--RAASL-AHVCR---------------TVCRRAERSIVALGR----TDTL----
---------NDAPRRYV-------NRLS-------DL-------------LF--VLARVL
N--RADG--GSDVL----------------------------------------------
----------------------------------WERGRVR-------------------
------------------------------------------------------
>gi|29830822|ref|NP_825456.1| hypothetical protein SAV_4279 [Streptomyces
avermitilis MA-4680]
------------------------------------------------------------
---------------MSTTAV-----TPLSTEDAEV---LVSAARRAAEAAGVT-VS---
----------------------------------------ITVLDA----GGHLLA----
----------------FRRDDRAVLISGETST--------------------------RK
AYTALQLNAS------------TADL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------V
E--AV--QPGGL-FH------------------TLPTALDRPLLFIAG------------
---------GVPVHRD--------GRLI-------GA-------------LG--VGGGAP
E--QDHG-----------------------------------------------------
----------------------------------FAAAAVKALS----------------
------------------------------------------------------
>gi|121602988|ref|YP_980317.1| ATP--cobalamin adenosyltransferase [Polaromonas
naphthalenivorans CJ2]
-----------------------------------------------------------M
ANRLSQIATRT--GDNGTTGL--GDNTRVSKDSLRV--HAMGDVDELNSNIGVL-LC--E
-D------------MPGG---------VR--EVLVEVQ--HQLFNL----GGELSI--PG
----------------FELLKPEAVALLDEAL--------------------------ET
YNAQLP-RLA------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GS--RAASL-AHVCR---------------TVARRAERAVVALDK----VETL----
---------KEAPRLYL-------NRLS-------DL-------------LF--VLSRVL
N--RMNG--GDDVY----------------------------------------------
----------------------------------WKSERMVRMAREDQKDQDSQP-----
------------------------------------------------------
>gi|134294809|ref|YP_001118544.1| ATP:cob(I)alamin adenosyltransferase [Burkholderia
vietnamiensis G4]
-----------------------------------------------------------M
GNRLSKIATRT--GDDGTTGL--GDGRRIGKDDARI--VAIGDVDELNSNLGVL-LA--E
-P------------LPDD---------VR--TALVTIQ--HDLFDL----GGELCI--PG
----------------HTVLDDTHLARLDRWL--------------------------AD
YNATLP-PLR------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GS--RAASL-AHVCR---------------TVCRRAERSIVALGR----ADTL----
---------NDAPRRYV-------NRLS-------DL-------------LF--VLARVL
```

```
N--RAGG--GSDVL----------------------------------------------
----------------------------------WERGRVR-------------------
------------------------------------------------------
>gi|206561625|ref|YP_002232390.1| cobalamin adenosyltransferase protein [Burkholderia cenocepacia J2315]
-----------------------------------------------------------M
GNRLSKIATRT--GDDGTTGL--GDGRRIGKDDARI--AAIGDVDELNSNLGVL-LA--E
-T------------LPDD---------VR--AALVTIQ--HDLFDL----GGELCI--PG
----------------HAVLDDTHLARLDRWL--------------------------AD
YNATLP-PLK------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GS--RAASL-AHVCR---------------TVCRRAERSIVALGR----SDTL----
---------NDAPRRYV-------NRLS-------DL-------------LF--VLARVL
N--RAGG--GADVL----------------------------------------------
----------------------------------WERGRVR-------------------
------------------------------------------------------
>gi|89053040|ref|YP_508491.1| ATP:cob(I)alamin adenosyltransferase [Jannaschia sp. CCS1]
------------------------------------------------------------
MVVLNKIYTRT--GDAGETAL--GDGSRVAKFSQRV--TAYGTVDELNATLGVARLH---
--------------ADGL-----------MAERIAMIQ--NDLFDL----GADLCT--PN
MEMDADREYP------PLRMADAQVARLEAEI--------------------------DE
MNPNLE-PLR------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--PLASH-LHICR---------------TVCRRAERLSVELGG----VESV----
---------NPAGVKYL-------NRLS-------DW-------------FF--VAGRIA
N---NNG--KDDIL----------------------------------------------
----------------------------------WVPGANR-------------------
------------------------------------------------------
>gi|92118942|ref|YP_578671.1| ATP--cobalamin adenosyltransferase [Nitrobacter hamburgensis X14]
------------------------------------------------------------
MVVLNRIYTRT--GDDGTTAL--GTGERRPKYDLRV--GAYGTVDETNAAIGVVRLH---
--------------LSGA---------PDLDGMLGCIQ--NDLFDL----GADLAV--PQ
REGKAE----------RLRMVSSQVVGLENDI--------------------------DR
LNAGLA-DLT------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--PAAAY-LHLAR---------------TICRRAERMMVELAA--QPGESV----
---------NDAAVRYM-------NRLS-------DF-------------LF--VASRFM
N---DKG--EGDVL----------------------------------------------
----------------------------------WVPGQNR-------------------
------------------------------------------------------
>gi|28871531|ref|NP_794150.1| ATP:cob(I)alamin adenosyltransferase, putative [Pseudomonas syringae pv. tomato str. DC3000]
-----------------------------------------------------------M
GFRLSKIYTRT--GDTGETGL--GDGRRVPKDHPRV--EAIGEVDTLNSQLGLL-LA---
-G------------LIDEARRVPALNEVI--EVLVPCQ--HRLFDL----GGELAM--PT
----------------YKALNSAEVERLEAAI--------------------------DV
WNEELG-PLE------------NFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--TLIAQ-AHICR---------------SLARSAERRCQHLNA----VEPL----
---------EGAGLAYI-------NRLS-------DL-------------LF--VAARLI
A--RRQG--IAEIL----------------------------------------------
----------------------------------WEPAPKPV------------------
------------------------------------------------------
>gi|115350680|ref|YP_772519.1| ATP--cobalamin adenosyltransferase [Burkholderia ambifaria AMMD]
-----------------------------------------------------------M
GHRLSKIATRT--GDDGTTGL--GDGRRIGKDDVRI--AAIGDVDELNSALGVL-LA--E
```

```
-P------------LPDD---------VR--TALVTIQ--HDLFDL----GGELCI--PG
----------------HGVLDDTHLARLDRWL--------------------------AD
YNATLP-PLK------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GS--RAASL-AHVCR---------------TVCRRAERSIVALGR----TDTL----
---------NDAPRRYV-------NRLS-------DL-------------LF--VLARVL
N--RADG--GSDVL----------------------------------------------
----------------------------------WERGRVR-------------------
------------------------------------------------------
>gi|209551135|ref|YP_002283052.1| ATP/cobalamin adenosyltransferase [Rhizobium
leguminosarum bv. trifolii WSM2304]
------------------------------------------------------------
MVKLNKIYTKT--GDDGTTGL--VSGPRRAKDDLRV--EAYGTIDEANSAIGLARLH---
--------------TSGL---------PELDAMLMSIQ--NDLFDL----GADLAT--PD
TGEPPAYE--------PLRIVEKQVDRVEHDI--------------------------DR
LNAGLQ-PLT------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--PAAAQ-LHLAR---------------TIVRRAERLMVALAR--TDGEIV----
---------SEPARKYI-------NRLS-------DF-------------LF--VAARHA
N---DRG--HADVL----------------------------------------------
----------------------------------WVPGKNR-------------------
------------------------------------------------------
>gi|169236264|ref|YP_001689464.1| hypothetical protein OE3203R [Halobacterium
salinarum R1]
------------------------------------------------------------
----MKIYTKR--GDDGDTDL--RTMDRVSKASPRI--EAYGTVDELNAAVGAI-RP---
-T------------DIAD---------LD--AWLREAQ--NHLHVV----QADFAN--PE
PEPDD------------PQITAEHVTHVEKWI--------------------------DH
CEARLD-PLE------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--EAGAA-LHQAR---------------AVCRRAERRAVALQD-HEPDDAV----
---------NDTAVAYL-------NRLS-------DA-------------LF--VFARLA
N--DVAGVHEESPS----------------------------------------------
----------------------------------Y-------------------------
------------------------------------------------------
>gi|150021644|ref|YP_001306998.1| ATP--cobalamin adenosyltransferase [Thermosipho
melanesiensis BI429]
------------------------------------------------------------
-----MISTKK--GDLGFTSL--ANGERVDKDNLRV--EAYGTIDELVSNLGIA-RA-YL
---------------SGK---------IR--DIIEEIQ--KDLFRM----ATELA---KG
EKF-------------VKLIDNEDVERVTKYV--------------------------ED
FEKDLN--LN------------TFVI----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--MK--KESAY-MDVCR---------------TIARRAERNIVRLSK----NEKI----
---------RKEILAYI-------NRVS-------DL-------------FY--VIARYL
EKDEINK--IKVSE----------------------------------------------
----------------------------------L-------------------------
------------------------------------------------------
>gi|110678708|ref|YP_681715.1| cob(I)alamin adenosyltransferase, putative
[Roseobacter denitrificans OCh 114]
------------------------------------------------------------
MVVLNKIYTKT--GDAGETAL--GNGARVAKHAVRV--ASYGTSDELNSFVGVARLE---
--------------AEGE---------MD--EALSRIQ--NDLFDL----GADLCR--PD
MDQDAEAEYP------PLRMIEAQVERLESEI--------------------------DA
MNKNLE-PLR------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--RLAAH-LHVCR---------------TVSRRAERLCVELAT----MEAI----
---------NPSAVKYL-------NRLS-------DW-------------FF--VAARTV
```

```
N---NGG--KDDVL----------------------------------------------
----------------------------------WVPGANR-------------------
------------------------------------------------------
>gi|91781869|ref|YP_557075.1| ATP:cob(I)alamin adenosyltransferase [Burkholderia
xenovorans LB400]
-------------------------------------------------------MGDMM
GNRLSKIATRT--GDDGTTGL--GDGSRVRKDSARI--AAIGDVDELNSNVGVL-LC--E
-T------------LPDK---------VR--AALVTIQ--HDLFDL----GGELCI--PG
----------------HTMITDRQLAQLDDWL--------------------------AD
YNAALP-PLK------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GS--RAASL-AHVCR---------------TVCRRAERAIVALGE----HDTI----
---------NAAPRQYV-------NRLS-------DL-------------LF--VLARVL
N--RADG--GTDVL----------------------------------------------
----------------------------------WQHERRAG------------------
------------------------------------------------------
>gi|83644749|ref|YP_433184.1| hypothetical protein HCH_01926 [Hahella chejuensis
KCTC 2396]
-----------------------------------------------------------M
GHRLSKIYTRT--GDKGTTGL--GNGERIAKNALRV--EAMGAVDETNSVLGVV-IC---
-E------------LTQD---------DPLHAQLQSIQ--NDLFDL----GGELSI--PG
----------------HIIIIDKHISRLEEWL--------------------------DQ
INEELP-PLK------------NFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GD--RAASH-CHMAR---------------SICRRAERTVVSLAQ----QEQL----
---------NPCLQGYL-------NRLS-------DY-------------LF--VAARAL
A--RRNG--GEEIL----------------------------------------------
----------------------------------WVQTKWEA------------------
------------------------------------------------------
>gi|45657407|ref|YP_001493.1| hypothetical protein LIC11534 [Leptospira interrogans
serovar Copenhageni str. Fiocruz L1-130]
------------------------------------------------------------
----MKIYTKK--GDFGQTSL--ATGVKVPKSDRRV--ELYGTADELNSTIGVV-KS--F
LR------------KESI---------LH--SSLETIQ--NLLFEL----GAELAGFRPK
Q---------------ESCILEEDITFLENQI--------------------------DQ
MQEKLE-PLK------------KFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--KAAAF-LHISR---------------TVSRRLEREMVKFKE---EGLEI----
---------LSSPMIFI-------NRLS-------DY-------------FF--VAARFA
N--LEEN--IQEPL----------------------------------------------
----------------------------------WTSRTKT-------------------
------------------------------------------------------
>gi|38234458|ref|NP_940225.1| hypothetical protein DIP1888 [Corynebacterium
diphtheriae NCTC 13129]
-----------------------------------------------------------M
AVHLTKIYTRT--GDDGTTAL--SDFSRVSKNDPRL--AAYADCDELNASIGQA-LALTT
--------------LPEE---------VV--TVLKRVQ--NELFDA----GADLST--PI
QENLKYP---------PLRIEQSYIDALEADC--------------------------DR
FNEQLE-ALN------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--PGAAM-LHVAR---------------TIARRAERAAWAAVE--AVPETT----
---------SVLPARYL-------NRLS-------DL-------------LF--IMSRLA
N-----D--SNDVK----------------------------------------------
----------------------------------WVPGGSRT------------------
------------------------------------------------------
>gi|33594016|ref|NP_881660.1| hypothetical protein BP3090 [Bordetella pertussis
Tohama I]
-----------------------------------------------------------M
ANRLSVIATRT--GDDGSTGL--GDGSRVGKDTARI--AALGDVDELNSVLGLL-RA--E
```

```
-T------------LPAE---------MD--ADLSTIQ--HDLFDM----GAELCI--PG
----------------HIALADEQVAHLDARL--------------------------AH
YNAGLA-PLR------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--RAAAL-CHLGR---------------TVARRAERSVVALAR----AEVV----
---------NAPVRQYL-------NRLS-------DL-------------LF--VLARHV
N--QAQG--ARDVY----------------------------------------------
----------------------------------WASRHARPAD----------------
------------------------------------------------------
>gi|33594892|ref|NP_882535.1| hypothetical protein BPP0174 [Bordetella parapertussis
12822]
-----------------------------------------------------------M
ANRLSVIATRT--GDDGSTGL--GDGSRVGKDTARI--AALGDVDELNSVLGLL-RA--E
-T------------LPAE---------MD--ADLSTIQ--HDLFDM----GAELCI--PG
----------------HIALADEQVAHLDARL--------------------------SH
YNAGLA-PLR------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--RAAAL-CHLGR---------------TVARRAERSVVALAR----AEVV----
---------NAPVRQYL-------NRLS-------DL-------------LF--VLARHV
N--QAQG--ARDVY----------------------------------------------
----------------------------------WASRHARPAD----------------
------------------------------------------------------
>gi|220935810|ref|YP_002514709.1| ATP:cob(I)alamin adenosyltransferase
[Thioalkalivibrio sp. HL-EbGR7]
-----------------------------------------------------------M
GNRLTRIYTRT--GDDGSTGL--ATGLRVPKDSARI--EVMGDVDELNSLLGVM-LA--E
-P------------VPVQ---------LS--ELLLEVQ--HDLFDL----GGELAM--PG
----------------ESLMQAARVAWLETRL--------------------------DQ
INETLP-PLK------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GG--RAAAL-CQLAR---------------AVCRRAERHLVHLSR----DEPV----
---------TEVSRQYL-------NRLS-------DL-------------LF--VMARVL
A--REVG--EGEVF----------------------------------------------
----------------------------------WKSRRMKDAEK---------------
------------------------------------------------------
>gi|170720142|ref|YP_001747830.1| ATP--cobalamin adenosyltransferase [Pseudomonas
putida W619]
-----------------------------------------------------------M
GYRLSKIYTRT--GDTGETGL--GDGRRVPKDHPRI--EAIGEVDSLNSQLGLL-LA---
-G------------LAEQ-----GLDEVS--EVLAPCQ--HRLFDL----GGELAM--PS
----------------YKALNEAEVERLEAAI--------------------------DG
WNEELG-PLT------------NFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
S--GS--ALIAQ-AHVCR---------------SLARSAERRCQQLNA----VEPL----
---------EGVGLAYI-------NRLS-------DL-------------LF--VAARII
G--RRQG--IAEVL----------------------------------------------
----------------------------------WQAAPKPAG-----------------
------------------------------------------------------
>gi|71735374|ref|YP_276218.1| ATP:cob(I)alamin adenosyltransferase, putative
[Pseudomonas syringae pv. phaseolicola 1448A]
-----------------------------------------------------------M
GFRLSKIYTRT--GDAGETGL--GDGRRVSKDHPRV--EAIGEVDTLNSQLGLL-LA---
-G------------LIDEAKSVPALNEVI--EVLAPCQ--HRLFDL----GGELAM--PI
----------------YKALNDAEVGRLEAAI--------------------------DV
WNEELG-PLE------------NFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--SLIAQ-AHICR---------------SLARSAERRCQHLNA----VEPL----
---------EGAGLAYI-------NRLS-------DL-------------LF--VAARLI
```

```
A--RRQG--IAEIL----------------------------------------------
----------------------------------WQPAPKPV------------------
------------------------------------------------------
>gi|56695625|ref|YP_165976.1| ATP:cob(I)alamin adenosyltransferase, putative
[Ruegeria pomeroyi DSS-3]
------------------------------------------------------------
MVVLNKIYTRT--GDKGQTAL--GNGARVAKYSDRV--ATYGTTDELNAFVGVARLE---
--------------ADGD---------MD--AALSRIQ--NDLFDL----GADLCR--PE
MEKDAEAEYP------PLRMIAAQVARLEQEI--------------------------DA
MNSDLD-PLR------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--ALAAH-LHVCR---------------TVARRAERLAVELAE----GETV----
---------NPQAITYL-------NRLS-------DW-------------FF--VAARTA
N---NGG--KDDVL----------------------------------------------
----------------------------------WIPGANR-------------------
------------------------------------------------------
>gi|78065298|ref|YP_368067.1| ATP:cob(I)alamin adenosyltransferase [Burkholderia sp.
383]
-----------------------------------------------------------M
GNRLSKIATRT--GDDGTTGL--GDGRRIGKDDTRI--AAIGDVDELNSNLGVL-LA--E
-T------------LPDE---------IR--SALVTIQ--HDLFDL----GGELCI--PG
----------------HTVLDDTHLARLDRWL--------------------------AD
YNATLP-PLK------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GS--RAASL-AHVCR---------------TVCRRAERSIVALGR----TETL----
---------NDAPRRYV-------NRLS-------DL-------------LF--VLARVL
N--RTDG--GSDVL----------------------------------------------
----------------------------------WERGRVR-------------------
------------------------------------------------------
>gi|24215115|ref|NP_712596.1| hypothetical protein LA2415 [Leptospira interrogans
serovar Lai str. 56601]
------------------------------------------------------------
----MKIYTKK--GDFGQTSL--ATGVKVPKSDRRV--ELYGTADELNSTIGVV-KS--F
LR------------KESI---------LH--SSLEIIQ--NLLFEL----GAELAGFRPK
Q---------------ESCILEEDITFLENQI--------------------------DQ
MQEKLE-PLK------------KFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--KAAAF-LHISR---------------TVSRRLEREMVKFKE---EGLEI----
---------LSSPMIFI-------NRLS-------DY-------------FF--VAARFA
N--LEEN--IQEPL----------------------------------------------
----------------------------------WTSRTKT-------------------
------------------------------------------------------
>gi|23098359|ref|NP_691825.1| hypothetical protein OB0904 [Oceanobacillus iheyensis
HTE831]
------------------------------------------------------------
----MRIYTRS--GDKGLTSL--VYGQRVPKNHLRV--EAYGTCDEANSAIGLAVSVLGN
KE------------WEGK---------QDFLDQLHRVQ--TILFHV----GAELST--PM
DKEV------------YWKLKQSHIDEMEKQI--------------------------DN
WHEELE-PLN------------NFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
S--GH--LASSA-LHNAR---------------TIVRRAERIVVGLDE----EIE-----
---------NKLVLSYL-------NRLS-------DF-------------LF--VAARYV
N--KKLG--GQEQG----------------------------------------------
----------------------------------LHVDLTK-------------------
------------------------------------------------------
>gi|148549580|ref|YP_001269682.1| ATP--cobalamin adenosyltransferase [Pseudomonas
putida F1]
-----------------------------------------------------------M
GYRLSKIYTRT--GDKGETGL--GDGRRVPKDHPRI--EAIGEVDSLNSQLGLL-LA---
```

```
-G------------LAEQ-----GLNEVT--TVLAPCQ--HRLFDL----GGELAM--PS
----------------YQALNLAEVERLEAAI--------------------------DV
WNEELG-PLK------------NFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
S--GS--ALVAQ-AHVCR---------------SLARSAERRCQQLNA----MEPL----
---------EGVGLAYI-------NRLS-------DL-------------LF--VAARII
G--RRQG--VAEVL----------------------------------------------
----------------------------------WQPAEKPKG-----------------
------------------------------------------------------
>gi|222087342|ref|YP_002545879.1| hypothetical protein Arad_4189 [Agrobacterium
radiobacter K84]
------------------------------------------------------------
MVKLNKIYTKT--GDDGTTGL--VSGPRRLKHDLRV--ESYGTIDETNSVIGVARLH---
--------------TADM---------PELDAMLMRIQ--NDLFDL----GADLSA--PE
TDEPLPYE--------PLRIIDNQVSRIEHDI--------------------------DA
LNAGLE-PLN------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GS--PASAH-LHLAR---------------TIARRAERLMVALSH--TTGERV----
---------SPAALKYV-------NRLS-------DF-------------LF--VAARHA
N---DRG--RADVL----------------------------------------------
----------------------------------WVPGKNR-------------------
------------------------------------------------------
>gi|162452129|ref|YP_001614496.1| hypothetical protein sce3856 [Sorangium cellulosum
'So ce 56']
--------------------------------MSDDDTRGTGAQTPDGGESGGARVFKAP
KITINRVYTRQ--GDGGLTRL--VGGQLVPKDDARI--ETYGTVDELNALVGAA-RQ-TL
IE------------LLPGAPSEGAQRLVELGRTLLRVQ--HELFNL----GSILAT--LP
------EDVHPK----QPRVTQAEIDLLEAEM--------------------------DR
CQADLP-PLR------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--RLNTD-LHVAR---------------TVCRRAERCCVRLAQ----AGHA----
---------DPHAVRYL-------NRLS-------DA-------------LF--VWSRWA
A--ALLG--TPELL----------------------------------------------
----------------------------------WEPDASASGGKAPPA-----------
------------------------------------------------------
>gi|126441453|ref|YP_001060305.1| ATP:cob(I)alamin adenosyltransferase, putative
[Burkholderia pseudomallei 668]
----------------------------------------------------------MM
GNRLSKIATRT--GDDGTTGL--GDGSRVRKDDARI--AAIGDVDELNSQLGVL-LA--E
-P------------LPDD---------VR--AALSSIQ--HDLFDL----GGELCI--PG
----------------HAAITDAHLARLDDWL--------------------------AH
YNAQLP-PLE------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GA--RGAAL-AHVCR---------------TVCRRAERAIVALGV----HAPL----
---------DAAPRRYV-------NRLS-------DL-------------LF--VLARVL
N--RAAG--GADVL----------------------------------------------
----------------------------------WDRTRAHGTR----------------
------------------------------------------------------
>gi|121600479|ref|YP_991684.1| putative ATP:cob(I)alamin adenosyltransferase
[Burkholderia mallei SAVP1]
----------------------------------------------------------MM
GNRLSKIATRT--GDDGTTGL--GDGSRVRKDDARI--AAIGDVDELNSQLGVL-LA--E
-P------------LPDD---------VR--AALSSIQ--HDLFDL----GGELCI--PG
----------------HAAITDAHLARLDDWL--------------------------AH
YNAQLP-PLE------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GA--RGAAL-AHVCR---------------TVCRRAERAIVALGV----HAPL----
---------DAAPRRYV-------NRLS-------DL-------------LF--VLARVL
```

```
N--RAAG--GADVL----------------------------------------------
----------------------------------WDRTRAHGTPHGTR------------
------------------------------------------------------
>gi|110833488|ref|YP_692347.1| hypothetical protein ABO_0627 [Alcanivorax
borkumensis SK2]
-------------------------------------------------------MSDTN
KTRINRVITRT--GDAGETGL--ADGSRVSKHDPRI--VVLGELDELNSALGVL-RA---
--------------RPQD---------ADLDALLGLIQ--QMLFDI----GSELAI--PG
----------------HRVIDDHDLVEMESQA--------------------------DT
INAELP-PLK------------EFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GH--PDAAW-CHHCR---------------TVARRLERHVIALRD--ADEDAV----
---------NPVSQALI-------NRLS-------DL-------------LF--VMARLI
N--LRHE--HPETL----------------------------------------------
----------------------------------WVPKADR-------------------
------------------------------------------------------
>gi|55378269|ref|YP_136119.1| cobalamin adenosyltransferase [Haloarcula marismortui
ATCC 43049]
------------------------------------------------------------
----MTIYTGR--GDQGQTDL--RNMERVSKDSRRI--EAYGTVDEVNALVGVV-RP---
-T------------GHDD---------ID--EKLRVVQ--NHLHIV----QADFAN--PS
PEEGD------------PRIQESHVETLEELI--------------------------DE
ADSELD-PLE------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
S--GS--EPGAK-LHHAR---------------AVCRRAERRCVSFAA---EEAGV----
---------NETAIIYL-------NRLS-------DA-------------LF--TLARLV
N--KREGIREENPE----------------------------------------------
----------------------------------Y-------------------------
------------------------------------------------------
>gi|53713793|ref|YP_099785.1| putative ATP:cob(I)alamin adenosyltransferase
[Bacteroides fragilis YCH46]
------------------------------------------------------------
--MMKRIYTRT--GDRGTTGI--HGGERVEKDDIRI--EANGTIDELNAVIGIIRSL---
--------------LPQE---------HDWQKLLHHLQ--RELMVV----MSHVAT--PS
AIRDKN----------PNVLSPGLAAFCEQEM--------------------------DT
MTAGLK-ENG------------YFLL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--PVSAQ-LQFAR---------------TVARRAERRLWTLNR----QDAV----
---------PEEILSFI-------NRLS-------DL-------------FF--VMARFD
M--QQQD--WPEER----------------------------------------------
----------------------------------WQAFAYKTKKK---------------
------------------------------------------------------
>gi|13473010|ref|NP_104577.1| hypothetical protein mlr3485 [Mesorhizobium loti
MAFF303099]
------------------------------------------------------------
MVKLNKIYTRT--GDDGTTGL--GTGERRLKSDLRV--DAYGTVDEANACIGMARVH---
--------------TAAN--------HPAIDAMLSRIQ--NDLFDL----GADLAV--PD
DGKTLDYE--------PLRIVAAQTDRVEKDI--------------------------DL
LNKDLQ-PLK------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------N
G--GT--PAAAA-LHLAR---------------TVARRAERLMVALAQ--DPGEHV----
---------NREGLKYI-------NRVS-------DF-------------LF--VAARAV
N---DNG--NADVL----------------------------------------------
----------------------------------WVPGKNR-------------------
------------------------------------------------------
>gi|115526838|ref|YP_783749.1| ATP--cobalamin adenosyltransferase [Rhodopseudomonas
palustris BisA53]
------------------------------------------------------------
MVVLNRIYTRT--GDDGTTAL--ANGERRPKCDARI--SAYGTVDETNAAIGVARLH---
```

```
--------------LAQM---------PVVDAMMGRVQ--NDLFDL----GADLAV--PE
RQGNAE----------RLRMLETQVTRLEREI--------------------------DE
LNAALA-PLN------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--AAASY-LHVAR---------------TICRRAERAMVELAG--RPNEPL----
---------SSFAIKYV-------NRLS-------DL-------------LF--VASRAA
N-----GNGADDVL----------------------------------------------
----------------------------------WVPGQNR-------------------
------------------------------------------------------
>gi|53720449|ref|YP_109435.1| hypothetical protein BPSL2841 [Burkholderia
pseudomallei K96243]
-----------------------------------------------------------M
GNRLSKIATRT--GDDGTTGL--GDGSRVRKDDARI--AAIGDVDELNSQLGVL-LA--E
-P------------LPDD---------VR--AALSSIQ--HDLFDL----GGELCI--PG
----------------HAAITDAHLARLDDWL--------------------------AH
YNAQLP-PLE------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GA--RGAAL-AHVCR---------------TVCRRAERAIVALGV----HAPL----
---------DAAPRRYV-------NRLS-------DL-------------LF--VLARVL
N--RAAG--GADVL----------------------------------------------
----------------------------------WDRTRAHGTPHGTR------------
------------------------------------------------------
>gi|197105595|ref|YP_002130972.1| hypothetical protein PHZ_c2132 [Phenylobacterium
zucineum HLK1]
------------------------------------------------------------
-------MTLT--IPHASISQ---------AAADRL--IEAATAKAAEMGLSMV------
----------------------------------------IAVVDD----AGVMKA----
----------------FRRMDGAPLLSVEIAK--------------------------DK
AYTAAAYKIP------------THAW----------------------------------
------------------------------------------------------------
-----------------------------------------------------------F
D--FI--KSDPPLLH------------------GIVHTN--RLVVFGG------------
---------GYPV-EVD-------GQVV-------GG-------------IG--VSGGHY
SQDQEVAEAALAAL----------------------------------------------
-----------------------------------------------K------------
------------------------------------------------------
>gi|26988083|ref|NP_743508.1| ATP--cobalamin adenosyltransferase [Pseudomonas putida
KT2440]
-----------------------------------------------------------M
GYRLSKIYTRT--GDKGETGL--GDGRRVPKDHPRI--EAIGEVDSLNSQLGLL-LA---
-G------------LAEH-----GLNEVT--TVLAPCQ--HRLFDL----GGELAM--PS
----------------YQALNLAEVERLEAAI--------------------------DV
WNEELG-PLK------------NFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
S--GS--ALVAQ-AHVCR---------------SLARSAERRCQQLNA----MEPL----
---------EGVGLAYI-------NRLS-------DL-------------LF--VAARII
G--RRQG--IAEVL----------------------------------------------
----------------------------------WQPAPKPEG-----------------
------------------------------------------------------
>gi|170750778|ref|YP_001757038.1| hypothetical protein Mrad2831_4389
[Methylobacterium radiotolerans JCM 2831]
------------------------------------------------------------
----MHVTIEQ--AE-----------------------KAIAAARAKAVELGTQ-MC---
----------------------------------------IAVVDS----GGNLKA----
----------------FHRMDDAWVGSIDIAH--------------------------KK
AKTSVFFGMM------------TGQI----------------------------------
------------------------------------------------------------
-----------------------------------------------------------G
Q--LS--QPGGP-LY------------------GIEHSNDG-LITFPG------------
---------GIPIVDAD-------GVMS-------GA-------------IG--VSGSTV
```

```
ENDHTVAEAGAKAI----------------------------------------------
-------------------------GRTELPAHPWRT-----------------------
------------------------------------------------------
>gi|17986376|ref|NP_539010.1| adenosylcobalamin-dependent diol dehydratase gamma
subunit [Brucella melitensis 16M]
----------------------------------------------MARSISRVMQADNK
MVKLNKIYTRT--GDKGTTGL--ASGPRRLKCDLRV--EAYGTVDEANACVGMARIHTGA
--------------QDAH---------AEIDAMLARIQ--NDLFDL----GADLST--PD
DGQPLSYE--------PLRIVASQVSRVEADI--------------------------DR
LNANLQ-PLR------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--PASAA-LHLAR---------------TVSRRAERLMVALSR--MEGEKV----
---------SPEALQYI-------NRLS-------DF-------------LF--VAGRAV
N---DNG--ASDIL----------------------------------------------
----------------------------------WVPGAQSLSERGGSVLERVSI-----
------------------------------------------------------
>gi|23502823|ref|NP_698950.1| ATP:cob(I)alamin adenosyltransferase, putative
[Brucella suis 1330]
------------------------------------------------------------
MVKLNKIYTRT--GDKGTTGL--ASGPRRLKCDLRV--EAYGTVDEANACVGMARIHTGA
--------------QDAH---------AEIDAMLARIQ--NDLFDL----GADLST--PD
DGQPLSYE--------PLRIVASQVSRVEADI--------------------------DR
LNANLQ-PLR------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--PASAA-LHLAR---------------TVSRRAERLMVALSR--MEGEKV----
---------SPEALQYI-------NRLS-------DF-------------LF--VAGRAV
N---DNG--ASDIL----------------------------------------------
----------------------------------WVPGANR-------------------
------------------------------------------------------
>gi|27376487|ref|NP_768016.1| hypothetical protein blr1376 [Bradyrhizobium japonicum
USDA 110]
------------------------------------------------------------
MVVLNRIYTKT--GDDGTTAL--GSGERRPKYDLRI--EAYGTVDETNAAIGVVRLH---
--------------THDA---------PEFDAMLGRIQ--NDLFDL----GADLAV--PE
REGKVE----------RLRVVASQVERLEHDI--------------------------DA
LNDKLA-PLT------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--PAAAY-LHVAR---------------TICRRAERVMVELAA--QPGEPV----
---------GAAGIQYM-------NRLS-------DF-------------LF--VASRAA
N---HNG--AGDVL----------------------------------------------
----------------------------------WVPGQNR-------------------
------------------------------------------------------
>gi|21222323|ref|NP_628102.1| hypothetical protein SCO3916 [Streptomyces coelicolor
A3(2)]
------------------------------------------------------------
---------------MSTTAV-----TPLTTQDAEA---LVTAAHHAAEAAGVT-VS---
----------------------------------------VTVLDA----GGHLLA----
----------------FRRDDRAVLISGETST--------------------------RK
AYTALQLNAP------------TADL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------V
D--AV--QPGGL-FH------------------TLPTALDRPLLFLAG------------
---------GVPVHRE--------GRLI-------GA-------------IG--VGGGAP
D--QDHG-----------------------------------------------------
----------------------------------FASAAVRALA----------------
------------------------------------------------------
>gi|120553889|ref|YP_958240.1| ATP--cobalamin adenosyltransferase [Marinobacter
aquaeolei VT8]
-----------------------------------------------------------M
GNRLSKIYTRT--GDDGSTGL--ADGNRIAKNAQRV--EAMGMADELNCHIGVL-IE---
```

```
-T------------LPSG---------DRLIDTFRRIQ--HHLFDL----GGEFAI--PG
----------------SKVISDNHIEWLEQTL--------------------------DE
YNTDLP-PLK------------NFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GC--PAAAQ-CHLAR---------------AVCRRAERVVVALGH----EDSI----
---------NTASRHYL-------NRLS-------DL-------------LF--VIARVL
A--RRDG--SQEIL----------------------------------------------
----------------------------------WEQKKPGL------------------
------------------------------------------------------
>gi|222109288|ref|YP_002551552.1| ATP/cobalamin adenosyltransferase [Diaphorobacter
sp. TPSY]
-----------------------------------------------------------M
GNRLTQIATRT--GDDGSTGL--GDNTRVSKASGRP--QAMGDVDELNSHIGLL-LC--E
-P------------LPAD---------MR--ELLIDVQ--HQLFNL----GGELSM--PG
----------------YELLKDDALLQLDNAL--------------------------AR
YNAELP-RLL------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GT--RAACQ-AHVCR---------------TVARRAERAVVALQQ----HETM----
---------RAAPRQYL-------NRLS-------DL-------------LF--VLSRAL
N--RMDG--GSEVY----------------------------------------------
----------------------------------WKSERLARQNDATE------------
------------------------------------------------------
>gi|111020544|ref|YP_703516.1| hypothetical protein RHA1_ro03555 [Rhodococcus jostii
RHA1]
------------------------------------------------------------
---------MT--VNQTSVSL---------DDAQRVIAAGQAKADEIESPSNIA------
------------------------------------------VVDA----GGNLVA----
----------------HVRMDGAWIASIDISI--------------------------SK
AFTARALDIS------------TEDL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------A
A--NA--GPGGQ-FY------------------GIHVSNGGRTMIFTG------------
----------GVPLRHN-------GQVV-------GA-------------VG--VSGGTG
EQDKTVAEAAAAAL----------------------------------------------
------------------------------------------------------------
------------------------------------------------------
>gi|15614158|ref|NP_242461.1| hypothetical protein BH1595 [Bacillus halodurans
C-125]
------------------------------------------------------------
----MRLYTRT--GDKGKTSV---IGGRLAKDDTRV--VAYGTTDELNSFVGLAITQ---
--------------LDEN-------TFADIRGELFKIQ--HELFDC----GGDLAMLKVK
EDR-------------PYKAKQEIVDFLEQRI--------------------------DA
YIKEAP-ELE------------RFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--EAAAS-LHVCR---------------TIARRAERYVVRLQQ----EGEI----
---------NPIVLKYL-------NRLS-------DY-------------FF--AVARVV
N--SRLQ--VPDVE----------------------------------------------
----------------------------------YERSAIVFREGKRKEDKK--------
------------------------------------------------------
>gi|194290650|ref|YP_002006557.1| putative Cob(I)yrinic acid a,c-diamide
adenosyltransferase [Cupriavidus taiwanensis]
-----------------------------------------------------------M
GNRLSKIATRT--GDAGTTGL--GDGSRTGKDSLRI--AAIGDVDELNCHVGVL-LT--E
-D------------LPAD---------VR--AALLHIQ--HDLFDL----GGELSI--PG
----------------YTLLKPGQVAQLDTWL--------------------------AD
YNANLP-RLA------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--RAAAQ-AHVCR---------------TVCRRAERALVALGA----AEAL----
---------NEAPRQYL-------NRLS-------DL-------------MF--VLARVL
```

```
N--RAAG--GSDVL----------------------------------------------
----------------------------------WQRDRDAS------------------
------------------------------------------------------
>gi|163853555|ref|YP_001641598.1| hypothetical protein Mext_4158 [Methylobacterium
extorquens PA1]
------------------------------------------------------------
----MHVTIEQ--AE-----------------------KAIQAARAKAVELGTQ-MC---
----------------------------------------IAIVDS----GGNLKA----
----------------FHRMDGAWVGSIDIAQ--------------------------KK
AKTAVFFGMK------------TGQI----------------------------------
------------------------------------------------------------
-----------------------------------------------------------G
A--LS--QPGGS-LY------------------GIEHSNQG-LITFPG------------
---------GIPIVDAD-------GEMS-------GA-------------IG--VSGSSV
ENDDAVALAGASAI----------------------------------------------
-------------------------GDTELPDHPWRT-----------------------
------------------------------------------------------
>gi|146305970|ref|YP_001186435.1| ATP:cob(I)alamin adenosyltransferase [Pseudomonas
mendocina ymp]
-----------------------------------------------------------M
GMRLSKIYTRT--GDKGETGL--ADGRRVGKDHPRI--EAIGELDTLNSQLGLL-LA---
-D------------LEEAAATWPGLQEIG--EVLSPCQ--HRLFDL----GGELAM--PE
----------------YQALQQGEIERLEAAI--------------------------DR
WNEEVG-PLE------------NFIM----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--RLIAQ-AHVCR---------------SFARSAERRCQHLNA----VEPL----
---------RAEGLAYV-------NRLS-------DL-------------LF--VAARLI
A--RRQG--VNEVL----------------------------------------------
----------------------------------WKAADKP-------------------
------------------------------------------------------
>gi|114570908|ref|YP_757588.1| ATP:cob(I)alamin adenosyltransferase [Maricaulis
maris MCS10]
------------------------------------------------------------
MVRLTKIYTRT--GDAGSTRL--GDMSQTVKHDPRV--DAYGDVDEANSSIGLARAA---
--------------LILN---------DPLDPPLARIQ--NDLFDL----GADLCV--PE
SDTPPDYE--------PLRVTAAQVDWLETEI--------------------------DR
LNARLE-PLN------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--EAAAR-LHVCR---------------TVCRRAERKVSALMA---GGVTL----
---------NPIVLTYL-------NRLS-------DL-------------LF--VMARTA
N---EEG--RADVL----------------------------------------------
----------------------------------WVPGKDR-------------------
------------------------------------------------------
>gi|121592479|ref|YP_984375.1| ATP:cob(I)alamin adenosyltransferase [Acidovorax sp.
JS42]
-----------------------------------------------------------M
GNRLTQIATRT--GDDGSTGL--GDNTRVSKASGRP--QAMGDVDELNSHIGLL-LC--E
-P------------LPAD---------MR--ELLIDVQ--HQLFNL----GGELSM--PG
----------------YELLKDDALLQLDNAL--------------------------AR
YNAELP-RLL------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GT--RAACQ-AHVCR---------------TVARRAERAVVALQQ----QETM----
---------RPAPRQYL-------NRLS-------DL-------------LF--VLARVL
N--RMDG--GSEVY----------------------------------------------
----------------------------------WKSERLARQNHATE------------
------------------------------------------------------
>gi|209543120|ref|YP_002275349.1| protein of unknown function DUF336
[Gluconacetobacter diazotrophicus PAl 5]
------------------------------------------------------------
----------------MTCSL---------EDARRV----IATAEAEARAIGQP-MN---
```

```
----------------------------------------IAVVDA----GGHLVA----
----------------HARMDGARIGAIDIAI--------------------------NK
AFTARAFDMS------------TADL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------A
E--HS--QPGGP-FF------------------GIHTSNNGRVMIFAG------------
----------GVPLRRG-------EQIV-------GA-------------IG--ISGGSG
EQDERVAQAGVLAF----------------------------------------------
------------------------------------------------------------
------------------------------------------------------
>gi|167035491|ref|YP_001670722.1| ATP--cobalamin adenosyltransferase [Pseudomonas
putida GB-1]
-----------------------------------------------------------M
GYRLSKIYTRT--GDKGETGL--GDGRRVPKDHPRI--EAIGEVDSLNSQLGLL-LA---
-G------------LDEQ-----GLDELS--AVLVPCQ--HRLFDL----GGELAM--PS
----------------YQALTLAEVERLEAAI--------------------------DV
WNEELG-PLK------------NFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
S--GS--ALVAQ-AHVCR---------------SLARSAERRCQQLNA----IEPL----
---------QGVGLAYI-------NRLS-------DL-------------LF--VAARII
G--RRQG--VAEVL----------------------------------------------
----------------------------------WQPAEKPKG-----------------
------------------------------------------------------
>gi|94969796|ref|YP_591844.1| hypothetical protein Acid345_2769 [Acidobacteria
bacterium Ellin345]
------------------------------------------------------------
---------------MSAVKL---------EDARRV----IGAAEKKAKEIGQP-MN---
----------------------------------------IAVADE----GGNIVA----
----------------HVRMDNAWIGSIDISM--------------------------KK
AYTSRAFDIE------------TKDL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------A
T--HS--QSGGQ-FF------------------GIHASNDGKIMIFAG------------
----------GIPLKRD-------GKVV-------GA-------------IG--VSGGSG
DQDHAVAMAGAAAY----------------------------------------------
------------------------------------------------------------
------------------------------------------------------
>gi|73542471|ref|YP_296991.1| ATP:cob(I)alamin adenosyltransferase [Ralstonia
eutropha JMP134]
-----------------------------------------------------------M
GHRLSKIATRT--GDAGTTGL--GDGSRTGKDSLRI--AAIGDVDELNCQIGVL-LT--E
-T------------LPDD---------VR--AALLHMQ--HDLFDL----GGELSI--PG
----------------YTLLKPEQVAQLDVWL--------------------------EH
YNAGLP-RLA------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--RAAAL-AHVCR---------------TVCRRAERALVALGA----MEAL----
---------NEAPRQYL-------NRLS-------DL-------------MF--VLARVL
N--RLDG--GSDVL----------------------------------------------
----------------------------------WQRGRDTANAPEKSD-----------
------------------------------------------------------
>gi|15897506|ref|NP_342111.1| hypothetical protein SSO0588 [Sulfolobus solfataricus
P2]
------------------------------------------------------------
------MFTRT--GDDGNTNV---ISKRVGKDSPVV--NLLGDIDELNSFIGLA-LT---
--------------KIEW---------EDMQSDLMRVQ--TELFIL----GEEIIQD---
----------------KGRINEETIKWLESRT--------------------------VE
YRKESG-PVK------------LFVI----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--EQASY-LHVVR---------------SIARRVERNAVAYSK----ELNF----
---------NKWIIVYL-------NRLS-------SL-------------LF--SMAIVA
```

```
N--KRKN--VKERI----------------------------------------------
----------------------------------YDIGKYF-------------------
------------------------------------------------------
>gi|212223783|ref|YP_002307019.1| cobalamin adenosyltransferase [Thermococcus
onnurineus NA1]
------------------------------------------------------------
----MPITTKT--GDKGLTGL--FTGDRIAKYSPIM--EANGTIDELSSFLGEA-KH--Y
--------------VPKE---------MA--EVLEKIQ--VELYSL----MAEIAS--KG
K---------------YKKVGEGEVKWLEELI--------------------------HK
YEEEVQ--LR------------AFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--ST--IASAK-LDVCR---------------TVARRAERAVARLVL----DYGF----
---------GSSALIYL-------NRLS-------DL-------------LF--IMARAI
E--KREG-KIKEVK----------------------------------------------
------------------------------------------------------------
------------------------------------------------------
>gi|152979973|ref|YP_001352023.1| hypothetical protein mma_0333 [Janthinobacterium
sp. Marseille]
-----------------------------------------------------------M
GNRLSKIATRT--GDKGTTGL--GDGSRVDKDALRI--HAMGDVDELNSHLGLL-LC--E
-D------------LPAA---------LR--EELISIQ--HDLFDL----GGEICI--PG
----------------YTLIHDEQVARLDGLL--------------------------AK
YNSTLP-PLK------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GS--RAASQ-AHICR---------------TVCRRAERTIVSLGK----AEKI----
---------NDNPRQYM-------NRLS-------DL-------------MF--VLSRVL
N--RYAG--GGDVL----------------------------------------------
----------------------------------WEKDRVRDIAS---------------
------------------------------------------------------
>gi|145298764|ref|YP_001141605.1| ATP:cob(I)alamin adenosyltransferase, putative
[Aeromonas salmonicida subsp. salmonicida A449]
------------------------------------------------------------
----MRIYTRQ--GDKGMTRL--ADGVQLAKDELRV--ETYGYIDELNSHIGLL-IA-EV
PA------------AETG---------LL--ADLVLLQ--QELFDL----GGELAFSSDG
QHEA------------IWQVNNEWTLRLEQQI--------------------------DA
YSANLP-LLR------------NFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
S--GS--RAASQ-AHVVR---------------TLTRRCERLLLSLSR----AEQI----
---------NPAILPYV-------NRLS-------DW-------------FF--TIARYL
L--ACTG--TPEVL----------------------------------------------
----------------------------------WVKAAERG------------------
------------------------------------------------------
>gi|70607307|ref|YP_256177.1| hypothetical protein Saci_1571 [Sulfolobus
acidocaldarius DSM 639]
------------------------------------------------------------
------MFTRS--GDDGKTSI---VNKKVGKDSPVV--ELLGDIDELNSHIGYT-IT---
--------------RLSW---------EDMKEDLQKIQ--VHLFEV----GEDIAS--DS
K---------------KKKIDESYVKWIEERT--------------------------IA
YRKESG-PVK------------LFVI----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--EEASL-LHITR---------------TVCRRVERNMVRYSK---ELQEL----
---------NKQNIVYL-------NRLS-------SL-------------LF--AMALVA
N--KRKN--VQEKY----------------------------------------------
----------------------------------YDIGKFW-------------------
------------------------------------------------------
>gi|17547382|ref|NP_520784.1| hypothetical protein RSc2663 [Ralstonia solanacearum
GMI1000]
-----------------------------------------------------------M
GNRLSKIATRT--GDDGTTGL--GDGSRTGKDGLRI--AAIGEVDELNSHLGVL-LT--E
```

```
-P------------LPDD---------VH--AALTAIQ--HDLFDL----GGELCI--PG
----------------HTMVTPAHVLRLDQWL--------------------------AD
YNADLP-RLA------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--RAAAQ-AHVCR---------------TVCRRAERAIVALGR----AETL----
---------GEAPRQYV-------NRLS-------DL-------------LF--VLARVL
N--RAGG--GQDVL----------------------------------------------
----------------------------------WEHERHKPV-----------------
------------------------------------------------------
>gi|182677150|ref|YP_001831296.1| ATP--cobalamin adenosyltransferase [Beijerinckia
indica subsp. indica ATCC 9039]
------------------------------------------------------------
MVVLTRIYTRG--GDGGTTSL--GTGERRKKQDLRI--ETYGTVDEANACIGLARIHTAS
--------------EAAH---------AKLDAMLLCIQ--NDLFDL----GADLCM--PE
NTAANPKVE-------ALRILPAQVERLERDI--------------------------DT
INAGLE-PLS------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--PAAAA-LHLAR---------------TVARRAERLLCALRE--TPGESV----
---------GAPTLAYL-------NRLS-------DF-------------LF--VAARHV
N---QQG--AGDVL----------------------------------------------
----------------------------------WVPGLNR-------------------
------------------------------------------------------
>gi|158421682|ref|YP_001522974.1| cobalamin adenosyltransferase [Azorhizobium
caulinodans ORS 571]
------------------------------------------------------------
MVKLNKIYTRT--GDDGSTGL--GTGERVRKDDLRV--AAYGTVDETNATIGLVRLH---
--------------LAAY---------PQVDAILARVQ--NDLFDL----GADLCV--PE
RPGAPPPPYE------PLRITAPQVRRLEEDI--------------------------DR
LNAELD-PLK------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--PAAAH-LHLAR---------------TVARRAERDMVTLAE--SDGEQV----
---------GMEALRYI-------NRLS-------DL-------------LF--VAGRYV
N-----GHGANDVL----------------------------------------------
----------------------------------WVPGAHR-------------------
------------------------------------------------------
>gi|188583856|ref|YP_001927301.1| protein of unknown function DUF336
[Methylobacterium populi BJ001]
------------------------------------------------------------
----MHVTIEQ--AE-----------------------KAIEAARAKAVELGTQ-MC---
----------------------------------------IAVVDS----GGNLKA----
----------------FHRMDGAWVGSIDIAQ--------------------------KK
AKTSVFFGMK------------TGQI----------------------------------
------------------------------------------------------------
-----------------------------------------------------------G
S--LS--QPGGS-LY------------------GIEHSNQG-LITFPG------------
---------GIPIVDAD-------GEMS-------GA-------------IG--VSGSSV
ENDDAVALAGASAI----------------------------------------------
-------------------------GDTELPDHPWRT-----------------------
------------------------------------------------------
>gi|134093562|ref|YP_001098637.1| putative Cob(I)yrinic acid a,c-diamide
adenosyltransferase [Herminiimonas arsenicoxydans]
-----------------------------------------------------------M
GNRLSKIATRT--GDNGTTGL--GDGSRIDKDALRV--HAMGDVDELNSHIGLL-LC--E
-D------------LPPA---------LR--EELISIQ--HDLFDM----GGELCI--PG
----------------YTMIHDAQVTRLDALL--------------------------AK
YNADLP-ALK------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GS--RAASQ-SHVCR---------------TVCRRAERTIVSLGK----AEKM----
---------NDNPRQYM-------NRLS-------DL-------------LF--VLSRVL
```

```
N--RHAG--DGDVL----------------------------------------------
----------------------------------WEKDRVRDIES---------------
------------------------------------------------------
>gi|72163425|ref|YP_291082.1| hypothetical protein Tfu_3026 [Thermobifida fusca YX]
------------------------------------------------------------
----------------MSVTL---------AEARRV----IEAGEAKAAEIGQP-MN---
----------------------------------------IAVVDA----GGNLVA----
----------------HVRMDGAWIGSIDISI--------------------------NK
AYTSRAFDIS------------TKEL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------A
E--HS--QSGGQ-FF------------------GIHASNGGRVMIFAG------------
----------GVPLRRN-------GTVV-------GA-------------VG--VSGGTG
EQDQAVAEAAAAAF----------------------------------------------
------------------------------------------------------------
------------------------------------------------------
>gi|15921748|ref|NP_377417.1| hypothetical protein ST1454 [Sulfolobus tokodaii str. 7]
------------------------------------------------------------
------MFTKS--GDDGNTNV--INK-RVGKDSPLV--NFLGDLDELNSFIGFA-IS-KI
--------------PWED---------MK--KDLERVQ--VELFEI----GEDLST--QS
S---------------KKKIDEKYVKWLEERT--------------------------VE
YRKESG-PVK------------LFVI----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--EEASV-LHVTR---------------SVARRVERNAVKYTK---ELPEI----
---------NRMIIVYL-------NRLS-------SL-------------LF--AMALVA
N--KRRN--VSEKI----------------------------------------------
----------------------------------YDIGKFW-------------------
------------------------------------------------------
>gi|217977938|ref|YP_002362085.1| protein of unknown function DUF336 [Methylocella silvestris BL2]
------------------------------------------------------------
------------------MHV------TIAHAEAAI--EA-ARKKAVETKTQMC------
----------------------------------------IAVVDS----GANLKA----
----------------FYRMDDAWVGSIDISI--------------------------KK
AKTALYFGMP------------TGAI----------------------------------
------------------------------------------------------------
-----------------------------------------------------------G
Q--LS--QPGGS-LF------------------GIEHSNDG-LITFPG------------
---------GLPIVDEE-------GVLV-------GA-------------IG--VSGSSV
ENDNIVAQAGVAVL----------------------------------------------
-------------------------GVSELPDHPWRT-----------------------
------------------------------------------------------
>gi|187735414|ref|YP_001877526.1| ATP/cobalamin adenosyltransferase [Akkermansia muciniphila ATCC BAA-835]
------------------------------------------------------------
----MSVITKR--GDSGETDL--MFGRRSPKTAPRI--EAYGTVDELNSLIGVV-RH---
--------------SGVS---------SRTVEMLDGVQ--ARLVGA----MGELATMEED
LPKYDAKG--------YARIKAEDVAWLEEQA--------------------------HL
LEKECDIRFK------------GWAR----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
GKEGS--LGSAY-LDLAR---------------SVCRRAERRVVALRL---DHALS----
---------NVNTALFL-------NRLS-------DL-------------CW--VLARFE
A--LAAG--EKIQA----------------------------------------------
------------------------------------------------------------
------------------------------------------------------
>gi|153008342|ref|YP_001369557.1| ATP--cobalamin adenosyltransferase [Ochrobactrum anthropi ATCC 49188]
------------------------------------------------------------
MVKLNKIYTRT--GDKGTTGL--ASGPRRLKSDLRV--EAYGTVDETNACIGMARLH---
--------------TGGE-----DNPHAQIDAMLGRIQ--NDLFDL----GADLST--PD
```

```
DGKPLAYE--------PLRIVASQVSRVEADI--------------------------DL
LNTDLQ-PLR------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--AASAA-LHLAR---------------TVSRRAERLMVALAR--VEGEVV----
---------SAEALQYI-------NRLS-------DF-------------LF--VASRTV
N---DNG--AQDVL----------------------------------------------
----------------------------------WVPGANR-------------------
------------------------------------------------------
>gi|94311855|ref|YP_585065.1| ATP:cob(I)alamin adenosyltransferase [Ralstonia
metallidurans CH34]
-----------------------------------------------------------M
GNRLSKIATRT--GDAGTTGL--GDGSRVGKNSLRI--VAIGDVDELNSHIGLL-LT--E
PD------------LPED---------VR--AALLHIQ--HDLFDL----GGELSI--PG
----------------YTLLKAPQVAQLDDWL--------------------------AH
YNAALP-RLA------------EFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--RPAAQ-AHICR---------------TVCRRAERALVELGA----AEAL----
---------NEAPRQYL-------NRLS-------DL-------------LF--VLARVL
N--RAGG--GSDVL----------------------------------------------
----------------------------------WQRERES-------------------
------------------------------------------------------
>gi|150397728|ref|YP_001328195.1| ATP--cobalamin adenosyltransferase [Sinorhizobium
medicae WSM419]
------------------------------------------------------------
MVKLNKIYTRT--GDNGTTGL--VSGPRRLKSDLRV--EAYGAIDEANAFVGLARQH---
--------------THAM---------PDLDATLMRVQ--NDLFDL----GADLAT--PD
TGEKPEYE--------PLRIVAAQVARLEEEI--------------------------DR
LNADLE-PLR------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GS--AASAA-LHVAR---------------TVARRAERQMVALSR--VEGEVV----
---------SAEAVAYV-------NRLS-------DF-------------LF--VAARWT
N---DKG--HADVL----------------------------------------------
----------------------------------WVPGKNR-------------------
------------------------------------------------------
>gi|54023035|ref|YP_117277.1| hypothetical protein nfa10680 [Nocardia farcinica IFM
10152]
-----------------------------------------------------------M
SVHLTRIYTRT--GDDGTTGL--SDFSRVPKTDPRL--VAYADCDETNAAIGVALAL---
--------------GDPD---------ERVRPVLRQVQ--NDLFDA----GADLST--PV
VAEPKHP---------PLRITQDYIDRLEKWC--------------------------DE
FNAELA-PLN------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--PLAAL-LHTAR---------------TVARRAERSAWAAVR--SYPDDT----
---------SVLPARYL-------NRLS-------DL-------------LF--ILSRYT
N-------PDGDVL----------------------------------------------
----------------------------------WRPGGAESAR----------------
------------------------------------------------------
>gi|196157240|ref|YP_002126729.1| putative vitamin B12 related Cobalamin
adenosyltransferase [Alteromonas macleodii 'Deep ecotype']
------------------------------------------------------------
----MKIYTRT--GDKGSTQIYADKAVRVDKDDLVV--QSYGDMDELNSHIGLLAAH---
--------------VPAT---------HN--SLLHDIQ--RSLFQA----GFAISA----
----------------SSTLTPNDVEKLESAI--------------------------DS
LTSQMP-PNT------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--KAAAQ-AHVCR---------------AVCRRAERSVISLSK----HYDV----
---------PEVVHAYL-------NRLS-------DF-------------LF--TFARFL
N--IEAG--VDEVP----------------------------------------------
```

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----------------------------------V-------------------------
------------------------------------------------------
>gi|209963670|ref|YP_002296585.1| ATP:cob(1)alamin adenosyltransferase, putative
[Rhodospirillum centenum SW]
------------------------------------------------------------
-MSKTKVVTRT--GDGGETSL--GRGVRVPKCSDRV--EAYGSVDEVGAMIGVL-RS--M
LE------------DNAA---------VD--ARLRAIQ--IDLYNI----CADLHM--PG
EAGA------------ALRIDGSGLERIEAEL--------------------------GE
MNEGLP-RLA------------NFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------A
G--GT--RAAAF-AHLTR---------------TVTRRAERRVVALAR----AEEV----
---------NPEVLRYM-------NRLS-------DY-------------LF--ILARTL
N---ENG--AKDDL----------------------------------------------
----------------------------------WAPRGVR-------------------
------------------------------------------------------
>gi|193215910|ref|YP_001997109.1| ATP/cobalamin adenosyltransferase [Chloroherpeton
thalassium ATCC 35110]
------------------------------------------------------------
----MKIYTRK--GDTGETGL--FGGKRVPKDDVRV--ECYGTFDEVNATVGLL-RA---
-------------KLPID---------HVWQANLHRIQ--KDMMNV----MSHLAR--PS
DTAKEN----------PNPLPLDGAAFCEQWI--------------------------DE
LEATVAAPSD------------YFLL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GN--EISAL-CQVIR---------------TQFRRGERRLVTLMR----TDEV----
---------HPSIPEYV-------NRLS-------DL-------------FF--VLARAE
M--ATAG--MEEER----------------------------------------------
----------------------------------WNLFIYKRKKKA--------------
------------------------------------------------------
>gi|111018470|ref|YP_701442.1| cobalamin adenosyltransferase [Rhodococcus jostii
RHA1]
-----------------------------------------------------------M
AVHLTKIYTRT--GDDGTTGL--SDFSRVSKNDPRL--IAYADCDEANASIGVAVAL---
--------------GDPP---------EEIRSILRQIQ--NDLFDA----GADLST--PV
EEEPKYP---------PLRISDEYIDRLEGWC--------------------------DE
LNERLE-PLN------------SFIL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GT--ALGAL-LHVAR---------------TVTRRAERSAWAAVD--ANPETT----
---------NALPAKYL-------NRLS-------DL-------------LF--IVSRLA
N-------PEGDVL----------------------------------------------
----------------------------------WKPGAGKS------------------
------------------------------------------------------
>gi|99082268|ref|YP_614422.1| ATP:cob(I)alamin adenosyltransferase [Silicibacter sp.
TM1040]
------------------------------------------------------------
MVVLNKIYTRT--GDKGDTAL--GNGARVAKHSARV--TAYGTTDELNAQVGVARLA---
--------------AEAE---------MD--AALARIQ--NDLFDL----GADLCR--PD
MHLDETAEYP------PLRIAQSQVDRLEAEI--------------------------DA
MNKDLS-PLR------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
G--GS--ALSAH-LHVCR---------------TVARRAERLTTELAG----AEDV----
---------NAAALIYL-------NRLS-------DW-------------FF--VASRVA
N---EHG--AKDVL----------------------------------------------
----------------------------------WVPGANR-------------------
------------------------------------------------------
>gi|222149949|ref|YP_002550906.1| hypothetical protein Avi_4008 [Agrobacterium vitis
S4]
------------------------------------------------------------
MVKLNKIYTRT--GDDGTTAL--VCGPRRFKHDLRV--DAYGTIDEANSAIGVARLY---
--------------TAGD---------EVLDAMLFRIQ--NDLFDL----GADLAT--PD
```

```
TGEKLEWE--------PLRVVQSQVDRIEQEI--------------------------DA
LNAHLE-PLK------------SFVL----------------------------------
------------------------------------------------------------
-----------------------------------------------------------P
A--GS--PASAN-LHLAR---------------TIARRGERIIVDLMQ--IPGEAV----
---------SAPALKYV-------NRLS-------DF-------------LF--VAARYA
N---EIG--KADVL----------------------------------------------
----------------------------------WVPGKNR-------------------
------------------------------------------------------
========================================

%%  PduP [targeting tail implicated]

>gi++|16765381|ref|NP_460996.1| CoA-dependent propionaldehyde dehydrogenase
[Salmonella typhimurium LT2]
------------MNTSELETLIRTIL-----------------SEQLTTPAQTPVQPQGK
-----------------------------------------------------GIFQSVS
EAIDAAHQAFLRYQ-QCPLKTRSAIISAMRQEL--TPLLAPLAEESANETGMGNKEDKFL
KNKAALDNTPGV--EDLTTTALTGDGGMVLFEYS-PFGVIGSVAPSTNPTETIINNSISM
LAAGNSIYFSPHPGAKKVSLKLISLIEEIAFRCCGIRNLVVTVAEPTFEATQQMMAHPRI
AVLAITGGPGIVAMGMK-SGKKVIGAGAGNPPCIVDETADLVKAAEDIINGASFDYNLPC
IAEKSLIVVESVAERLVQQM-QTFGALLL-SPADTDKLRAVCL-------PEGQA-----
NKKLVGKSPSAMLEAAGIA--VPAKAPRLLIAL-VN--ADDPWVTSEQLMPMLPVVKVSD
FDSALALALKVEE--GLHHTAIMHSQNV---SRLNLAARTLQTSIFVKNGPSYAG-IGVG
GE----GFTTFTIATPTGEGTT-----SARTFARSRRCV---------------------
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---------------------------------LTNGFSIR-------------------
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----------------------
>gi++|198246036|ref|YP_002216136.1| ethanolamine utilization protein EutE
[Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853]
------------MNTSELETLIRTIL-----------------SEQLTTPAQTPAQPQGK
-----------------------------------------------------GIFQSVS
EAIDAAHQAFLRYQ-QCPLKTRSAIISAMRQEL--TPLLATLAEESANETGMGNKEDKFL
KNKAALDNTPGV--EDLTTTALTGDGGMVLFEYS-PFGVIGSVAPSTNPTETIINNSISM
LAAGNSVYFSPHPGAKKVSLKLISLIEEIAFRCCGIRNLVVTVAEPTFEATQQMMAHPRI
AVLAITGGPGIVAMGMK-SGKKVIGAGAGNPPCIVDETADLVKAAEDIINGASFDYNLPC
IAEKSLIVVESVAERLVQQM-QTFGALLL-SPADTDKLRAVCL-------PEGQA-----
NKKLVGKSPSAMLEAAGIA--VPAKAPRLLIAL-VN--ADDPWVTSEQLMPMLPVVKVSD
FDSALALALKVEE--GLHHTAIMHSQNV---SRLNLAARTLQTSIFVKNGPSYAG-IGVG
GE----GFTTFTIATPTGEGTT-----SARTFARSRRCV---------------------
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
---------------------------------LTNGFSIR-------------------
------------------------------------------------------------
----------------------
>gi++|197250063|ref|YP_002147008.1| ethanolamine utilization protein EutE
[Salmonella enterica subsp. enterica serovar Agona str. SL483]
------------MNTSELETLIRTIL-----------------SEQLTTPAQTPAQPQGK
-----------------------------------------------------GIFQSVS
EAIDAAHQAFLRYQ-QCPLKTRSAIISAMRQEL--TPLLATLAEESANETGMGNKEDKFL
KNKAALDNTPGV--EDLTTTALTGDGGMVLFEYS-PFGVIGSVAPSTNPTETIINNSISM
LAAGNSIYFSPHPGAKKVSLKLISLIEEIAFRCCGIRNLVVTVAEPTFEATQQMMAHPRI
AVLAITGGPGIVAMGMK-SGKKVIGAGAGNPPCIVDETADLVKAAEDIINGASFDYNLPC
IAEKSLIVVESVAERLVQQM-QTFGALLL-SPADTDKLRAVCL-------PEGQA-----
NKKLVGKSPSAMLEAAGIA--VPAKAPRLLIAV-VN--ADDPWVTSEQLMPMLPVVKVSD
```

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FDSALALALKVEE--GLHHTAIMHSQNV---SRLNLAARTLQTSIFVKNGPSYAG-IGVG
GE----GFTTFTIATPTGEGTT-----SARTFARSRRCV---------------------
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------------------------------------------------------------
---------------------------------LTNGFSIR-------------------
------------------------------------------------------------
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>gi++|205353194|ref|YP_002226995.1| putative CoA-dependent proprionaldehyde
dehydrogenase [Salmonella enterica subsp. enterica serovar Gallinarum str. 287/91]
------------MNTSELETLIRTIL-----------------SEQLTTPAQTPVQPQGK
-----------------------------------------------------GIFQSVS
EAIDAAHQAFLRYQ-QCPLKTRSAIISAMRQEL--TPLLATLAEESANETGMGNKEDKFL
KNKAALDNTPGV--EDLTTTALTGDGGMVLFEYS-PFGVIGSVAPSTNPTETIINNSISM
LAAGNSVYFSPHPGAKKVSLKLISLIEEIAFRCCGIRNLVVTVAEPTFEATQQMMAHPRI
AVLAITGGPGIVAMGMK-SGKKVIGAGAGNPPCIVDETADLVKAAEDIINGASFDYNLPC
IAEKSLIVVESVAERLVQQM-QTFGALLL-SPTDTDKLRAVCL-------PEGQA-----
NKKLVGKSPSAMLEAAGIA--VPAKAPRLLIAV-VN--ADDPWVTSEQLMPMLPVVKVSD
FDSALALALKVEE--GLHHTAIMHSQNV---SRLNLAARTLQTSIFVKNGPSYAG-IGVG
GE----GFTTFTIATPTGEGTT-----SARTFARSRRCV---------------------
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---------------------------------LTNGFSIR-------------------
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----------------------
>gi++|197361971|ref|YP_002141608.1| putative CoA-dependent proprionaldehyde
dehydrogenase [Salmonella enterica subsp. enterica serovar Paratyphi A str.
AKU_12601]
------------MNTSELETLIRTIL-----------------SEQLTTPAQTPAQPQGK
-----------------------------------------------------GIFQSVS
EAIDAAHQAFLRYQ-QCPLKTRSAIISAMRQEL--TPLLATLAEESANETGMGNKEDKFL
KNKAALDNTPGV--EDLTTTALTGDGGMVLFEYS-PFGVIGSVAPSTNPTETIINNSISM
LAAGNSIYFSPHPGAKKVSLKLISLIEEIAFRCCGIRNLVVTVAEPTFEATQQMMAHPRI
AVLAITGGPGIVAMGMK-SGKKVIGAGAGNPPCIVDETADLVKAAEDIINGASFDYNLPC
IAEKSLIVVESVAERLVQQM-QTFGALLL-SPADTDKLRAVCL-------PEGQA-----
NKKLVGKSPSAMLEAAGIA--VPAKAPRLLIAM-VN--ADDPWVTSEQLMPMLPVVKVND
FDSALALALKVEE--GLHHTAIMHSQNV---SRLNLAARTLQTSIFVKNGPSYAG-IGVG
GE----GFTTFTIATPTGEGTT-----SARTFARSRRCV---------------------
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---------------------------------LTNGFSIR-------------------
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----------------------
>gi++|16760983|ref|NP_456600.1| putative CoA-dependent proprionaldehyde
dehydrogenase [Salmonella enterica subsp. enterica serovar Typhi str. CT18]
------------MNTSELETLIRTIL-----------------SEQLTTPAQTPAQPQGK
-----------------------------------------------------GIFQSVS
EAIDAAHQAFLRYQ-QCPLKTRSAIISAMRQEL--TPLLAALAEESANETGMGNKEDKFL
KNKAALDNTPGV--EDLTTTALTGDGGMVLFEYS-PFGVIGSVAPSTNPTETIINNSISM
LAAGNSIYFSPHPGAKKVSLKLISLIEEIAFRCCGIRNLVVTVAEPTFEATQQMMAHPRI
AVLAITGGPGIVAMGMK-SGKKVIGAGAGNPPCIVDETADLVKAAEDIINGASFDYNLPC
IAEKSLIVVESVAERLVQQM-QTFGALLL-SPADTDKLRAVCL-------PEGQA-----
NKKLVGKSPSAMLEAAGIA--VPAKAPRLLIAL-VN--ADDPWVTREQLMPMLPVVKVND
FDSALALALKVEE--GLHHTAIMHSQNV---SRLNLAARTLQTSIFVKNGPSYAG-IGVG
GE----GFTTFTIATPTGEGTT-----SARTFARSRRCV---------------------
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---------------------------------LTNGFSIR-------------------
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>gi++|62180629|ref|YP_217046.1| propanediol utilization: CoA-dependent
propionaldehyde dehydrogenase [Salmonella enterica subsp. enterica serovar
Choleraesuis str. SC-B67]
------------MNTSELETLIRTIL-----------------SEQLTTPAQTPAQPQGK
-----------------------------------------------------GIFQSVS
EAIDAAHQAFLRYQ-QCPLKTRSAIISAIRQEL--TPLLATLAEESANETGMGNKEDKFL
KNKAALDNTPGV--EDLTTTALTGDGGMVLFEYS-PFGVIGSVAPSTNPTETIINNSISM
LAAGNSVYFSPHPGAKKVSLKLISLIEEIAFRCCGIRNLVVTVAEPTFEATQQMMAHPRI
AVLAITGGPGIVAMGMK-SGKKVIGAGAGNPPCIVDETADLVKAAEDIINGASFDYNLPC
IAEKSLIVVESVAERLVQQM-QTFGALLL-SPADTDKLRAACL-------PEGQA-----
NKKLVGKSPSAMLEAAGIA--VPAKAPRLLIAL-VN--ADDPWVTSEQLMPMLPVVKVSD
FDSALALALKVEE--GLHHTAIMHSQNV---SRLNLAARTLQTSIFVKNGPSYAG-IGVG
GE----GFTTFTIATPTGEGTT-----SARTFARSRRCV---------------------
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------LTNGFSIR-------------------
------------------------------------------------------------
----------------------
>gi++|56413047|ref|YP_150122.1| putative CoA-dependent proprionaldehyde
dehydrogenase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC
9150]
------------MNTSELETLIRTIL-----------------SEQLTTPAQTPAQPQGK
-----------------------------------------------------GIFQSVS
EAIDAAHQAFLRYQ-QCPLKTRSAIISAMRQEL--TPLLATLAEESANETGMGNKEDKFL
KNKAALDNTPGV--EDLTTTALTGDGGMVLFEYS-PFGVIGSVAPSTNPTETIINNSISM
LAAGNSIYFSPHPGAKKVSLKLISLIEEIAFRCCGIRNLVVTVAEPTFEATQQMMAHPRI
AVLAITGGPGIVAMGMK-SGKKVI--GAGNPPCIVDETADLVKAAEDIINGASFDYNLPC
IAEKSLIVVESVAERLVQQM-QTFGALLL-SPADTDKLRAVCL-------PEGQA-----
NKKLVGKSPSAMLEAAGIA--VPAKAPRLLIAM-VN--ADDPWVTSEQLMPMLPVVKVND
FDSALALALKVEE--GLHHTAIMHSQNV---SRLNLAARTLQTSIFVKNGPSYAG-IGVG
GE----GFTTFTIATPTGEGTT-----SARTFARSRRCV---------------------
------------------------------------------------------------
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---------------------------------LTNGFSIR-------------------
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>gi++|161502785|ref|YP_001569897.1| hypothetical protein SARI_00836 [Salmonella
enterica subsp. arizonae serovar 62:z4,z23:--]
------------MNTSELEMLIRNIL-----------------SEQLTPEKTQTKGN---
-----------------------------------------------------GIFQTVD
EAIRAAHQAFLRYQ-QCPLKTRSAIIHAMREEL--APHLASLAEESAAETGMGNKEDKLL
KNKAALDNTPGI--EDLTTTALTGDGGMVLFEYS-PFGVIGSVAPSTNPTETIINNSISM
LAAGNSVYFSPHPGAKSVSLKLIGMIEEIAFRCCGIRNLLVTVAEPTFEATQQMMSHPDI
AVLAITGGPGIVAMGMK-SGKKVIGAGAGNPPCIVDETADLVKAAEDIINGAAFDYNLPC
IAEKSLIVVESVAERLIQQM-QAFGALLL-SPSDTDKLRTVCL-------QDGHA-----
NKKLVGKSPATLLEASGIA--TPAKTPRLLIAA-VN--ANDPWVTCEQLMPMLPIVKVSD
FDSALALALKVEA--GLHHTAIMHSENV---SRLNLAARTLQTSIFVKNGPSYAG-IGVG
GE----GFTTFTIATPTGEGTT-----SARTFARSRRCV---------------------
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---------------------------------LTNGFSIR-------------------
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>gi++|218549353|ref|YP_002383144.1| putative CoA-dependent proprionaldehyde
dehydrogenase pduP [Escherichia fergusonii ATCC 35469]
------------MNTRELENIIRNIL-----------------REQLSTTADAPTN----
-----------------------------------------------------GIFDSVD
EAINAAHQAFLRYQ-QCPLKTRSAIISAIRQEL--TPHLDMLATESANETGMGNKEDKFL
KNKAALDNTPGI--EDLTTTALTGDGGMVLFEYS-PFGVIGSVTPSTNPTETIINNSISM
LAAGNSVYFSPHPGAKNISLKLIAMIEEIAFRCSGIHNLIVTVAEPTFEATQQMMTHPNI
AVLAITGGPGIVAMGMK-SGKKVIGAGAGNPPCIVDETADLVKAAEDIINGASFDYNLPC
IAEKSLIVVEEIAGTLVQQM-QNFGALLL-NKEETDKLRDVCL-------PQGMA-----
NKQLVGKSPAALLQAAGIA--VPLKTPRLLIAL-VD--ACDKWVTSEQLMPMLPIVKVKD
FDSALTLALKVEE--GLHHTAIMHSQNV---SRLNLAARTLQTSIFVKNGPSYAG-IGVG
GE----GFTTFTIATPTGEGTT-----SAKTFARSRRCV---------------------
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---------------------------------LTSGFSIR-------------------
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>gi++|206577507|ref|YP_002236771.1| propanediol utilization protein PduP [Klebsiella
pneumoniae 342]
------------MNTAELETLIRTIL-----------------SEKLAPAPVSQEQQ---
-----------------------------------------------------GIYRDVG
SAIDAAHQAFLRYQ-QCPLKTRSAIISALRETL--APELATLAEESATETGMGNKEDKYL
KNKAALENTPGI--EDLTTSALTGDGGMVLFEYS-PFGVIGAVAPSTNPTETIINNSISM
LAAGNSVYFSPHPGAKKVSLTLIARIEEIAYRCSGIRNLVVTVAEPTFEATQQMMAHPLI
AVLAITGGPGIVAMGMK-SGKKVIGAGAGNPPCIVDETADLVKAAEDIISGAAFDYNLPC
IAEKSLIVVASVADRLIQQM-QDFDALLL-SPQETDTLRAVCL-------PDGAA-----
NKKLVGKSPAELLAAAGLA--VPSRPPRLLIAE-VQ--ANDPWVTCEQLMPVLPIVRVAD
FDSALALALRVEE--GLHHTAIMHSQNV---SRLNLAARTLQTSIFVKNGPSYAG-IGVG
GE----GFTTFTIATPTGEGTT-----SARTFARLRRCV---------------------
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---------------------------------LTNGFSIR-------------------
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>gi++|152971735|ref|YP_001336844.1| propanediol utilization: CoA-dependent
propionaldehyde dehydrogenase [Klebsiella pneumoniae subsp. pneumoniae MGH 78578]
------------MNTAELETLIRTIL-----------------SEKLAPTPPAPQQEQ--
-----------------------------------------------------GIFCDVG
SAIDAAHQAFLRYQ-QCPLKTRSAIISALRETL--APELATLAEESATETGMGNKEDKYL
KNKAALENTPGI--EDLTTSALTGDGGMVLFEYS-PFGVIGAVAPSTNPTETIINNSISM
LAAGNSVYFSPHPGAKKVSLKLIARIEEIAYRCSGIRNLVVTVAEPTFEATQQMMSHPLI
AVLAITGGPGIVAMGMK-SGKKVIGAGAGNPPCIVDETADLVKAAEDIISGAAFDYNLPC
IAEKSLIVVASVADRLIQQM-QDFDALLL-SRQEADTLRAVCL-------PDGAA-----
NKKLVGKSPAALLAAAGLA--VPPRPPRLLIAE-VE--ANDPWVTCEQLMPVLPIVRVAD
FDSALALALRVEE--GLHHTAIMHSQNV---SRLNLAARTLQTSIFVKNGPSYAG-IGVG
GE----GFTTFTIATPTGEGTT-----SARTFARLRRCV---------------------
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---------------------------------LTNGFSIR-------------------
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>gi++|215487224|ref|YP_002329655.1| CoA-dependent proprionaldehyde dehydrogenase
[Escherichia coli O127:H6 str. E2348/69]
------------MNNSELETLIRNIL-----------------REQLVPATPRMQRN---
-----------------------------------------------------AIFQTVD
EAVCAAHQAFLRFQ-QCPLKTRSAIISAIREEL--MPRLTELAEESAKETGMGNKEDKYL
KNKAALDNTPGI--EDLTTTALTGDGGMVLFEYS-PFGVIGSVTPSTNPTETIINNSISM
LAAGNSVYFSPHPGAKNVSLKLIAIIEDIAFRCSGIHNLIVTVSEPTFAATEQMMAHPKI
SVLAITGGPGIVAMGMK-SGKKVIGAGAGNPPCIVDETADIVKAAEDIINGASFDYNLPC
IAEKSLIVVASVADYLIQQM-QSFGALLL-NHEQTEKLRAICL-------PDGSA-----
NKKLVGKSPSALLEAASLP--LPAKAPRLLIAV-VD--ADDSWVTCEQLMPMLPIVKVND
FDSALALALKVED--GLHHTAIMHSQNV---SRLNLAARVMQTSIFVKNGPSWAG-IGVG
GE----GFTTFTIATPTGEGTT-----SARTFARSRRCV---------------------
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---------------------------------LTSGFSIR-------------------
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>gi++|157158089|ref|YP_001463352.1| propanediol utilization protein PduP
[Escherichia coli E24377A]
------------MNNSELETLIRNIL-----------------REQLVPATPRTQRN---
-----------------------------------------------------AIFQTVD
EAVCAAHQAFLRFQ-QCPLKTRSAIISAIREEL--MPRLTELAEESAKETGMGNKEDKYL
KNKAALDNTPGI--EDLTTTALTGDGGMVLFEYS-PFGVIGSVTPSTNPTETIINNSISM
LAAGNSVYFSPHPGAKNVSLKLITTIEDIAFRCSGIHNLIVTVSEPTFAATEQMMAHPKI
SVLAITGGPGIVAMGMK-SGKKVIGAGAGNPPCIVDETADIVKAAEDIINGASFDYNLPC
IAEKSLIVVASVADYLIQQM-QSFGALLL-NYEQTEKLRAICL-------PDGSA-----
NKKLVGKSPSALLEAAGLP--LPAKAPRLLIAV-VD--ANDSWVTCEQLMPMLPIVKVND
FDSALTLALKVED--GLHHTAIMHSQNV---SRLNLAARVMQTSIFVKNGPSWAG-IGVG
GE----GFTTFTIATPTGEGTT-----SARTFARSRRCV---------------------
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---------------------------------LTSGFSIR-------------------
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>gi++|218705543|ref|YP_002413062.1| putative CoA-dependent proprionaldehyde
dehydrogenase pduP [Escherichia coli UMN026]
------------MNNSELETLIRNIL-----------------REQLVPATPRMQRN---
-----------------------------------------------------AIFQTVD
EAVCAAHQAFLRFQ-QCPLKTRSAIISAIREEL--IPRLTELAEESAKETGMGNKEDKYL
KNKAALDNTPGI--EDLTTTALTGDGGMVLFEYS-PFGVIGSVTPSTNPTETIINNSISM
LAAGNSVYFSPHPGAKYVSLKLITTIEDIAFRCSGIHNLIVTVSEPTFAATEQMMAHPKI
SVLAITGGPGIVAMGMK-SGKKVIGAGAGNPPCIVDETADIVKAAEDIINGASFDYNLPC
IAEKSLIVVASVADYLIQQM-QSFGALLL-NYEQTEKLRAICL-------PDGSA-----
NKKLVGKSPSALLEAAGLP--LPAKAPRLLIAV-VD--ANDSWVTCEQLMPMLPIVKVND
FDSALTLALKVED--GLHHTAIMHSQNV---SRLNLAARVMQTSIFVKNGPSWAG-IGVG
GE----GFTTFTIATPTGEGTT-----SARTFARSRRCV---------------------
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---------------------------------LTSGFSIR-------------------
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>gi++|123442957|ref|YP_001006932.1| putative propanediol utilization protein: 
CoA-dependent propionaldehyde dehydrogenase [Yersinia enterocolitica subsp. 
enterocolitica 8081]
------------MNTNDLESLIRTIL-----------------TEQLTPVTAPASS----
-----------------------------------------------------AIFASVD
EAINAAHSAFLRYQ-QSPMKTRSAIIRAIREQL--KPQLVSLSERGASETGMGNKEDKFL
KNKAALENTPGI--EDLSTTALTGDGGMVLFEYS-PFGVIGSVTPSTNPTETIINNSISM
LAAGNAVYFSPHPGAKAVSLDLIAQIEEIIFNSCGIRNLVVTVKEPSFEATQQMMAHDKI
ALLAITGGPAIVAMSMK-SGKKVIGAGAGNPPCLVDETAELVKAAQDIVAGASFDYNLPC
IAEKSLIVVESVADRLLQQM-QAFDALLISNPQEIDSLRKACL------TPQGHA-----
NKNLVGKSPIELLKAAGIT--CPAKAPRLLLVE-VA--GDDPLVTTEQLMPLLPVVRVKD
FDAALTLALHVEG--GLHHTATMHSQNV---SRLNLAARLLQTSIFVKNGPSYAG-IGVG
GE----GFTTFTIATPTGEGTT-----SARTFARQRRCV---------------------
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---------------------------------LTNGFSIR-------------------
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>gi++|74312543|ref|YP_310962.1| putative propanediol utilization protein: 
CoA-dependent propionaldehyde dehydrogenase [Shigella sonnei Ss046]
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-----------------------------------MPRLTELAEESAKETGMGNKEDKYL
KNKAALDNTPGI--EDLTTTALTGDGGMVLFEYS-PFGVIGSVTPSTNPTETIINNSISM
LAAGNSVYFSPHPGAKNVSLKLITTIEDIAFRCSGIHNLIVTVSEPTFAATEQMMAHPKI
SVLAITGGPGIVAMGMK-SGKKVIGAGAGNPPCIVDETADIVKAAEDIINGASFDYNLPC
IAEKSLIVVASVADYLIQQM-QSFGALLL-NYEQTEKLRAICL-------PDGSA-----
NKKLVGKSPSALLEAAGLP--LPAKAPRLLIAV-VD--ADDSWVTCEQLMPMLPIVKVKD
FDSALTLALKVED--GLHHTAIMHSQNV---SRLNLAARVMQTSIFVKNGPSWAG-IGVG
GE----GFTTFTIATPTGEGTT-----SARTFARSRRCV---------------------
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---------------------------------LTSGFSIR-------------------
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>gi++|116872539|ref|YP_849320.1| CoA-dependent propionaldehyde dehydrogenase 
[Listeria welshimeri serovar 6b str. SLCC5334]
------------MESLELEQLVKKVL-----------------LEKLAEQKDVPVKTTTQ
GAKS-------------------------------------------------GIFDTVD
EAVQAAVQAQNSYK-EKSLEERRNVVKAIREAL--YPEIESIATRAVAETGMGNVTDKIL
KNTLAIEKTPGV--EDLYTEVATGDNGMTLYELS-PYGVIGAVAPSTNPTETLICNTIGM
LAAGNAVFYSPHPGAKNISLWLIEKLNTIVRESCGIDNLVVTVEKPSIQAAQEMMNHPKV
PLLVITGGPGVVLQAMQ-SGKKVIGAGAGNPPSIVDETANIEKAAADIVDGASFDHNILC
IAEKSVVAVDSITDFLLFQM-EKNGALHVTNPSDIKKLEKVAV------TDKGVT-----
NKKLVGKSASEILKEAGIT--CDF-TPRLIIVE-TD--KSHPFATVELLMPIVPVVRVPD
FDEALKVAIELEQ--GLHHTATMHSQNI---SRLNKAARDMQTSIFVKNGPSFAG-LGFR
GE----GSTTFTIATPTGEGTT-----TARHFARRRRCV---------------------
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---------------------------------LTDGFSIR-------------------
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>gi++|16800198|ref|NP_470466.1| hypothetical protein lin1129 [Listeria innocua 
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Clip11262]
------------MESLELEQLVKKVL-----------------LEKLAEQKEVPTKTTTQ
GAKS-------------------------------------------------GVFDTVD
EAVQAAVIAQNCYK-EKSLEERRNVVKAIREAL--YPEIETIATRAVAETGMGNVTDKIL
KNTLAIEKTPGV--EDLYTEVATGDNGMTLYELS-PYGVIGAVAPSTNPTETLICNSIGM
LAAGNAVFYSPHPGAKNISLWLIEKLNTIVRDSCGIDNLIVTVAKPSIQAAQEMMNHPKV
PLLVITGGPGVVLQAMQ-SGKKVIGAGAGNPPSIVDETANIEKAAADIVDGASFDHNILC
IAEKSVVAVDSIADFLLFQM-EKNGALHVTNPSDIQKLEKVAV------TDKGVT-----
NKKLVGKSATEILKEAGIA--CDF-TPRLIIVE-TE--KSHPFATVELLMPIVPVVRVPD
FDEALEVAIELEQ--GLHHTATMHSQNI---SRLNKAARDMQTSIFVKNGPSFAG-LGFR
GE----GSTTFTIATPTGEGTT-----TARHFARRRRCV---------------------
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---------------------------------LTDGFSIR-------------------
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>gi++|46907383|ref|YP_013772.1| CoA-dependent propionaldehyde dehydrogenase
[Listeria monocytogenes str. 4b F2365]
------------MESLELEQLVKKVL-----------------LEKLAEQKDAPVKTTVK
GAKS-------------------------------------------------GVFDTVD
EAVQAAVIAQNNYK-EKSLEERRNVVKAIREAL--YPEIESIAARAVAETGMGNVADKIL
KNTLAIEKTPGV--EDLYTEVATGDNGMTLYELS-PYGVIGAVAPSTNPTETLICNTIGM
LAAGNAVFYSPHPGAKNISLWLIEKLNTIVRESCGIDNLVVTVEKPSIQAAQEMMNHPKV
PLLVITGGPGVVLQAMQ-SGKKVIGAGAGNPPSIVDETANIEKAAADIVDGASFDHNILC
IAEKSIVAVDSIADFLMFQM-EKNGALHVTNPSDIQKLEKVAV------TDKGVT-----
NKKLVGKSASEILKEAGIV--CDF-SPRLIIVE-TE--KTHPFATVELLMPIVPVVRVPN
FDEALDVAIELEQ--GLHHTATMHSQNI---SRLNKAARDMQTSIFVKNGPSFAG-LGFR
GE----GSTTFTIATPTGEGTT-----TARHFARRRRCV---------------------
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---------------------------------LTDGFSIR-------------------
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>gi++|217964766|ref|YP_002350444.1| ethanolamine utilization protein EutE [Listeria
monocytogenes HCC23]
------------MESLELEKLVKKVL-----------------LEKLAEQKDIPVKTTVK
GAKS-------------------------------------------------GVFDTVD
EAVQAAVIAQNSYK-EKSLEERRNVVKAIREAL--YPEIESIAARAVAETGMGNVADKIL
KNTLAIEKTPGV--EDLYTEVATGDNGMTLYELS-PYGVIGAVAPSTNPTETLICNTIGM
LAAGNAVFYSPHPGAKNISLWLIEKLNTIVRESCGVDNLVVTVEKPSIQAAQEMMNHPKV
PLLVITGGPGVVLQAMQ-SGKKVIGAGAGNPPSIVDETANIEKAAADIVDGASFDHNILC
IAEKSIVAVDSIADFLMFQM-EKNGALHVTNPSDIQKLEKVAV------TDKGVT-----
NKKLVGKSASEILKEAGIV--CDF-SPRLIIVE-TE--KTHPFATVELLMPIVPVVRVPN
FDEALDVAIELEQ--GLHHTATMHSQNI---SRLNKAARDMQTSIFVKNGPSFAG-LGFR
GE----GSTTFTIATPTGEGTT-----TARHFARRRRCV---------------------
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---------------------------------LTDGFSIR-------------------
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>gi++|16803205|ref|NP_464690.1| hypothetical protein lmo1165 [Listeria monocytogenes
EGD-e]
------------MESLELEKLVKKVL-----------------LEKLAEQKGIPVKTMTK
GAKS-------------------------------------------------GVFDTVD
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EAVQAAVIAQNSYK-EKSLEERRNVVKAIREAL--YPEIESIAARAVAETGMGNVADKIL
KNTLAIEKTPGV--EDLYTEVATGDNGMTLYELS-PYGVIGAVAPSTNPTETLICNTIGM
LAAGNAVFYSPHPGAKNISLWLIEKLNTIVRESCGVDNLVVTVEKPSIQAAQEMMNHPKV
PLLVITGGPGVVLQAMQ-SGKKVIGAGAGNPPSIVDETANIEKAAADIVDGASFDHNILC
IAEKSVVAVDSIADFLMFQM-EKNGALHVTNPSDIQKLEKVAV------TDKGVT-----
NKKLVGKSASEILKEAGIA--CDF-SPRLIIVE-TE--KTHPFATVELLMPIVPVVRVPN
FEEALEVAIELEQ--GLHHTATMHSQNI---SRLNKAARDMQTSIFVKNGPSFAG-LGFR
GE----GSTTFTIATPTGEGTT-----TARHFARRRRCV---------------------
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---------------------------------LTDGFSIR-------------------
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>gi++|188590535|ref|YP_001921227.1| ethanolamine utilization protein EutE
[Clostridium botulinum E3 str. Alaska E43]
---------MNDFNMIDIESIVKNIV-----------------KELTGNEKEQGTITTAA
VPKEVNPLVDIEKKIMGFVNTPTMPIGEH------------------------GVFEDIN
DAIEQAWIAEQEYR-KVGLDKRTEIIEAFKAEV--RKNVEEISRRTFEETGMGRYEDKIL
KNNLALDKTPGV--EDLEAGVKTGDGGLTLYEMS-PFGVIGAIAPSTNPTETIINNGISM
LAGGNTVVFSPHPGAKDVSVFIIQLINKAIERVNGPKNLIVTVRNPNIESTNIMLAHPKV
NMICATGGPGIVKVALS-SGKKAIGAGAGNPPVVVDETADIEKAAVDIIDGCSFDNNLPC
ICEKEVIVVDKVADYLKTCM-SKYCALEITDKNMLAQLEKLVL------TENGTI-----
NKKFVGKNADYIMSKLGVN--IDP-SIRVIFAE-VE--ANHPFAVEELMMPILPVIRVRN
VDEAIDLGVELEH--GNRHTAIMHSKHI---DNLSKFAKAVQTTIFVKNAPSYAG-IGYG
AE----GHGTFTIAGPTGEGLT-----SARTFTRKRRCV---------------------
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---------------------------------MVDNFSIK-------------------
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>gi++|83592250|ref|YP_426002.1| aldehyde dehydrogenase [Rhodospirillum rubrum ATCC
11170]
------------MNDGQIAAAVAKVL--------EAYGVPADPSAAAPAPAAPVAPAAPT
AGSVSEMIARGIAKASSDDQIAQIVAKVVGDYSAQAAKPAVVPGAAASTEAGDGVFDTMD
AAVDAAVLAQQQYL-LCSMTDRQRFVDGIREVILQKDTLELISRMAAEETGMGNYEHKLI
KNRLAAEKTPGT--EDLTTEAFSGDDGLTLVEYS-PFGAIGAVAPTTNPTETIICNSIGM
LAAGNSVIFSPHPRATKVSLLTVKLINQKLACLGAPANLVVTVSKPSVENTNAMMAHPKI
RMLVATGGPGIVKAVMS-TGKKAIGAGAGNPPVVVDETADIEKAALDIINGCSFDNNLPC
IAEKEIIAVAQIADYLIFSM-KKQGAYQITDPAVLRKLQDLVL------TAKGGP-----
QTSCVGKSAVWLLNKIGIE--VDS-SVKVILME-VP--KEHPFVQEELMMPILPLVRVSD
VDEAIAVAIEVEH--GNRHTAIMHSTNV---RKLTKMAKLIQTTIFVKNGPSYAG-LGVG
GE----GYTTFTIAGPTGEGLT-----SAKSFARKRKCV---------------------
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---------------------------------MVEALNIR-------------------
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>gi++|187933041|ref|YP_001885942.1| ethanolamine utilization protein EutE
[Clostridium botulinum B str. Eklund 17B]
---------MNDFNMIDIESIVKNIV-----------------KELTGNEKEQGAIITAT
APKEVN------------------------PLVDIEKKIMGFMNTPTMQAGEYGVFEDIN
DAIEQAWLAEQEYR-KVGLDKRTEIIEVFKAEV--RKNVEEISRRTFEETGMGRYEDKIL
KNNLALDKTPGV--EDLEAGVKTGDGGLTLYEMS-PFGVIGAIAPSTNPTETIINNGISM
LAGGNTVVFSPHPGAKDVSVFIIQLINKAIERVNGPKNLIVTVRNPNIESTNIMLSHPKV
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NMICATGGPGIVKVALS-SGKKAVGAGAGNPPVVVDETADIEKAAVDIIDGCSFDNNLPC
ICEKEVIVVDKVTDYLKTCM-SKYCALEITDKNMLAQLEKLVL------TENGTI-----
NKKFVGKNADYIMSKLGIN--IDP-SIRVIFAE-VG--ANHPFAVEELMMPILPIIRVRN
VDEAIELGVELEH--GNRHTAIMHSKHI---DNLSKFAKAVQTTIFVKNAPSYAG-IGYG
AE----GHGTFTIAGPTGEGLT-----SARTFTRKRRCV---------------------
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---------------------------------MVDNFSIK-------------------
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>gi++|117626447|ref|YP_859770.1| ethanolamine utilization protein EutE [Escherichia
coli APEC O1]
------------MNDIEIAQAVSTIL-----------------SKFTKATPDEAP--ATS
EAARVDGLDEIVAKALAQHSSVRDASAI-----------SQVAKVAKVANASTGAFDTMD
EAISAAVLAQVQYR-HCSMQDRASFINGIRDVFLQEDVLCALSRMAVEETGMGNYEDKLI
KNRVAALKTPGI--EDLTTSAVSGDGGLTLIEYS-AFGVIGSITPTTNPTETIINNSIGM
LAAGNTVVFSPHPRSRKVSLYAVELINNKLAQLGAPANMVVTVTKPSIDNTNVLINDPRI
NMLVATGGPAIVKTVMS-SGKKAIGAGAGNPPAVVDETADIEKAARDIIKGCSFDNNLPC
VAEKEVIVVNQVADYLIHCM-KKSGAYLLCDKKLSQQLQSLVL-----NEKGTGP-----
NTAFVGKDARYILQQLGIQ--VGD-DIKVILIE-AE--KTHPFVVHELMMPVLPVVRVDN
VDEAIELAVKVEH--GNRHTAVMHSTNV---EKLTKMARLIQTTIFVKNGPSYAG-LGVG
GE----GHATFTIAGPTGEGLT-----SARSFARRRRCV---------------------
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---------------------------------MVEALNIR-------------------
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>gi++|26250354|ref|NP_756394.1| ethanolamine utilization protein eutE [Escherichia
coli CFT073]
------------MNDIEIAQAVSTIL-----------------SKFTKATPDEAP--ATS
EAARVDGLDEIVAKALAQHSSVRDASAI-----------SQ---VAKVANASTGAFDTMD
EAISAAVLAQVQYR-HCSMQDRASFINGIRDVFLQEDVLCALSRMAVEETGMGNYEDKLI
KNRVAALKTPGI--EDLTTSAVSGDGGLTLIEYS-AFGVIGSITPTTNPTETIINNSIGM
LAAGNTVVFSPHPRSRKVSLYAVELINNKLAQLGAPANMVVTVTKPSIDNTNVLINDPRI
NMLVATGGPAIVKTVMS-SGKKAIGAGAGNPPAVVDETADIEKAARDIIKGCSFDNNLPC
VAEKEVIVVNQVADYLIHCM-KKSGAYLLCDKKLSQQLQSLVL-----NEKGTGP-----
NTAFVGKDARYILQQLGIQ--VGD-DIKVILIE-AE--KTHPFVVHELMMPVLPVVRVDN
VDEAIELAVKVEH--GNRHTAVMHSTNV---EKLTKMARLIQTTIFVKNGPSYAG-LGVG
GE----GHATFTIAGPTGEGLT-----SARSFARRRRCV---------------------
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---------------------------------MVEALNIR-------------------
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>gi++|167040571|ref|YP_001663556.1| aldehyde dehydrogenase [Thermoanaerobacter sp.
X514]
-----------MIDENLVVTITKKIL-----------------NEINLKEAEEKKEKDNP
DL---------------------------------------------------GIFNDVN
EAVECAKEAQKKFA-LMDLEKREEIIAAIREAC--VNNARLLAEIACSETGRGRVEDKVA
KNILAAKKTPGT--EDLKPTAWTGDRGLTLVEMA-PVGVIASITPVTNPTATIINNTISM
LAAGNAVVFNPHPSAKKTSNKAVEIINEAILKVGAPNGLVCSINNPTIQTAQKLMEHPEV
NMVVVTGGKAVVQTALR-CGKKVIGAGAGNPPVVVDETADIVKAAHDIACGASFDNNLPC
IAEKEIIAVERIADTLLERM-KREGAYVL-HGKDIDRMTELIF-------QGGAI-----
NKDLIGRDAHFILSQIGIE--TGK-DIRLVVMP-VD--VSHPLVYHEQLMPVIPFVTVPT
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VEEAINLAVKAEG--GNRHTAMMHSKNV---ENMTAFARAIQTTIFVKNAPSYAG-IGFG
GE----GYTTFTIAGPTGEGLT-----SARTFTRQRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|90422686|ref|YP_531056.1| aldehyde dehydrogenase [Rhodopseudomonas palustris
BisB18]
----------------MVAKAIRDHA-----------------GTAQPSGNAATSSAAVS
D----------------------------------------------------GVFETMD
AAVEAAALAQQQYL-LCSMSDRARFVQGIRDVILNQDTLEKMSRMAVEETGMGNYEHKLI
KNRLAGEKTPGI--EDLTTDAFSGDNGLTLVEYS-PFGVIGAITPTTNPTETIVCNSIGM
LAAGNSVVFSPHPRARQVSLLLVRLINQKLAALGAPENLVVTVEKPSIENTNAMMAHPKV
RMLVATGGPAIVKAVLS-TGKKAIGAGAGNPPVVVDETANIEKAACDIVNGCSFDNNLPC
VAEKEIIAVAQIADYLIFNL-KKNGAYEIKDPAVLQQLQDLVL------TAKGGP-----
QTKCVGKSAVWLLSQIGIS--VDA-SIKIILME-VP--REHPFVQEELMMPILPLVRVET
VDDAIDLAIEVEH--DNRHTAIMHSTDV---RKLTKMAKLIQTTIFVKNGPSYAG-LGAG
GE----GYSTFTIAGPTGEGLT-----SAKSFARRRKCV---------------------
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---------------------------------MVEALNIR-------------------
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>gi++|116334184|ref|YP_795711.1| CoA-dependent propionaldehyde dehydrogenase
[Lactobacillus brevis ATCC 367]
------------MNTENIEQAIRKIL-----------------SEELSNPQSSTATNTTV
PGKN-------------------------------------------------GIFKTVN
EAIAATKAAQENYA-DQPISVRNKVIDAIREGF--RPYIEDMAKRIHDETGMGTVSAKIA
KLNNALYNTPGP--EILQPEAETGDGGLVMYEYA-PFGVIGAVGPSTNPSETVIANAIMM
LAGGNTLFFGAHPGAKNITRWTIEKLNELVADATGLHNLVVSLETPSIESVQEVMQHPDV
AMLSITGGPAVVHQALI-SGKKAVGAGAGNPPAMVDATANIALAAHNIVDSAAFDNNILC
TAEKEVVVEAAVKDELIMRM-QQEGAFLVTDSADIEKLAQMTI------GPKGAP-----
DRKFVGKDATYILDQAGIS--YTG-TPTLIILE-AA--KDHPLVTTEMLMPILPVVCCPD
FDSVLATATEVEG--GLHHTASIHSENL---PHINKAAHRLNTSIFVVNGPTYCG-TGVA
TNGAHSGASALTIATPTGEGTA-----TSKTYTRRRRLN---------------------
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---------------------------------SPEGFSLRTWEA---------------
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>gi++|150018857|ref|YP_001311111.1| aldehyde dehydrogenase [Clostridium beijerinckii
NCIMB 8052]
----------MDVDVVLVEKLVRQAI-----------------EEVKNKNLLNLDKFESV
KNY--------------------------------------------------GIFGTMD
AAVEASFVAQKQLL-NASMTDKQKYVDTIKATILKKENLELISRMSVEETEIGKYEHKLI
KNRVAAEKTPGI--EDLTTEAMTGDNGLTLVEYC-PFGVIGAITPTTNPTETIICNSISM
IAGGNTVVFSPHPRAKNVSIKLVTMLNKALEEAGAPDNLIATVKEPSIENTNIMMEHPKI
RMLVATGGPAIVNKVMS-TGKKAIGAGAGNPPVVVDETADIEKAAIDIVNGCSFDNNVPC
IAEKEVFAVDQICDYLIHYM-KLNGAYEIKDRDLIQKLLDLVT------NENGGP-----
KVSFVGKSAPYILNKLGIS--VDE-NIKVIIME-VE--KNHHFVLEEMMMPILPIVRTKD
VDEAIECAYVAEH--GNRHTAIMHSKNV---DKLTKMARLLETTIFVKNAPSYAG-IGVG
GE----GTTTFTIAGPTGEGLT-----TARSFCRKRRCV---------------------
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---------------------------------MVDAFNIR-------------------
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>gi++|26248822|ref|NP_754862.1| ethanolamine utilization protein eutE [Escherichia
coli CFT073]
------------MNQQDIEQVVKAVL-----------------LKMQSSDTPPAAVHEM-
-----------------------------------------------------GVFASLD
DAVAAAKVAQQGLK---SVAMRQLAIAAIREAG--EKHARDLAELAVSETGMGRVEDKFA
KNVAQARGTPGV--ECLSPQVLTGDNGLTLIENA-PWGVVASVTPSTNPAATVINNAISL
IAAGNSVIFAPHPAAKKVSQRAITLLNQAIVAAGGPENLLVTVANPDIETAQRLFKFPGI
GLLVVTGGEAVVEAARKHTNKRLIAAGAGNPPVVVDETADLARAAQSIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQHAVKL-TAEQAQQLQSVLL-KNIDERGKGTV-----
SRDWVGRDAAKIAAAIGLN--VPS-ETRLLFVE-TT--AEHPFAVTELMMPVLPVVRVAN
VADAIALAVKLEG--GCHHTAAMHSRNI---ENMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|218700911|ref|YP_002408540.1| putative aldehyde dehydrogenase, ethanolamine
utilization protein [Escherichia coli IAI39]
------------MNQQDIEQVVKAVL-----------------LKMQSSDTPPAAVHEM-
-----------------------------------------------------GVFASLD
DAVAAAKVAQQGLK---SVVMRQLAIAAIREAG--EKHARDLAELAVSETGMGRVEDKFA
KNVAQARGTPGV--ECLSPQVLTGDNGLTLIENA-PWGVVASVTPSTNPAATVINNAISL
IAAGNSVIFAPHPAAKKVSQRAITLLNQAIVAAGGPENLLVTVANPDIETAQRLFKFPGI
GLLVVTGGEAVVEAARKHTNKRLIAAGAGNPPVVVDETADLARAAQSIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQHAVKL-TAEQAQQLQSVLL-KNIDECGKGTV-----
SRDWVGRDAAKIAAAIGLK--VPE-QTRLLFVE-TT--AEHPFAVTELMMPVLPVVRVAN
VADAIALAVKLEG--GCHHTAAMHSRNI---ENMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|170681242|ref|YP_001744637.1| ethanolamine utilization protein EutE
[Escherichia coli SMS-3-5]
------------MNQQDIEQVVKAVL-----------------LKMQSSDTPPAAVHEM-
-----------------------------------------------------GVFASLD
DAVAAAKVAQQGLK---SVAMRQLAIAAIREAG--EKHARDLAELAVSETGMGRVEDKFA
KNVAQARGTPGV--ECLSPQVLTGDNGLTLIENA-PWGVVASVTPSTNPAATVINNAISL
IAAGNSVIFAPHPAAKKVSQRAITLLNQAIVAAGGPENLLVTVANPDIETAQRLFKFPGI
GLLVVTGGEAVVEAARKHTNKRLIAAGAGNPPVVVDETADLARAAQSIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQHAVKL-TAEQAQQLQSVLL-KNIDECGKGTV-----
SRDWVGRDAAKIAAAIGLK--VPE-QTRLLFVE-TT--AEHPFAVTELMMPVLPVVRVAN
VADAIALAVKLEG--GCHHTAAMHSRNI---ENMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|161612791|ref|YP_001586756.1| hypothetical protein SPAB_00490 [Salmonella
enterica subsp. enterica serovar Paratyphi B str. SPB7]
------------MNQQDIEQVVKAVL-----------------LKMKDSSQPASTVHEM-
-----------------------------------------------------GVFASLD
DAVAAAKRAQQGLK---SVAMRQLAIHAIREAG--EKHARELAELAVSETGMGRVDDKFA
KNVAQARGTPGV--ECLSPQVLTGDNGLTLIENA-PWGVVASVTPSTNPAATVINNAISL
IAAGNSVVFAPHPAAKKVSQRAITLLNQAVVAAGGPENLLVTVANPDIETAQRLFKYPGI
GLLVVTGGEAVVDAARKHTNKRLIAAGAGNPPVVVDETADLPRAAQSIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQHAVKL-TAAQAEQLQPVLL-KNIDERGKGTV-----
SRDWVGRDAGKIAAAIGLN--VPD-QTRLLFVE-TS--ANHPFAVTELMMPVLPVVRVAN
VEEAIALAVQLEG--GCHHTAAMHSRNI---DNMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|152971320|ref|YP_001336429.1| ethanolamine utilization protein [Klebsiella
pneumoniae subsp. pneumoniae MGH 78578]
------------MNQQDIEQVVKAVL-----------------LKMKDSSQPAGTVHDM-
-----------------------------------------------------GVFASLD
DAVAAATVAQQGLK---RVAMRQQVIQAIREAG--EKYARELAELAVTETGMGRVEDKFA
KNVAQARGTPGV--ECLTPQVLTGDNGLTLIENA-PWGVVASVTPSTNPAATVINNAISL
IAAGNSVVFAPHPAAKKISQRAITLLNQAVVAAGGPANLLVTVANPDIDTAQRLFKYPGI
GLLVVTGGEAVVEAARKHTNKRLIAAGAGNPPVVVDETADLPRAAQAIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQQAVKL-TAAQAEQLQPLLL-KNIDERGKGTV-----
SRDWVGRDAGKIAAAIGLQ--VPA-QTRLLFVE-TP--ASHPFAVTELMMPVLPVVRVAN
VEEAIALAVQLEG--GCHHTAAMHSRNI---DNMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|110642627|ref|YP_670357.1| ethanolamine utilization protein EutE [Escherichia
coli 536]
------------MNQQDIEQVVKAVL-----------------LKMQSSDTPPAAVHEM-
-----------------------------------------------------GVFASLD
DAVAAAKVAQQGLK---SVAMRQLAIAAIREAG--EKHARDLAELAVSETGMGRVEDKFA
KNVAQARGTPGV--ECLSPQVLTGDNGLTLIENA-PWGVVASVTPSTNPAATVINNAISL
IAAGNSVIFAPHPAAKKVSQRAITLLNQAIVAAGGPENLLVTVANPDIETAQRLFKFPGI
GLLVVTGGEAVVEAARKHTNKRLIAAGAGNPPVVVDETADLARAAQSIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQHAVKL-TAEQAQQLQSVLL-KNIDERGKGTV-----
SRDWVGRDAAKIAAAIGLK--VPE-QTRLLFVE-TT--AEHPFAVTELMMPVLPVVRVAN
VADAIALAVKLEG--GCHHTAAMHSRNI---ENMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|218705953|ref|YP_002413472.1| putative aldehyde dehydrogenase, ethanolamine
utilization protein [Escherichia coli UMN026]
------------MNQQDIEQVVKAVL-----------------LKMQSSDTPPAAVHEM-
-----------------------------------------------------GVFASLD
DAVAAAKVAQQGLK---SVAMRQLAIAAIREAG--EKHARDLAELAVSETGMGRVEDKFA
KNVAQARGTPGV--ECLSPQVLTGDNGLTLIENA-PWGVVASVTPSTNPAATVINNAISL
IAAGNSVIFAPHPAAKKVSQRAITLLNQAIVAAGGPENLLVTVANPDIETAQRLFKFPGI
GLLVVTGGEAVVEAARKHTNKRLIAAGAGNPPVVVDETADLARAAQSIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQHAVKL-TAEQAQQLQPVLL-KNIDEHGKGTV-----
SRDWVGRDAAKIAAAIGLT--VPE-QTRLLFVE-TT--AEHPFAVTELMMPVLPVVRVAN
VADAIALAVKLEG--GCHHTAAMHSRNI---ENMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|218782808|ref|YP_002434126.1| Aldehyde Dehydrogenase [Desulfatibacillum
alkenivorans AK-01]
----------MSVKEFALEDMVASVI-----------------MEMMNKDDDSCQPTGD-
-----------------------------------------------------GIYETID
EAVAKAKAAQPRLI-SLSLEKREAILTAIRKIS--LEKNEEWAKATVAETGLGRVEDKIA
ENILAATKTPGT--EDLDAKALSGDAGLTLIEYA-PFGVIGSLTPVTNATGTLINNTISM
LAGGNTVVYNVHPSALKISTEVIRTFHKVIVENGGPEGCVGMVATPTMETAGEIMAHPDI
NVLVATGGAGVVKAVLS-SGKKAIGAGAGNPPVLVDETACIRKAAEEIIAGHSINNNIFC
ISEKEVIAVDEVADNLLKFM-EETGKAAILTPEEAQKVTETVI-------HDNHV-----
VKDYVGKNASVIIEGAGLTRLAGKKDLRCLVFE-AD--CKHPMVWIEQMMPVLPMVRVKD
VWEGIDLAVKVEQ--GNRHTAMMHSTNV---EHLTALARAIQTTIFVKNGPSYSG-IGLN
GE----GHATFTIAGPTGEGIT-----SAKSFCRQRRCV---------------------
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---------------------------------LIDSFRIV-------------------
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>gi++|16765783|ref|NP_461398.1| putative aldehyde oxidoreductase [Salmonella
typhimurium LT2]
------------MNQQDIEQVVKAVL-----------------LKMKDSSQPASTVHEM-
-----------------------------------------------------GVFASLD
DAVAAAKRAQQGLK---SVAMRQLAIHAIREAG--EKHARELAELAVSETGMGRVDDKFA
KNVAQARGTPGV--ECLSPQVLTGDNGLTLIENA-PWGVVASVTPSTNPAATVINNAISL
IAAGNSVVFAPHPAAKKVSQRAITLLNQAVVAAGGPENLLVTVANPDIETAQRLFKYPGI
GLLVVTGGEAVVDAARKHTNKRLIAAGAGNPPVVVDETADLPRAAQSIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQHAVKL-TAAQAEQLQPVLL-KNIDERGKGTV-----
SRDWVGRDAGKIAAAIGLN--VPD-QTRLLFVE-TP--ANHPFAVTEMMMPVLPVVRVAN
VEEAIALAVQLEG--GCHHTAAMHSRNI---DNMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|206580835|ref|YP_002237208.1| ethanolamine utilization protein EutE
[Klebsiella pneumoniae 342]
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------------MNQQDIEQVVKAVL-----------------LKMKDSSQPADAVHDR-
-----------------------------------------------------GVFASLD
DAVAAATVAQQGLK---RVAMRQQVIQAIREAG--EKHARELAELAVTETGMGRVEDKFA
KNVAQARGTPGV--ECLTPQVLTGDNGLTLIENA-PWGVVASVTPSTNPAATVINNAISL
IAAGNSVVFAPHPAAKQVSQRAITLLNQAVVAAGGPANLLVTVANPDIDTAQRLFKYPGI
GLLVVTGGEAVVEAARKHTNKRLIAAGAGNPPVVVDETADLPRAAQAIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQQAVKL-TAAQAEQLQPLLL-KNIDERGKGTV-----
SRDWVGRDAGKIAAAIGLQ--VPA-QTRLLFVE-TP--ASHPFAVTELMMPVLPVVRVAN
VEEAIALAVQLEG--GCHHTAAMHSRNI---DNMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|91211784|ref|YP_541770.1| ethanolamine utilization protein EutE acetaldehyde
dehydrogenase [Escherichia coli UTI89]
------------MNQQDIEQVVKAVL-----------------LKMQSSDTPPAAVHEM-
-----------------------------------------------------GVFASLD
DAVAAAKVAQQGLK---SVAMRQLAIAAIREAG--EKHARDLAELAVSETGMGRVEDKFA
KNVAQARGTPGV--ECLSPQVLTGDNGLTLIENA-PWGVVASVTPSTNPAATVINNAISL
IAAGNSVIFAPHPAAKKVSQRAITLLNQAIVAAGGPENLLVTVANPDIETAQRLFKFPGI
GLLVVTGGEAVVEAARKHTNKRLIAAGAGNPPVVVDETADLARAAQSIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQHAVKL-TAEQAQQLQPVLL-KNIDERGKGTV-----
SRDWVGRDAAKIAAAIGLK--VPE-QTRLLFVE-TT--AEHPFAVTELMMPVLPVVRVAN
VADAIALAVKLEG--GCHHTAAMHSRNI---ENMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|74312980|ref|YP_311399.1| EutE [Shigella sonnei Ss046]
------------MNQQDIEQVVKAVL-----------------LKMQSSDTPPAAVHEM-
-----------------------------------------------------GVFASLD
DAVAAAKVAQQGLK---SVAMRQLAIAAIREAG--EKHARDLAELAVSETGMGRVEDKFA
KNVAQARGTPGV--ECLSPQVLTGDNGLTLIENA-PWGVVASVTPSTNPAATVINNAISL
IAAGNSVIFAPHPAAKKVSQRAITLLNQAIVAAGGPENLLVTVANPDIETAQRLFKFPGI
GLLVVTGGEAVVEAARKHTNKRLIAAGAGNPPVVVDETADLARAAQSIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQHAVKL-TAEQAQQLQPVLL-KNIDERGKGTV-----
SRDWVGRDAAKIAAAIGLN--VPQ-ETRLLFVE-TT--AEHPFAVTELMMPVLPVVRVAN
VADAIALAVKLEG--GCHHTAAMHSRNI---ENMNQMANAIDTSIFVKNGPRIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SVRTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|82544904|ref|YP_408851.1| ethanolamine utilization [Shigella boydii Sb227]
------------MNQQDIEQVVKAVL-----------------LKMQSSDTPPAAVHEM-
-----------------------------------------------------GVFASLD
DAVAAAKVAQQGLK---SVAMRQLAIAAIREAG--EKHARDLAELAVSETGMGRVEDKFA
KNVAQARGTPGV--ECLSPQVLTGDNGLTLIENA-PWGVVASVTPSTNPAATVINNAISL
IAAGNSVIFAPHPAAKKVSQRAITLLNQAIVAAGGPENLLVTVANPDIETAQRLFKFPGI
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GLLVVTGGEAVVEAARKHTNKRLIAAGAGNPPVVVDETADLARAAQSIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQHAVKL-TAEQAQQLQPVLL-KNIDERGKGTV-----
SRDWVGRDAAKIAAAIGLN--VPQ-ETRLLFVE-TT--AEHPFAVTELMMPVLPVVRVAN
VADAIALAVKLEG--GCHHTAAMHSRNI---ENMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|161502387|ref|YP_001569499.1| hypothetical protein SARI_00421 [Salmonella
enterica subsp. arizonae serovar 62:z4,z23:--]
------------MNQQDIEQVVKAVL-----------------LKMQDSSKPTSTVHEM-
-----------------------------------------------------GVFASLD
DAVAAAKLAQQGLK---SVAMRQLAIHAIREAG--EKHARELAELAVSETGMGRVDDKFA
KNVAQARGTPGV--ECLSPQVLTGDNGLTLIENA-PWGVVASVTPSTNPAATVINNAISL
IAAGNSVVFAPHPAAKKVSQRAITLLNQAVVAAGGPENLLVTVANPDIETAQRLFKYPGI
GLLVVTGGEAVVDAARKHTNKRLIAAGAGNPPVVVDETADLSRAAQSIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQHAVKL-TAAQAEQLQPVLL-KNIDERGKGTV-----
SRDWVGRDAGKIAAAIGLN--VPQ-QTRLLFVE-TP--ASHPFAVTEMMMPVLPVVRVAN
VEEAIALAVQLEG--GCHHTAAMHSRNI---DNMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|16130380|ref|NP_416950.1| predicted aldehyde dehydrogenase, ethanolamine
utilization protein [Escherichia coli str. K-12 substr. MG1655]
------------MNQQDIEQVVKAVL-----------------LKMQSSDTPSAAVHEM-
-----------------------------------------------------GVFASLD
DAVAAAKVAQQGLK---SVAMRQLAIAAIREAG--EKHARDLAELAVSETGMGRVEDKFA
KNVAQARGTPGV--ECLSPQVLTGDNGLTLIENA-PWGVVASVTPSTNPAATVINNAISL
IAAGNSVIFAPHPAAKKVSQRAITLLNQAIVAAGGPENLLVTVANPDIETAQRLFKFPGI
GLLVVTGGEAVVEAARKHTNKRLIAAGAGNPPVVVDETADLARAAQSIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQHAVKL-TAEQAQQLQPVLL-KNIDERGKGTV-----
SRDWVGRDAGKIAAAIGLK--VPQ-ETRLLFVE-TT--AEHPFAVTELMMPVLPVVRVAN
VADAIALAVKLEG--GCHHTAAMHSRNI---ENMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|15802977|ref|NP_289007.1| ethanolamine utilization; acetaldehyde dehydrogenase
[Escherichia coli O157:H7 EDL933]
------------MNQQDIEQVVKAVL-----------------LKMQSSDTPPAAVHEM-
-----------------------------------------------------GVFASLD
DAVAAAKIAQQGLK---SVAMRQLAIAAIREAG--EKHARDLAELAVSETGMGRVEDKFA
KNVAQARGTPGV--ECLSPQVLTGDNGLTLIENA-PWGVVASVTPSTNPAATVINNAISL
IAAGNSVIFAPHPAAKKVSQRAITLLNQAIVAAGGPENLLVTVANPDIETAQRLFKFPGI
GLLVVTGGEAVVEAARKHTNKRLIAAGAGNPPVVVDETADLARAAQSIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQHAVKL-TAEQAQQLQPVLL-KNIDERGKGTV-----
SRDWVGRDAGKIAAAIGLK--VPQ-ETRLLFVE-TT--AEHPFAVTELMMPVLPVVRVAN
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VADAIALAVKLEG--GCHHTAAMHSRNI---ENMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|157161914|ref|YP_001459232.1| ethanolamine utilization protein EutE
[Escherichia coli HS]
------------MNQQDIEQVVKAVL-----------------LKMQSSDTPPAAVHEM-
-----------------------------------------------------GVFASLD
DAVAAAKVAQQGLK---SVAMRQLAIAAIREAG--EKHARDLAELAVSETGMGRVEDKFA
KNVAQARGTPGV--ECLSPQVLTGDNGLTLIENA-PWGVVASVTPSTNPAATLINNAISL
IAAGNSVIFAPHPAAKKVSQRAITLLNQAIVAAGGPENLLVTVANPDIETAQRLFKFPGI
GLLVVTGGEAVVEAARKHTNKRLIAAGAGNPPVVVDETADLARAAQSIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQHAVKL-TAEQAQQLQPVLL-KNIDERGKGTV-----
SRDWVGRDAAKIAAAIGLN--VPQ-ETRLLFVE-TT--AEHPFAVTELMMPVLPVVRVAN
VADAIALAVKLEG--GCHHTAAMHSRNI---ENMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|157154906|ref|YP_001463775.1| ethanolamine utilization protein EutE
[Escherichia coli E24377A]
------------MNQQDIEQVVKAVL-----------------LKMQSSDTPSAAVHEM-
-----------------------------------------------------GVFASLD
DAVAAAKVAQQGLK---SVAMRQLAIAAIREAG--EKHARDLAELAVSETGMGRVEDKFA
KNVAQARGTPGV--ECLSPQVLTGDNGLTLIENA-PWGVVASVTPSTNPAATVINNAISL
IAAGNSVIFAPHPAAKKVSQRAITLLNQAIVAAGGPENLLVTVANPDIETAQRLFKFPGI
GLLVVTGGEAVVEAARKHTNKRLIAAGAGNPPVVVDETADLARAAQSIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQHAVKL-TAEQAQQLQPVLL-KNIDERGKGTV-----
SRDWVGRDAAKIAAAIGLN--VPQ-ETRLLFVE-TT--AEHPFAVTELMMPVLPVVRVAN
VADAIALAVKLEG--GCHHTAAMHSRNI---ENMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|215487756|ref|YP_002330187.1| predicted aldehyde dehydrogenase, ethanolamine
utilization protein [Escherichia coli O127:H6 str. E2348/69]
------------MNQQDIEQVVKAVL-----------------LKMQSSDTPPAAVHEM-
-----------------------------------------------------GVFASLD
DAVAAAKVAQQGLK---SVAMRQLAIAAIREAG--EKHARDLAELAVSETGMGRVEDKFA
KNVAQARGTPGV--ECLSPQVLTGDNGLTLIENA-PWGVVASVTPSTNPAATVINNAISL
IAAGNSVIFAPHPAAKKVSQRAITLLNQAIVAAGGPENLLVTVANPDIETAQRLFKFPGI
GLLVVTGGEAVVEAARKHTNKRLIAAGAGNPPVVVDETADLARAAQSIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQHAVKL-TAEQAQQLQSVLL-KNIDERGKGTV-----
SRDWVGRDAAKIAAAIGLN--VPS-ETRLLFVE-TT--AEHPFAVTELMMPVLPVVRVAN
VADAIALAVKLEG--GCHHTAAMHSRNI---ENMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----SWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|218548112|ref|YP_002381903.1| putative aldehyde dehydrogenase, ethanolamine
utilization protein [Escherichia fergusonii ATCC 35469]
------------MNQQDIEQVVKAVL-----------------LKMQSSDTPPASVHEM-
-----------------------------------------------------GVFASLD
DAVAAAKIAQQGLK---SVAMRQLAIAAIREAG--EKHARDLAELAVSETGMGRVEDKFA
KNVAQARGTPGV--ECLSPQVLTGDNGLTLIENA-PWGVVASVTPSTNPAATVINNAISL
IAAGNSVIFAPHPAAKKVSQRAITLLNQAIVAAGGPENLLVTVANPDIETAQRLFKFPGI
GLLVVTGGEAVVEAARKHTNKRLIAAGAGNPPVVVDETADLARAAQSIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQHAVKL-TAEQAQQLQPVLL-KNIDERGKGTV-----
SRDWVGRDAAKIAAAIGLN--VPQ-ETRLLFVE-TP--AEHPFAMTELMMPVLPVVRVAN
VADAIALAVKLEG--GCHHTAAMHSRNI---ENMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|16761381|ref|NP_456998.1| putative aldehyde dehydrogenase [Salmonella enterica
subsp. enterica serovar Typhi str. CT18]
------------MNQQDIEQVVKAVL-----------------LKMKDSSQPASTVHEM-
-----------------------------------------------------GVFASLD
DEVAAAKRAQQGLK---SVAMRQLAIHAIREAG--EKHARELAELAVSETGMGRVDDKFA
KNVAQARGTPGV--ECLSPQVLTGDNGLTLIENA-PWGVVASVTPSTNPAATVINNAISL
IAAGNSVVFAPHPAAKKVSQRAITLLNQAVVAAGGPENLLVTVANPDIETAQRLFKYPGI
GLLVVTGGEAVVDAARKHTNKRLIAAGAGNPPVVVDETADLPRAAQSIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQHAVKL-TAAQAEQLQPVLL-KNIDERGKGTV-----
SRDWVGRDAGKIAAAIGLN--VPD-QTRLLFVE-TP--ANHPFAVTEMMMPVLPVVRVAN
VEDAIALAVQLEG--GCHHTAAMHSRNI---DNMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|187730631|ref|YP_001881246.1| ethanolamine utilization protein EutE [Shigella
boydii CDC 3083-94]
------------MNQQDIEQVVKAVL-----------------LKMQSSDTPPAAVHEM-
-----------------------------------------------------GVFASLD
DAVAAAKVAQQGLK---SVAMRQLAIAAIREAG--EKHARDLAELAVSETGMGRVEDKFA
KNVAQARGTPGV--ECLSPQVLTGDNGLTLIENA-PWGMVASVTPSTNPAATVINNAISL
IAAGNSVIFAPHPAAKKVSQRAITLLNQAIVAAGGPENLLVTVANPDIETAQRLFKFPGI
GLLVVTGGEAVVEAARKHTNKRLIAAGAGNPPVVVDETADLARAAQSIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQHAVKL-TAEQAQQLQPVLL-KNIDERGKGTV-----
SRDWVGRDAAKIAAAIGLN--VPQ-ETRLLFVE-TT--AEHPFAVTELMMPVLPVVRVAN
VADAIALAVKLEG--GCHHTAAMHSRNI---ENMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|218690581|ref|YP_002398793.1| putative aldehyde dehydrogenase, ethanolamine
utilization protein [Escherichia coli ED1a]
------------MNQQDIEQVVKAVL-----------------LKMQSSDTPPAAVHEM-
-----------------------------------------------------GVFASLD
DAVAAAKVAQQGLK---SVAMRQLAIAAIREAG--EKHARDLAELAVSETGMGRVEDKFA
KNVAQARGTPGV--ECLSPQVLTGDNGLTLIENA-PWGVVASVTPSTNPAATVINNAISL
IAAGNSVIFAPHPAAKKVSQRAITLLNQAIVAAGGPENLLVTVANPDIETAQRLFKFPGI
GLLVVTGGEAVVEAARKHTNKRLIAAGAGNPPVVVDETADLARAAQSIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQHAVKL-TAEQAQQLQSVLL-KNIDECGKGTV-----
SRDWVGRDAAKIAAAIDLK--VPE-QTRLLFVE-TT--AEHPFAVTELMMPVLPVVRVAN
VADAIALAVKLEG--GCHHTAAMHSRNI---ENMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|62181029|ref|YP_217446.1| putative aldehyde oxidoreductase in ethanolamine
utilization [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
------------MNQQDIEQVVKAVL-----------------LKMKDSSQPASTVHEM-
-----------------------------------------------------GVFASLD
DAVAAAKRAQQGLK---SVAMRQLAIHAIREAG--EKHARELAELAVSETGMGRVDDKFA
KNVAQARGTPGV--ECLSPQVLTGDNGLTLIENA-PWGVVASVTPSTNPAATVINNAISL
IAAGNSVVFAPHPAAKKVSQRAITLLNQAVVAAGGPENLLVTVANPDIETAQRLFKYPGI
GLLVVTGGEAVVDAARKHTNKRLIAAGAGNPPVVVDETADLPRAAQSIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQHAVKL-TAAQAEQLQPVLL-KNIDECGKGTV-----
SRDWVGRDAGKIAAAIGLN--VPD-QTRLLFVE-TP--ANHPFAVTEMMMPVLPVVRVAN
VEEAIALAVQLEG--GCHYTAAMHSRNI---DNMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|170019261|ref|YP_001724215.1| aldehyde dehydrogenase [Escherichia coli ATCC
8739]
------------MNQQDIEQVVKAVL-----------------LKMQSSDTPPAAVHEM-
-----------------------------------------------------GVFASLD
DAVAAAKVAQQGLK---SVAMRQLAIAAIREAG--EKHARDLAELAVSETGMGRVEDKFA
KNVAQARGTPGV--ECLSPQVLTGDNGLTLIENA-PWDVVASVTPSTNPAATVINNAISL
IAAGNSVIFAPHPAAKKVSQRAITLLNQAIVAAGGPENLLVTVANPDIETAQRLFKFPGI
GLLVVTGGEAVVEAARKHTNKRLIAAGAGNPPVVVDETADLARAAQSIVKGASFDNNIIC
ADEKVLIVVDSVADELMRLM-EGQHAVKL-TAEQAQQLQPVLL-KNIDERGKGTV-----
SRDWVGRDAAKIAAAIGLN--VPQ-ETRLLFVE-TT--AEHPFAVTELMMPVLPVVRVAN
VADAIALAVKLEG--GCHHTAAMHSRNI---ENMNQMANAIDTSIFVKNGPCIAG-LGLG
GE----GWTTMTITTPTGEGVT-----SARTFVRLRRCV---------------------
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---------------------------------LVDAFRIV-------------------
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>gi++|148544941|ref|YP_001272311.1| 50S ribosomal protein L29P [Lactobacillus
reuteri DSM 20016]
------------MQINDIESAVRKIL-----------------AEELDNASSSSANVAAT
TDNGHR-----------------------------------------------GIFTNVN
DAIAAAKAAQEIYR-DKPIAVRQQVIDAIKEGF--RPYIEKMAKDIKEETGMGTVEAKIA
KLNNALYNTPGP--EILEPVVENGDGGMVMYERL-PYGVIGAVGPSTNPSETVIANAIMM
LAGGNTLYFGAHPGAKNVTRWTIEKMNDFIADATGLHNLVVSIETPTIESVQQMMKHPDI
AMLAVTGGPAVVHQAMT-SGKKAVGAGPGNPPAMVDATADIDLAAHNIITSASFDNDILC
TAEKEVVAESSIKDELIRKM-QDEGAFVV-NREQADKLADMCI------QENGAP-----
DRKFVGKDATYILDQANIP--YTG-HPVEIICE-LP--KEHPLVMTEMLMPILPVVSCPT
FDDVLKTAVEVEK--GNHHTATIHSNNL---KHINNAAHRMQCSIFVVNGPSYVG-TGVA
DNGAHSGASALTIATPTGEGTC-----TARTFTRRVRLN---------------------
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---------------------------------SPQGFSVRNWY----------------
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>gi++|150018866|ref|YP_001311120.1| aldehyde dehydrogenase [Clostridium beijerinckii
NCIMB 8052]
-----------------MDINYKFFN-----------------NEEL-------------
----KS-----------------------------------------------GVFSSVN
DAVLAAVGAYNQYS-KFTLNERQEIINSIKEKL--LSRVEEIAYMTVEETGMGNVHDKIE
KLILAIKKTPGI--EDLITEVRTGDNGMTLYELS-SYGVICAIHPCTNPCATLISNTIGM
LAAGNGVVHCPHPRAIKVSKYVTEIISIAIRERCGIDNLVVTLNENSITCTNEIMTHPDI
SMVVTTGGNNVLRQAMA-SGKKVIGAGPGNPTTIVDETGDIKKAARDIVRGASFDNNIMC
ISEKSIVAVSSIADLLVEEL-VRNKVYYVDNDEEMLKLTVATL------TSDMTL-----
NKTLEGKSANEILKAAGIV--CER-DIKLIV---VNTIKQHPFATVEMLMPLVPLIRVKN
FEIALDTALEIEQ--GFRHTATIHSQSI---ERLNVAAKVMQTAVFVKNGASLVG-IGCN
GE----GDTSFTIATITGEGTT-----TARHFARRRRCS---------------------
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---------------------------------LTNGFSIR-------------------
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>gi++|160879327|ref|YP_001558295.1| aldehyde dehydrogenase [Clostridium
phytofermentans ISDg]
----------MTVNEQLVQDIIKNVV-----------------ASMQLTQTNKTEL----
-----------------------------------------------------GVFDDMN
QAIEAAKEAQLVVK-KMSMDQREKIISAIRKKT--IEHAETLARMAVEETGMGNVGHKIL
KHQLVAEKTPGT--EDITTTAWSGDRGLTLVEMG-PFGVIGAITPCTNPSETIICNTIGM
LAGGNTVVFNPHPAAIKTSNFAVQLINEASLSAGGPVNIACSVRKPTLDSSKIMMSHQDI
PLIAATGGPGVVTAVLQ-SGKRGIGAGAGNPPVLVDETADIRKAAEDIINGCTFDNNLPC
IAEKEVVAIDAIANELMNYMVKEQGCYAI-TKEQQEKLTNLVI------TPKGL------
NRNCVGKDARTLLGMIGID--VPS-NIRCIIFE-GE--KEHPLISEELMMPILGIVRAKS
FDDAVEKAVWLEH--GNRHSAHIHSKNV---DRITTYAKAIDTAILVKNAPSYAA-IGFG
GE----GFCTFTIASRTGEGLT-----SASTFTKRRRCV---------------------
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---------------------------------MSDSLCIR-------------------
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>gi++|51246891|ref|YP_066775.1| ethanolamine utilization protein (EutE)
[Desulfotalea psychrophila LSv54]
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----------MSIGREQIESIVAEVI-----------------SQIGNVQQGAPVLSGSA
AGDW-------------------------------------------------GVFDELD
DAVAAAKAACKLID---TVAMRTRVVEVMRRAA--RMNARPLAEKAVAETGMGNIEDKVL
KTLLVANSTPGP--EILQPTAITGDDGFTLIENA-PWGVIASVTPSTNPGSTVINNGISM
ISGGNAVVFAPHPAAKRITQEAIKLMNKAIAEETGINNLLVCIKEPSLDAAQRLFTYPGI
NLLTVTGGEAVVKAARKVTDKRLIAAGAGNPPVVVDETADLARAAESIYIGASFDNNLIC
ANEKEIIVVESVADQFKREF-VAAGAFEI-SLEQAEAIGKTVL--LDYGTDKCRA-----
NPKWVGRDAYKLAELIGVT--IPA-GCKLLFVD-VKGDARHPFAVTEQMMPLIPVVRARN
FDQALEWALMLER--GLSHTAGLHSTNI---HNMERMAKAVNTSLFVKNGPHIAG-LGAG
GE----GWTSMTISTPTGEGVT-----NAATFVRLRRCA---------------------
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---------------------------------LVGSFRIV-------------------
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>gi++|51246880|ref|YP_066764.1| ethanolamine utilization protein (EutE)
[Desulfotalea psychrophila LSv54]
------MELEMSIGQAQIESIVSEVL-----------------AQLSKAQNGSLV--ASA
PAAGDW-----------------------------------------------GVFDELD
DAVAAAKVAYKLID---TVAMRNRVVDVMRRAA--RMNARRLSEMAVSETGMGNVEDKVA
KTLLVANRTPGP--EILQPTAITGDEGFTLIENA-PWGVIASVTPSTNPGSTVINNGISM
ISGGNSVVFAPHPAAKRITQETIKMMNKAIVEETGVHNLLVCIKEPSLDAARRLFTYEGI
NLLTVTGGEAVVAAARKITDKRLIAAGAGNPPVVVDETADLARAAESIYIGASFDNNLIC
ANEKEIIIVDSVADEFKREF-TAIGAFEI-SLAQAETIGKTVL--LDYGTDKCRA-----
NPKWVGRDAYKLADLAGIT--IPK-GCKLLFVD-VKGDARHPFAVTEQMMPLIPVVRARN
FDQALEWALMLER--GLSHTAGMHSTNI---HNMEKMAKAVNTSLFVKNGPHIAG-LGAG
GE----GWTSMTISTPTGEGVS-----NAATFVRLRRCA---------------------
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---------------------------------LVGSFRIV-------------------
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>gi++|120554161|ref|YP_958512.1| aldehyde dehydrogenase [Marinobacter aquaeolei VT8]
----------MQTDAQQIESIVRRVI-----------------EQLHSPQRDGESY----
-----------------------------------------------------GVFRTLD
DAVAGAQGAYKKIR---TMAQREAIIAAIRRTG--SENVQALSELAVQETGFGRVEDKIR
KHRLVLDKTPGI--EAIVPMAVTGDHGLSLIENA-PWGVIASVTPSTNPSATILNNAISM
IAAGNSVVFSPHPAARAVSQRTIQLINRASVSAGGPANLVTCVEEPTIEAATRLFSFPGI
QLLTITGGEGVVNAARKVTDKRLIAAGPGNPPVVVDETADIERAAISIVQGASFDNNIIC
VDEKEIIAVESIATELKTAM-CRHGAAEI-NADQADAVARLVL--AGYPGPNPHP-----
KPEWVGRDAEKIAAAAGFS--VPA-GTRLLVTE-TE--RDHAFATTEMMLPVISLIRARD
ADQAIDWAVELEA--GNRHTAAMHSRNI---DNLSRMGLEINCSLFVKNGPCLAG-LGAG
GE----GWTSMTISTPTGEGVT-----NASTFVRKRRCT---------------------
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---------------------------------MVDSFRIV-------------------
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>gi++|32472043|ref|NP_865037.1| ethanolamine utilization protein EutE
[Rhodopirellula baltica SH 1]
----------MQLDENTIRSVVAQVL-----------------AEVGPMPSMPDPANAFE
GSH--------------------------------------------------GIFGNAS
DAVAAARRAFEQLR-QRPMEDRKRVIDIIRKIS--IENCEELGLMEMRETGIGRPEHKIE
KLRALGELSPGT--EFLQTKAFSGDHGLAIIERA-PFGVIAAITPVTHSLPTITGNAVSM
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IAGGNAVVVNPHPSGRLVAAEGVRRFNEEIAREVGIDNLICVIAEPTLESAAELFGHRDV
ALICVTGGPAVGRAALN-SGKRAIVAGPGNPPVVVDETADLDNAARCIIQGGAYDNNLLC
IAEKEVFVVDSVFDDMMAAM-RRAGAVQL-DQAQIAKLTSVAITQVGDDNHDAAA-----
-KDFIGKDASVLAAAAGVK--VPE-SCELIFGE-TD--EHHPFVSVEQMMPFIPFVRARD
VDHAIAMAKHYEH--GFRHTAIIHSRNV---HNMTKMGKELDTTLYVKNGPCMAA-LGLG
GE----GYLSFSIAGPTGEGVT-----TPDTFTRERRCS---------------------
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---------------------------------MIDELRVV-------------------
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>gi++|182413114|ref|YP_001818180.1| aldehyde dehydrogenase [Opitutus terrae PB90-1]
-------MPSLPIDETLVRSVVEEVVRAFARNGGTIGTASASTAAAPSRAGAGPALVSTR
NSGPRY-----------------------------------------------GVFQDVP
SAVAAAQAAYLQLC-VKGVAARAKVVEIVKALA--TQNAEEWGKFEFAETKIGRLDHKIE
KLQIV-KLVPGV--EWLHPDARSGDHGITLEEYT-PFGVIAAILPMTHSIPTLSGNIINI
VAAGNAVIFNPHPGGARSAALAVRAYNEAITAATGIENLVCTIEQPTLESFDALCQAPEV
RVLCVTGGPAVVAAAMK-SGKRAICAGPGNPPVLVDDTVNFDKAARDIIQGAAYDNNLLC
VGEKEVFVLDKVADKLISAF-ARNGARQL-NSSQLERLTAAAF---TNKPDAGGCSHPVL
NRSFVGVDAAVLARHAGTE--VPA-NTPLLFAE-TD--ANHAFVIEEQMMPMIPIVRVKS
VEEGVAAAVKAEH--GYKHSAIIHSLNV---DHMTMMARALDTTVFIKNGPCVAG-LGLG
GE----GYLSYSIATTTGEGIT-----TPRTFTRTRRCV---------------------
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---------------------------------MVDNLRIY-------------------
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>gi++|116620455|ref|YP_822611.1| aldehyde dehydrogenase [Solibacter usitatus
Ellin6076]
----------MIANQELIQAIAREVI-----------------ARIEQRTGGATAVAATG
GED--------------------------------------------------GVFATVD
EAVKAAVVAQQRVA-AMGLEERARMNAIIRRIC--ADNADELARIELAETKIGRADHKAA
KLRNI-RLVLGA--EAMKTDASSDAAGLCLVEYA-PWGVIGMVLPATHSVPTMASNAINI
LAAGNTAVFSPHPAGAKVAARGLQMFNREIQRELGVGNVLTMAREATLQNAEQIFQHPDV
ALLCVTGGPAVVKAAMK-FGKRVIAAGPGNPPVVVDESADLDAAARAIIQGASFDNNLLC
IGEKEVFVVAPVADAFVESM-RRAGAMQL-DARAIEALTKAAF----TTGDDGKP---HV
KRDFIGKDAAVLAEAAGLR--APA-GTDLLFGE-TS--EEHPFVQEEQMMPFLPVVRVRD
VDAGIRASVRAEH--GYRHTAMIHSRNV---DNVTRMARAMNCTLFVQNAPCYAS-LNVP
------SYLSHSIATPTGEGVT-----TPMTFTRQRRIV---------------------
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--------------------------------IGGGALRIL-------------------
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>gi++|158321408|ref|YP_001513915.1| acetaldehyde dehydrogenase (acetylating)
[Alkaliphilus oremlandii OhILAs]
--------------MESFDKDLRSVQ----------------------------------
---------------------------------------------------------EAR
DLARLGKIATKQLA-DYTEEQINKILCNMVRVA--KENAVSLAKMAVEETGFGKVEDKTY
KNHMASVLLYEAIKDMKTIGVIKEDTEEQVIEIAEPMGLLMGIVPSTNPTSTAIFKSMIA
IKSRNGIVFSPHPSALKCTLKAVRLMHDAAVEAGAPENIIGSISIPTIQATNELMKHDDI
AMIIATGGPGMVKASYS-AGKPALGVGAGNSPAYIERTANIQKAVSNIIASKTFDYGTIC
ASEQSIIVEECNREAVVAEL-KKQGGYFM-TEAETKKVCNLLF-------KNGHT----M
NAQFVGRSPQVIAEAAGIT--IPE-GTKILIGE-QQGVGPAYPLSYEKLTTVIGFYTVKD
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WHEACDLSIALLQN-GIGHTMSLHTEDR---EMVMKFAKK-PAARILVNTGSAQG--GTG
AS--TGLMPSFTLGCGTWGGSATSENVTPMHLVNIKRVA---------------------
--YGLKDCT---------------------------------------TLASADASFNYP
ELNGSATVGCTTES----------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------TPSFNKVN----------
---SD------------------VLDQEKLMD-LVNGLLKAMKGED--------------
------------------------------------------------------------
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>gi++|150391551|ref|YP_001321600.1| acetaldehyde dehydrogenase (acetylating)
[Alkaliphilus metalliredigens QYMF]
--------------MEDFDRDLRSIQ----------------------------------
---------------------------------------------------------EAR
VLATKGKIASNQIS-EYSKEQIEKIICNMVKVA--KENAVMLAEMAVDETGFGTVKDKTY
KNHMASVMLYEEIKDMKTIGIIDEDQEKQVIDLAEPMGLLMGIIPSTNPTSTAIFKSIIS
IKSRNGIVFSPHPASLKCTVKAIQLMNDAAVQAGAPENIISSITTPSVEATNALMKHKNI
ALIIATGGPGMVKASYS-AGKPALGVGAGNSPAYIEKSANIPKAISNIIASKTFDHGTIC
ASEQSIIVEESNSDEVIEEL-KKQGAYFM-TEEETKRVCKIIF-------KDGHT----M
NANFVGKPPQVIGDAAGIV--IPQ-GTKLLVGE-QKGVGTGFPLSYEKLTTVIAFYKVKD
WEEACNLSIDLLQN-GIGHTMCLHTEDR---EMVMKFAKK-PASRILVNTGGAQG--GTG
AS--TGLFPSFTLGCGTWGGSSTSENVSPMDLINIKRVA---------------------
------------------------------------------------------------
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---------------------------------------------YGLSDCATLASRDRT
FNYFDVEKNNLDIPKNCEESMQNNDSTDIDNDKLVKMVYELVEAMKGAN-----------
------------------------------------------------------------
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>gi++|28211118|ref|NP_782062.1| acetaldehyde dehydrogenase (acetylating)
[Clostridium tetani E88]
--------------MEKYDKDLYSIQ----------------------------------
---------------------------------------------------------QAR
NLARLGKVAANKIA-NYTEEQIDKILRNMVRVA--EENAVSLAQMAVEETGFGKVEDKTY
KNHLAATILYDSIKDMKTIGVISEDKVNKMIEIAEPVGLIMGIVPSTNPTSTAIFKSIIA
IKSRNAIVFSPHPAAAKCTIRAVELMRDAAIEAGAPEDIIASLTNLTMEATNELMKNENV
SLIIATGGPGMVKAAYS-SGKPAIGVGAGNSPAYIERTANVEKAIRDIISSKSFDYGTIC
ASEQSIICEECNHDAVVEEL-KKQGGYFM-TAEETEKVCKLLF-------KNGHT----M
NAKFVGRSPQVIANAAGFT--VSE-DIKVLIGK-QNGVGNGNPLSFEKLTTVLAFYTVKD
WHEACELSIELLQN-GIGHTMSIHTQND---DIVMEFAKK-PASRILVNTGGSQG--GTG
AS--TGLKPAFTLGCGTWGGSSVSENVTPEHLINKKRVA---------------------
--YGLKDCA---------------------------------------TLVQNDPTFNCI
KTASN-------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----------------CRGVKNQFMNMSPAQIAAAAEVLNKCNDYAKNTGCSNESKE---
-----------------------KDANNEELLSLVNQIVAAMKGAN--------------
------------------------------------------------------------
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>gi++|125717387|ref|YP_001034520.1| aldehyde dehydrogenase [Streptococcus sanguinis
SK36]
--------------MFLEDKDLVSIQ----------------------------------
---------------------------------------------------------EVR
NLIRDAKKAQAELA-KMSQEQIDTIVKVVAKAC--YDERERLAKMAAQETGFGRWEDKVL
KNALASKGILEEIKDMKTVGVLSEDKEKKVLEVGVPVGVIAGLIPSTNPTSTVMYKALIA
LKAGNSIVFSPHPNALKCIEETVEIIKKAAKSAGCPDGAISAIHRVSIAATNELMRHKDT
NLILATGGNAMVKAAYS-SGTPAIGVGPGNGPAFIERTADVPKAVRQILDSKTFDNGVIC
ASEQSIIVEEDMKEKVVAEF-KKQGAYFV-PAEDAKKLGSFII------QPSGAM-----
NPKMVGKTPQVIGELAGIS--VPA-DARVLIAE-ETGVGKQYPYSMEKLAPVLGFYTVKD
WLEACELSIKILHHEGAGHTLAIHSQNE---EIIREFALKKPVSRLLINTPAALG--GVG
AT--TGLFPAFTLGCGAVGGSATSDNVSPLNLFNIRRVA---------------------
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------------------------------------------------------------
---------------------------------------------------------YGT
SELSDLRQAENMAVEEPKAVAVDGSNEEELVTLLVQRVLEKLK-----------------
------------------------------------------------------------
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>gi++|111026478|ref|YP_708761.1| aldehyde-alcohol dehydrogenase, N-terminal
[Rhodococcus jostii RHA1]
----------------MRTPEFDRSP----------------------------------
---------------------------------------------------------ELD
TVLDRAQVAATAFE-AYDRSQVDRIVRAVANVA--LQNARQLAEKAADETGFGVAEDKVA
KNEAVSSGFVREY-GDLDFVSHRADNEKKLLLSPKPAGVIFAVTPSTSPVANLYFKVLSS
LLTRNAVVISPHPAAVQTSLEAAQLLSRAATEAGAPEGAIQILNKPSVPLIEAAMGDARV
NLILATGGSAVVRAAYR-SGTPAIGVGPGNAAVVVDETADLERAADQISASKAFDNSVLC
TAESVLIMVESIASRMNELL-VRRGAHLC-RPDETRRLRNYMY-------PKGKF-----
NTEVVGRPAREIAKKAGIT--VAE-GTQLLLAP-IDSIRDDEPLTHEKLSPVLAVMTVSN
FDQALAAAASLVDIVGVGHSAVIHSEDP---QHVLDYSHRLPVHRVAVNIGGSLGNAGIG
TG----LPLTMSIGTGFAGGSSLGENLAPEHLVQWKRAA---------------------
------------------------------------------------------------
------------------------------------------------------------
----------------------------------YPVG----------------------
------------------------------------------------------------
-------------------------------------------------------AVFPQ
FASLQPTRGDRSGVSGVGLG---DGAVREELRRLI--VEELRGLIGQNHG----------
------------------------------------------------------------
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>gi++|187933220|ref|YP_001885659.1| acetaldehyde dehydrogenase (acetylating)
[Clostridium botulinum B str. Eklund 17B]
--------------MENFDRDLCSIQ----------------------------------
---------------------------------------------------------EAR
NLARLGKVAAEKIA-DYTEEQIDKILCNMVKVA--EANAVCLAQMAVEETGFGKVEDKTY
KNHMASTILYDSIKDMKTIGVIKEDEANKLIELAEPVGLVMGIVPSTNPTSTAIFKAIIA
IKSRNAIVFSPHPSAAQCTIKAAKLMNEAAIEAGAPENIIGCVSTPTIGATNELMKSKEV
AIIIATGGPGMVKAAYS-SGKPALGVGAGNSPAYIERSANVEKAIRNIIASKTFDNGTIC
ASEQSIICEECNHDEVVAEL-KKQGGYFM-TAEETDKVCKLLF-------KNGHS----M
NAKFVGRSPQVIASSAGIS--IPQ-DTKVLIGE-QKGVGEGYPLSFEKLTTVLAFYTVKD
WHEACELSIELLQN-GIGHTMSIHTEDR---DIVMKFARK-PASRILVNTGGSQG--GTG
AS--TGLIPSFTLGCGTWGGSSVSENVTPMHLINIKRVA---------------------
--YGLKDCA---------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------------TLASNDPTFNRIKTENNCHHTQN
QCGSLSPDQYAAASKCINTDDIKNANNEELLDMINKLVKVMKGEA---------------
------------------------------------------------------------
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>gi++|148380063|ref|YP_001254604.1| acetaldehyde dehydrogenase (acetylating)
[Clostridium botulinum A str. ATCC 3502]
--------------MENFDKDLRSIQ----------------------------------
---------------------------------------------------------QAR
DLARLGKVAADKIA-DYTEEQIDKILRNMVRVA--EENAVCLAQMAVEETGFGKVEDKTF
KNHLAATILYNSIKDMKTIGVINEDKENKLIELAEPVGLVMGIVPSTNPTSTAIFKAMIS
IKSRNAIVFAPHPAAAKCTIKAVELMRDAAIEAGAPENIISAVTIPTIGATNELMKSKEV
AIIIATGGPGMVKAAYS-SGTPAIGVGAGNSPAYIERTANVEKAVKNIIASKTFDNGTIC
ASEQSIICEECNHDLVVAEF-KKQGGYFM-TEEETEKVCKLLF-------KKGNA----M
NAKFVGRSPQVIASAAGFT--IPA-GTKVLIGR-QNGVGEGYPLSFEKLTTVLGFYTVKD
WHEACELSIKLLQN-GIGHTISIHTEDR---DMVMKFARK-PASRILVNTGGTQG--GTG
AS--TGLNPSFTLGCGTWGGSSVSENVTPKHLMNIKRVA---------------------
--YGIKDCT---------------------------------------NLASNDPTFNCI
KTAEN-------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
```

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----------------CHGVQNQFMNMSPAQIAAAAEVLNKANNCAENTNTCTECSN---
-----------------------ENTKNEELLDLVNQIVAAMKGAN--------------
------------------------------------------------------------
----------------------
>gi++|188587712|ref|YP_001920780.1| acetaldehyde dehydrogenase (acetylating)
[Clostridium botulinum E3 str. Alaska E43]
--------------MENFDRDLCSIQ----------------------------------
---------------------------------------------------------EAR
NLARLGKVAAEKIA-DYTEEQIDKILCNMVKVA--EANAVCLAQMAVEETGFGKVEDKTY
KNHMASTILYDSIKDMKTIGIIKEDEANKLIELAEPVGLVMGIVPSTNPTSTAIFKAMIA
IKSRNAIVFSPHPSAAQCTIKAAKLMNEAAIEAGAPENIIGCVSTPTIGATNELMKSKEV
AIIIATGGPGMVKAAYS-SGKPALGVGAGNSPAYIERSANVEKAIRNIIASKTFDNGTIC
ASEQSIICEECNHDEVVAEL-KKQGGYFM-TAEETDKVCNLLF-------KNGHS----M
NAKFVGRSPQVIASSAGIS--IPQ-DTKVLIGE-QKGVGEGYPLSFEKLTTVLAFYTVKD
WHEACELSIELLQN-GIGHTMSIHTEDR---DIVMKFARK-PASRILVNTGGSQG--GTG
AS--TGLIPSFTLGCGTWGGSSVSENVTPMHLINIKRVA---------------------
--YGLKDCA---------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------------TLASNDTTFNHIKTENNCHHTQN
QCGSLSPDQYAAASKCINTDDIKNANNEELLDMINKLVKVMKGEA---------------
------------------------------------------------------------
----------------------
>gi++|170759220|ref|YP_001787498.1| acetaldehyde dehydrogenase (acetylating)
[Clostridium botulinum A3 str. Loch Maree]
--------------MENFDKDLRSIQ----------------------------------
---------------------------------------------------------QAR
DLARLGKVAADKIA-DYTEEQIDKILRNMVRVA--EENAVCLAQMAVEETGFGKAEDKTF
KNHLAATILYNSIKDMKTIGVINEDEENKLIELAEPVGLVMGIVPSTNPTSTAIFKAMIS
IKSRNAIVFAPHPAAAKCTTKAVELMMDAAIEAGAPENIISAVTIPTIGATNELMKSKEV
AIIIATGGPGMVKAAYS-SGTPAIGVGAGNSPAYIERTANVEKAVKNIIASKTFDNGTIC
ASEQSIICEECNHDLVVAEF-KKQGGYFM-TEEETEKVCKLLF-------KKGNA----M
NAKFVGRSPQVIASAAGFT--IPA-GAKVLIGR-QNGVGEGYPLSFEKLTTVLGFYTVKD
WHEACELSIKLLQN-GIGHTMSIHTEDR---DMVMKFARK-PASRILVNTGGTQG--GTG
AS--TGLNPSFTLGCGTWGGSSVSENVTPKHLINIKRVA---------------------
--YGIKDCT---------------------------------------NLASNDPTFNCI
KTAEN-------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----------------CHGVQNQFMNMSPAQIAAAAEVLNKANNCAENTNTCTECSN---
-----------------------ENTKNEELLDLVNQIVAAMKGAN--------------
------------------------------------------------------------
----------------------
>gi++|91213915|ref|YP_543901.1| hypothetical protein UTI89_C4967 [Escherichia coli
UTI89]
--------------MIELDTDLRSRQ----------------------------------
---------------------------------------------------------NAR
VLVRNAKKAQAIMA-TFSQQQIDAIVKNVAQEA--AHHAEALAKMAAEETGFGNWQDKVL
KNRFASLRVYDAIKDMKTVGIIHDDQQQKVMDVGVPLGVICALVPSTNPTSTIFYKTLIA
LKAGNAIIFSPHPGARQCSWKAIEVVKRAAEAAGAPAGIVDGVTELTLEATQELMHSKDV
SLILATGGEGMVRAAYA-SGTPTISGGPGNGPAFIERSADIHHAVKDIITSKTFDNGVIC
ASEQSIIVERCIYNEVHREL-EAQGAYFM-NEDEAAKMAALLL------RPNGTI-----
NPKVVGKTALYLSQMAGFC--VPA-STRVLIAE-QTTVSHKNPYSREKLCPVLGLYIEED
WKAACHRVVELLTNEGLGHTLVIHTRNQ---DVIRQFCLEKPVNRILINTPAALG--GIG
AT--TNITPALTLGCGAVGGGSSSDNVGPMNLLNIRKVGYGVRSIDELRSPGSRAEPQPA
IAAPIVDPH---------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----------------------------------------------------RSILDDAR
FTSPAPATTSADDRFTVATTDPEGEINEQNVERVIRQVLERLGK----------------
------------------------------------------------------------
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>gi++|153938065|ref|YP_001391402.1| acetaldehyde dehydrogenase (acetylating) 
[Clostridium botulinum F str. Langeland]
--------------MENFDKDLRSIQ----------------------------------
---------------------------------------------------------QAR
DLARLGKVAADKIA-DYTEEQIDKILRNMVRVA--EENAVCLAQMAVEETGFGIVEDKTF
KNHLAATILYNSIKDMKTIGIIKEDETNKLIEIAEPVGLVMGIVPSTNPTSTAIFKAMIS
IKSRNAIVFAPHPAAAKCTIKAVELMRDAAIEAGAPENIISSVTIPTIGATNELMKSKEV
AIIIATGGPGMVKAAYS-SGTPAIGVGAGNSPAYIERTANVEKAVKNIIASKTFDNGTIC
ASEQSIICEECNHDLVVAEF-KKQGGYFM-TAEETEKVCKLLF-------KKGNA----M
NAKFVGRSPQVIASAAGFT--IPA-GTKVLIGR-QNGVGEGYPLSFEKLTTVLGFYTVKD
WHEACELSIKLLQN-GIGHTMSIHTEDR---DMVMKFARK-PASRILVNTGGTQG--GTG
AS--TGLNPSFTLGCGTWGGSSVSENVTPKHLINVKRVA---------------------
--YGIKDCT---------------------------------------NLASNDPSFNCI
KTAEN-------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----------------CHGVQNQFMNMSPAQIAAAAEVLNKANNCSESSNTCTECNS---
-----------------------ENGKNEELLDLVNQIVAAMKGAN--------------
------------------------------------------------------------
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>gi|50843201|ref|YP_056428.1| putative propionaldehyde dehydrogenase / ethanolamine 
utilization protein EutE [Propionibacterium acnes KPA171202]
------------MTTTAVPPTSTQLC----------------------------------
-----------------------------------------------------GVFADVN
AAVAAAREAFLAFS-DCSLAQRRTFINAVREAASQQERLEYMATAAVEETGMGNAHHKVL
KNLYAATRTPGV--EDLVMEARQGDDGLTTLEYS-PYGVIGAITPTTNPTETIICNTVGM
LAAGNTVVFSPHPRARHLSAWLVDVLNRAMVEAGAPDNLITVITEPTPDTTKALINHPDI
TMLVATGGPQIVNMVLS-SGKKAIGAGSGNPPAVVDETADAAKAASDIVQGASFDNNLPC
TAEKEVIVVAEVLPQLMTAM-TANGAQVVSDPEELAKLRSLLL-----DTSGTRP-----
NTAWVGQDAQKILRTAGIE---PHQDTRLVTMV-TD--PSDPFVQVEMLMPVVPVVPVTD
YLTAIDLAVELEH--GNRHTAIMHSKDV---SRLDLMARRIQTTIFVKNGPSFAG-IGIN
GE----GFATFTIAGPTGEGLT-----SARSFARRRRCV---------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------------LDAH-------------------
------------------------------------------------------------
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>gi|187934965|ref|YP_001886323.1| ethanolamine utilization protein EutE [Clostridium 
botulinum B str. Eklund 17B]
------MERNLSVLSQTNDLKITKRT-----------------EGDKSNNKESYL-----
-----------------------------------------------------GVFKKVE
NAITKAIYAQKKLSLYYTKEDRERIIKSIRKAT--LENKEILAKMIVDETHMGRYEDKIL
KHELVAKYTPGT--EDLITTAWSGDQGLTLVEMS-PYGVIGAITPSTNPTETVICNSIGM
IAAGDSVVFNGHPGAKKCVAFAVDMINKAVIREGGPENLVTTVENPTMESLNVIMKHPYI
KLLCGTGGPGLIKTLLN-SGKKAIGAGAGNPPVIVDDSADIDKAAKNIIEGCSFDNNLPC
IAEKEVFVFENVANDLIQNM-IKNNAVLI-NENQVSKLLDLVLLERKDETLEYAI-----
NKKWVGKDAKLFLDKIGIK--ASD-NVRCIICE-VD--ANHPFVMTELMMPILPIVRVKD
VDEAIECAKTAEQ--RKRHSAYMYSKNI---DNLNRFEKEIDTTIFVKNAKSFAG-VGFG
AE----GFTTFTIAGPTGEGIT-----SARNFTRQRRCV---------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------LAG------------------------
------------------------------------------------------------
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>gi|150018649|ref|YP_001310903.1| aldehyde dehydrogenase [Clostridium beijerinckii 
NCIMB 8052]
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------------MNKDTLIPTTKDLK-----------------VKTNGENINLKNYKDNS
SCF--------------------------------------------------GVFENVE
NAISSAVHAQKILSLHYTKEQREKIITEIRKAA--LQNKEVLATMILEETHMGRYEDKIL
KHELVAKYTPGT--EDLTTTAWSGDNGLTVVEMS-PYGVIGAITPSTNPTETVICNSIGM
IAAGNAVVFNGHPCAKKCVAFAVEMINKAIISCGGPENLVTTIKNPTMESLDAIIKHPSI
KLLCGTGGPGMVKTLLN-SGKKAIGAGAGNPPVIVDDTADIEKAGRSIIEGCSFDNNLPC
IAEKEVFVFENVADDLISNM-LKNNAVII-NEDQVSKLIDLVL------QKNNETQEYFI
NKKWVGKDAKLFLDEIDVE--SPS-NVKCIICE-VN--ANHPFVMTELMMPILPIVRVKD
IDEAIKYAKIAEQ--NRKHSAYIYSKNI---DNLNRFEREIDTTIFVKNAKSFAG-VGYE
AE----GFTTFTIAGSTGEGIT-----SARNFTRQRRCV---------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------LAG------------------------
------------------------------------------------------------
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>gi|27366378|ref|NP_761906.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Vibrio vulnificus CMCP6]
------------------------MA----------------------------------
---------------------------------------------------------ELD
AMIARVKKAQEEFA-TYSQEQVDAIFRAASLAA--NQARIPLAQMAVEESGMGIVEDKVI
KNHFASEFIYNKYKDEKTCGILEEDDNLGTMTIAEPVGIICGIVPTTNPTSTAIFKSLIS
LKTRNGIIFSPHPRAKNSTNDAAKLVLEAAVAAGAPKDIIGWIDQPSVELSNALMKHDDI
ALILATGGPGMVKAAYS-SGKPAIGVGAGNVPVVIDETADIKRAVASILMSKTFDNGVVC
ASEQAAIVVDAVYDEVKERF-ASHKAYVL-SKAEAEKVRKVLL-------IDGAL-----
NAKIVGQPAAAIAEMAGVK--VPA-DTKVLVGEGLGKVSYDDAFAHEKLSPTLGLFRADD
FEDAVAQAVTMVEIGGIGHTSGLYTNQDVNADRIRYFGDKLKTARILVNIPTTHG--GIG
DLYNFNVAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALSDLE---GKKRAFLVTDRFLFNNGYADDVVQLLKAQGMEVQTFFDVEADPTLSVV
EKGAAAMQSFQPDVILALGGGSPMDAAKIMWVMYEHPETHFEELAMRFMDIRKRIYKFPK
MGKKAELVCITTTSGTGSEVTPFAVVTDDKTGAKYPLADYELTPQMAIVDANLVMNMPKS
LTAFGGYDAVTHALEAYVSVLANEYSDGQALQALKMLKEYLPSSYANGAKDPIAREKVHN
AATIAGIAFANAFLGVCHSMAHKIGAEFHLPHGLANALLISNVVRYNANDNPTKQTAFSQ
YDRPQARRRYAEVADHLGLSQA-GDRTAQKIERLLAWLDELKGNLDIPMSIQAA-GVAEA
DFLAKVDELAVEAFDDQCTGANPRYPLIAELKEVLLASYYGKAFVEGETFEGTTVIKKKA
DQVAPKAKK-------------
>gi|37679359|ref|NP_933968.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Vibrio vulnificus YJ016]
-------------------MPVTNMA----------------------------------
---------------------------------------------------------ELD
AMIARVKKAQEEFA-TYSQEQVDAIFRAASLAA--NQARIPLAQMAVEESGMGIVEDKVI
KNHFASEFIYNKYKDEKTCGILEEDDNLGTMTIAEPVGIICGIVPTTNPTSTAIFKSLIS
LKTRNGIIFSPHPRAKNSTNDAAKLVLEAAVAAGAPKDIIGWIDQPSVELSNALMKHDDI
ALILATGGPGMVKAAYS-SGKPAIGVGAGNVPVVIDETADIKRAVASILMSKTFDNGVVC
ASEQAAIVVDAVYDEVKERF-ASHKAYVL-SKAEAEKVRKVLL-------IDGAL-----
NAKIVGQPAAAIAEMAGVK--VPA-DTKVLVGEGLGKVSYDDAFAHEKLSPTLGLFRADD
FEDAVAQAVTMVEIGGIGHTSGLYTNQDVNADRIRYFGDKLKTARILVNIPTTHG--GIG
DLYNFNVAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALSDLE---GKKRAFLVTDRFLFNNGYADDVVQLLKAQGMEVQTFFDVEADPTLSVV
EKGAAAMQSFQPDVILALGGGSPMDAAKIMWVMYEHPETHFEELAMRFMDIRKRIYKFPK
MGKKAELVCITTTSGTGSEVTPFAVVTDDKTGAKYPLADYELTPQMAIVDANLVMNMPKS
LTAFGGYDAVTHALEAYVSVLANEYSDGQALQALKMLKEYLPSSYANGAKDPIAREKVHN
AATIAGIAFANAFLGVCHSMAHKIGAEFHLPHGLANALLISNVVRYNANDNPTKQTAFSQ
YDRPQARRRYAEVADHLGLSQA-GDRTAQKIERLLAWLDELKGNLDIPMSIQAA-GVAEA
DFLAKVDELAVEAFDDQCTGANPRYPLIAELKEVLLASYYGKAFVEGETFEGTTVIKKKA
DQVAPKAKK-------------
>gi|15642035|ref|NP_231667.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Vibrio cholerae O1 biovar eltor str. N16961]
-------------------MPVTNLA----------------------------------
---------------------------------------------------------ELD
ALVARVKAAQAEFA-TFSQEQVDKIFRAASLAA--NQARIPLAQMAVEESGMGIVEDKVI
```

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KNHFASEFIYNKYKDEKTCGILEEDDNLGTMTIAEPVGIICGIVPTTNPTSTAIFKSLIS
LKTRNGIIFSPHPRAKNSTNAAAKLVLDAAIAAGAPKDIIGWIDQPSVELSNALMKHDGI
ALILATGGPGMVKAAYS-SGKPAIGVGAGNVPVVIDETADIKRAVASILMSKTFDNGVVC
ASEQAAIVVSEVYDEVKERF-ATHKAHVL-SKADADKVRKVLL-------IDGAL-----
NAKIVGQPAAAIAEMAGVK--VPA-DTKVLVGEGLGKVSYDDEFAHEKLSPTLGLFRADN
FEDAVAQAVTMVEIGGIGHTSGLYTNQDVNADRIRYFGDKLKTARILVNIPTTHG--GIG
DLYNFNVAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALSDLE---GKKRAFLVTDRFLFNNGYADDVVALLKAQGMEVQTFFEVEADPTLSVV
EKGAAAMQSFQPDVILALGGGSPMDAAKIMWVMYEHPDTHFEELAMRFMDIRKRIYKFPK
MGKKAELVCITTTSGTGSEVTPFAVVTDDKTGAKYPLADYELTPQMAIVDANLVMNMPKS
LTAFGGYDAVTHALEAYVSVLANEYSDGQALQALKMLKEYLPSSYANGAKDPIAREKVHN
AATIAGIAFANAFLGVCHSMAHKIGAEFHLPHGLANALLIANVVRYNANDNPTKQTAFSQ
YDRPQARRRYAEVADHLGLSQP-GDRTAQKIERLLTWLDELKVNLDIPKSIQAA-GVAEA
DFLAKVDELAVEAFDDQCTGANPRYPLIAELKEVLLASYYGKPFVEGQTFEGTTVIVKKA
DQEAAKAPKAKK----------
>gi|218708954|ref|YP_002416575.1| Alcohol dehydrogenase/acetaldehyde dehydrogenase
[Vibrio splendidus LGP32]
-------------------MPVTNLA----------------------------------
---------------------------------------------------------ELD
ALVARVKAAQEEFA-TFSQEKVDAIFRAASLAA--NHARIPLAQQAVAESGMGIVEDKVI
KNHFASEFIYNKYKDEKTCGILDEDESLGTMTIAEPVGIICGIVPTTNPTSTAIFKSLIS
LKTRNGIIFSPHPRAKNSTNDAAKLVLDAAVAAGAPKDIIGWIDQPSVELSNALMKHDGI
ALILATGGPGMVKAAYS-SGKPAIGVGAGNVPVVIDETADIKRAVASILMSKTFDNGVVC
ASEQAAIVVSEVYDEVKERF-ASHKAHVL-SKADADKVRKVLL-------IDGNL-----
NAKIVGQPAPAIAEMAGVK--VPA-DTKVLVGEGLGKVSYDDEFAHEKLSPTLGLFRADD
FEDAVAQAVTMVEIGGIGHTSGLYTNQDVNADRIRYFGDKMKTARILINIPTTHG--GIG
DLYNFNVAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIAMSDLE---GKKRAFLVTDRFLFNNGYADDVVQILKSQGIEVQVFFDVEADPTLSVV
EKGAEAMKSFQPDVILALGGGSPMDAAKIMWVMYEHPETHFEELAMRFMDIRKRIYKFPK
MGKKAELVCITTTSGTGSEVTPFAVVTDDKTGAKYPLADYEITPNMAVVDANLVMNMPKS
LTAFGGYDAVTHALEAYVSVLANEYSDGQALQALKMLKEYLPSSYKNGSADPIAREKVHN
AATIAGIAFANAFLGVCHSMAHKIGAEFHLPHGLANALLISNVVRYNANDNPTKQTAFSQ
YDRPQARRRYAEVADHLGLSQA-GDRTAQKIERLLTWLEELKVDLDIPLSIQAA-GVNES
DFIAKLDELAVEAFDDQCTGANPRYPLITELKEVLTTSYFGKAYVEGETFEGTTVILKKA
DQKPAEEKAAPKAKKEKANA--
>gi|187251182|ref|YP_001875664.1| bifunctional acetaldehyde-CoA/alcohol
dehydrogenase [Elusimicrobium minutum Pei191]
------------MTNKEIKKGTKPVF-----------------TEADIAKEQA-------
---------------------------------------------------------HIE
HVLTSVKDAQKQYA-QYTQEQVDKIFRAAAAAA--ASKRIFLSKMAVEETGMGVMEDKVI
KNQFASEYIYNTYKNEQTCGVLERDQAFGFARVAEPIGVIAGIIPTTNPTSTAIFKSLLA
LKTRNGIVFSPHPRAKKCTIAAAKIVLEAAVAAGAPKNIIGWIEASSTKASEYLMKHDKV
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDSTADIKMAVSSVIMSKTFDNGMIC
ASEQSVIVEKSIAEEVKKEF-VKRGCHFV-TGKDREKLAKTIV-------QDYHL-----
NSKIVGQSAHKIAELAGFT--VDP-KTKILIAE-AKDVNCDEPFAYEKLSPVLAFYTVKD
FYSGVELAQKLIEFGGAGHTSVLYTDEVNT-EHISIFGEKLTTGRILINMPSSQG--AIG
DVYNFKLVPSLTLGCGSWGGNSVSENIGVKHLMNIKSVAERRENMLWFRVPEKIYFKAGA
TTLALEELK---GRKRAFIITDKTMEQLGTVKNVAKVLAEAGIQVRIFSDVKPDPDLSNV
REALELVNLFQPDILIGFGGGSPMDAAKIIWLMYEHPEVKFEDIALRFMDIRKRITAFPK
LGIKATMVAIPTTSGTGSEVTPFTVITDDASGIKYPIADYELTPKMAIIDPEYVMTMPKS
LTAFSGMDVVTHAVESYTSVFANNFTDGHALEALRLVFKYLRQSYNEGAKAPIAREKMHY
AATIAGMAFANAFLGICHSMAHKIGGMYHTAHGLANAILLPYVIDYNATDNPVKQGLMPQ
YKYPFVKGRYAKIADFLGITEGCGDDTDKKVMRLIEAIQKLNKDLGVPVSLQES-GIPEA
EFLANLDALSEEAFDDQCTSGNPRYPLVSEIKDLYLKAYYGKPIKHKKN-----------
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>gi|28211045|ref|NP_781989.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Clostridium tetani E88]
-------------------MKVENVQ----------------------------------
---------------------------------------------------------QLM
EKIENVRKAQKEFA-NYNQKQVDEIFRSAAIAA--NEARIELAKLAVEETGMGIIEDKVI
KNHFASEYIYNKYKDEKTCGIIERDESFGISKVAEPRGVIAAIIPITNPTSTTIFKALIC
LKARNGIIFSPHPKAKKSTIAAAKIVLQAAIDAGAPKEIIAWIDEPSLELSQKLMHEGD-
-MILATGGPGMVKAAYS-SGKPAIGVGAGNTPAIIDETAHIKMAVNSIIMSKSFDNGVIC
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ASEQSVLVVDEVYEDVKQEF-EERGAYIL-KGDEVDKLRNIIL-------INGAV-----
NPDIVGQPPYKIAKLAGVE--IPQ-SSRIIIGE-VKSVEIDEPFAHEKLSPVLAMYRVKD
FNEALDKAVTLIEDGGRGHTSVLYTNIVKSKDRVDKFSLTMKTGRTIINMPASQG--AMG
DVYNFKLQPSLTLGCGTWGGNSVSENVGVKHLINIKSVAERRENMLWFRVPEKIYFKYGC
LAMALNELK-DMKKKRAFIVTDRVLYNLGFAEKIEKILEEIGIEFKVFFDVESDPTLKTA
KKGAEDMKSFKPDTIIALGGGSPMDAAKIMWIMYEHPDVKFEDLTMRFMDIRKRVYKFPK
MGEKAMMVAIPTTAGTGSEVTPFAVITDENTGIKYPLADYELTPDMAIIDAELMLNIPKE
LTAASGIDALTHGIEAYVSVLASEYTNGLALEAIRLVFKYLPDAYNEGANNIKAREKMAH
ASTMAGMAFANAFLGVCHSMAHKLGAMHNLSHGLSNALLINEVIKFNAVDNPRKQASYPQ
YKYPNAKWRYGRIADHLNLG---GNTDDEKVELLIKAIDELNEKVGIPKTISEA-GVPKE
KFYATLDEMSEQAFDDQCTVANPRYPLISEIKEMYINVYEDTDKEHKTEKHKNEECK---
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>gi|28898895|ref|NP_798500.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Vibrio parahaemolyticus RIMD 2210633]
-------------------MPVTNMA----------------------------------
---------------------------------------------------------ELD
AMIARVKKAQEEFA-TYSQEQVDKIFRAASLAA--NQARIPLAQQAVEESGMGIVEDKVI
KNHFASEFIYNKYKDEQTCGILEEDDNLGTMTIAEPVGIICGIVPTTNPTSTAIFKSLIS
LKTRNGIIFSPHPRAKNSTNDAAKLVLDAAVAAGAPKDIIGWIDQPSVELSNALMKHDDI
ALILATGGPGMVKAAYS-SGKPAIGVGAGNVPVVIDETADIKRAVASVLMSKTFDNGVVC
ASEQAVIVVDEVYDEVKERF-ASHKAHVL-SKTDADKVRKVLL-------IDGAL-----
NAKIVGQPATAIAEMAGVK--VPA-DTKVLIGEGLGKVSYDDAFAHEKLSPTLGMFRADN
FEDAVAQAVTMVEIGGIGHTSGLYTNQDVNADRIRYFGDKMKTARILINIPTTHG--GIG
DLYNFNVAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALGDLE---GKKRAFLVTDRFLFNNGYADDVVSLLKAQGMEVQTFFDVEADPTLSVV
EKGAAQMASYQPDVILALGGGSPMDAAKIMWVMYEHPETHFEELAMRFMDIRKRIYKFPK
MGKKAELVCITTTSGTGSEVTPFAVVTDDKTGAKYPLADYEITPNMAIVDANLVMNMPKS
LTAFGGYDAVTHALEAYVSVLANEYSDGQALQALKMLKEYLPSSYANGANDPIAREKVHN
AATIAGVAFANAFLGVCHSMAHKLGAEFHLPHGLANALLISNVVRYNANDNPTKQTAFSQ
YDRPQARRRYAEVADHLGLSQA-GDRTAQKIERLLAWLDELKVNLDIPMSIQAA-GVAEA
DFVAKLDELAVEAFDDQCTGANPRYPLISELKDVLLASYYGKAFVEGETFEGTTVIKKKA
DQEAAKSAPKAKKEKADA----
>gi|218440596|ref|YP_002378925.1| iron-containing alcohol dehydrogenase [Cyanothece
sp. PCC 7424]
-------------------MKVTNLE----------------------------------
---------------------------------------------------------ELE
ALIQRTKAAQEIYA-TYTQEQVDEIFKKAALAA--NAARIPLAKMAVAETGMGVIEDKVI
KNHFASEIIYNKYKSDKTCGVIEEDKSFGFQKIAEPVGLVAGIVPTTNPTATAIFKSLIT
LKTRNGIIFSPHPRAKTCTIEAARIVLEAAIEAGAPEHLIGWIDEPSVELSQRLMQHPNI
SLILATGGPGMVKAAYS-SGRPSLGVGAGNTPALIDDTAHIKMAVSSIILSKTFDNGMIC
ASEQSVVVLDRIYDIVKEEF-RERGAYFL-TPEEEEKLGKVLI-------VDGHI-----
NGEVVGQSVQKLAELGGFA--VPE-NTRVLIAE-VEEIGYDEPFAYEKLSPVLGMYRATD
FTDGLNKAEQLVEFAGRGHTAVLYTSPSNK-DHIRQFEETIETARVLINTPSSQG--AIG
DIYNFRLDPSLTLGCGTWGGNSISENVEPRHLLNIKTVAERRENMLWFRVPPKVYFKYGA
LPIAIRELA---GKQRAFIVTDKPLYNLGLTKGLEEVLEEIGMRYNVFYDVEPDPSLETV
NRGLGVMREFNPDVIIAIGGGSPMDAAKIMWLLYEHPEIEFEGLAMRFMDIRKRVYDLPP
LGQKAILVAVPTTSGTGSEVTPFAVVTDRRKNIKYPLADYALTPTMAVVDPELVLQMPKS
LTAYGGLDALTHATEAFVSVLASEFTTGLCLEAIRLIFKYLPSAYHNGAKDYKAREKVHY
AATMAGMAFANSFLGICHSMAHQLGAVFHVPHGLANAMMISHVIRYNATDAPFKQATFSQ
YKYPNAIWRYARIADYLGLG---GATKEDKVDRLIEVIEDLKRRLDVPMALKDVIHVTEA
EFLAKVDEIADQAFDDQCTGSNPRYPLIKDLRELLIKAYYGESPVTSNGNGRQYLTLEDV
KTDPQPIA--------------
>gi|189485598|ref|YP_001956539.1| aldehyde-alcohol dehydrogenase [uncultured Termite
group 1 bacterium phylotype Rs-D17]
----MTGTKGKNVKLSERDVSAGYVI----------------------------------
-----------------------------------------------------DSSEALN
MLIQRVKKAQEVYS-SFSQEQVDAIFKAVSIAA--NRSRIPLAKIAVEETGMGIVEDKVI
KNHFACEYIYNKHKDAKTCGIISEDKPNGIKILAEPVGVIAGIIPTTNPTSTVIFKSLIS
LKTRNAVIFSPHPKAKKSTVVAARIMLDAAVKAGAPSDIIGWIDVPSLELTNLLMTHKDI
AIILATGGPGMVKAAYS-SGKPALGVGAGNTPAVIDETADIKMAVSSILISKTFDNGMIC
SSEQSIIIVKDVYDEVIKEL-KFRGAYIL-NEQEKEKIAKTII-------LKGKL-----
NPAIVGQSACKIADMSGVK--VPS-NAKVLVGE-VSEISLEEEFAQEKLSPVIAVYMAEN
FEDAVEKAYRLVELCGAGHTSVLYTDERKQ-NRINAFAGKLRTGRILINTPSSQG--AIG
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DLYNFKLDPSLTLGCGSWGGNAVSENVGVKHLLNYKTVAERRENMLWFRIPPKIYFKRGV
TNSALRELQ---GKKRAFIVTDRFLFNSGVIYNITKVLEEINVDYQIFFDVKPDPTVSTV
NEALLLIRNYEPDVIIAFGGGSPIDAAKIIWLMYEHPETDFKNIAMRFMDIRKRICKIPE
LGKKAQMIAIPTTSGTGSEVTPFAVITDDETHIKYPIADYVLTPNVAIIDPDFADSMPKS
LCAASGIDALTHAIEAYVSVLAANFTNSPALEAAKLIFKYLPSSYAAGKDDPVAKEKVHY
ASTLAGMAFANAFLGLCHSVAHKLGAAFNLSHGIANALVINQVIRYNATERPGKQTVFPQ
YKFPNAKAKYGQIADELNLG-G-GYHDDEKVDLLINAITQLKKDIQIPLSIKDT-GVLEK
DFYDKLDELAEQAFDDQCTGANPVYPLIADIKNIFIKAYNGEV-----------------
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>gi|115525690|ref|YP_782601.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Rhodopseudomonas palustris BisA53]
--------MVRPLPDNQNGGFTVTLS-------------------------------APS
NSPLSN-----------------------------------------------SALTDLD
QLVARVKAAQLVFA-TYSQEKVDLIFRSAALAA--SDARISLAQMATAETGMGVVEDKVI
KNHFASEYIYNAYKDDKTCGIIEVNDEAGIMVVAEPIGLICGIVPTTNPTSTAIFKALIC
LKTRNGIIFSPHPRAARSTNAAAKLVLDAAVAAGAPADIIGWIDTPTLQLSDALMHHPDV
NLILATGGPAMVKAAYS-SGKPAIGVGAGNTPVVIDETADIKRAVASILMSKTFDNGVVC
ASEQSIIVVDSVYDAVRERF-ASHGGYML-KPAELDAVRAVLL-------VNGNV-----
NVNIVGQSAARIAELAGIS--VPR-DTKLLIGE-VDSTGVAEPFAHEKLSPTLAMYRRAD
YAQAVAAAVELVALGGIGHTSALYTDQDLQPERIADFGSRMKTARILINTPSSHG--GLG
DLYNFSLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGA
TSEALKDLA---GKKRALIVTDSFLFSKGYTDDVIRLLKKNGMEVETFYQVEADPTLTII
KKGVEIAHAFQPDVIVAFGGGSPMDAAKLIWVLYEHPDVQFEDLALRFMDIRKRIYKFPK
LGIKAELVAIPTTSGTGSEVTPFAVVTDDSTGVKYPIADYELTPSMAIVDANFVMNLPKS
LTAFGGIDAVVHSLEAYVSIMASEFTDGQALQALRLLKDHLPSAYANGAKDPVAREKVHS
GATIAGIAFANAFLGVCHSMAHKLGAAFHIPHGLSNALLICNVIRYNANDNPTKQTAFSQ
YDRPKSRHRYGEIAIALGLD---GVNTAARIDNLLEWLEGLKRELDIPASIQAA-GVPEA
AFLAKLDELAVEAFDDQCTGANPRFPLLDELKAILLASYYGRPFSEEYVEDEAVATAAAA
E---------------------
>gi|197335754|ref|YP_002155681.1| aldehyde-alcohol dehydrogenase 2 [Vibrio fischeri
MJ11]
-------------------MPVTNLA----------------------------------
---------------------------------------------------------ELD
ALVARVKAAQEEFA-TFSQEQVDAIFRAASLAA--NQARIPLAQQAVAESGMGIVEDKVI
KNHFASEFIYNKYKDEKTCGILEEDDNLGTMTIAEPVGIICGIVPTTNPTSTAIFKSLIS
LKTRNGIIFSPHPRAKNSTNDAAKLVLDAAVAAGAPKDIIGWIDQPSVELSNALMKHDGI
ALILATGGPGMVKAAYS-SGKPAIGVGAGNVPVVIDDTADVKRAVASVLMSKTFDNGVVC
ASEQAVIVMDEVYDEVKERF-ASHKGYVL-SKAEADKVRKVLL-------IDGNL-----
NANIVGQPATAIAEMAGVK--VPA-DTKILVGEGIGEVSYDDEFAHEKLSPTLGMFRASS
FENAVDQAVKMVEIGGIGHTSGLYTNQDVNADRIRYFGDKLKTARILVNIPTTHG--GIG
DLYNFNVAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIAMSDLE---GKKRAFLVTDRFLFNNGYADDVVQLLKAQGIEVQTFFDVEADPTLSVV
EKGAEAMKSFQPDVILALGGGSPMDAAKIMWVMYEHPETHFAELAMRFMDIRKRIYKFPK
MGKKAELVCITTTSGTGSEVTPFAVVTDDKTGAKYPLADYEITPNMAIVDANLVMNMPKS
LTAFGGYDAVTHALEAYVSVLANEYSDGQALQALKMLKEYLPSSYKNGANDPIAREKVHN
AATIAGIAFANAFLGVCHSMAHKIGAEFHLPHGLANALLISNVVRYNANDNPTKQTAFSQ
YDRPQARRRYAEVADHLGLSQA-GDRTAQKIERLLTWLEELKKDLDIPLSIKDA-GVNEA
DFIAKLDELSVEAFDDQCTGANPRYPLITELKEVLTTSYYGKPFVEGETFEGTTVIKKTE
EPKAKKAKK-------------
>gi|90425953|ref|YP_534323.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Rhodopseudomonas palustris BisB18]
-------------------MTLSTPS----------------------------------
---------------------------------------------------------DLD
KLVARVKAAQLIFA-TYSQEQVDLIFRSAALAA--SDARISLAQMATAETGMGVVEDKVI
KNHFASEYIYNAYKDDKTCGIIEVNDEAGIMVVAEPIGLICGIVPTTNPTSTAIFKALIC
LKTRNGIIFSPHPRAARSTNAAAKLVLDAAVAAGAPPDIIGWIEKPTLELSNALMHHPAV
NLILATGGPAMVKAAYS-SGKPAIGVGAGNTPVVIDETADIKRAVASILMSKTFDNGVVC
ASEQSIIVVDEVYDAVRQRF-ATHGGYML-KPAELDAVRRVLL-------VNGNV-----
NVDIVGQSAARIAELAGIS--VPH-DTKILIGE-VELTHTSEPFAHEKLSPTLAMYRRAD
YTQAVAAAVELVALGGIGHTSALYTDQDLQPERVADFGTKMKTARILINTPSSHG--GLG
DLYNFSLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGA
TSEALKDLA---GKKRALVVTDGFLFSKGYTDDVIRLLKKNGMEVETFFQVEADPTLSII
NKGVEIAHAFKPDVIVAFGGGSPMDAAKLIWVLYEHPDVQFEDLALRFMDIRKRIYKFPK
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LGQKAELVAIPTTSGTGSEVTPFAVVTDDASGIKYPIADYELTPSMAIVDANFVMHLPKS
LTAFGGIDAVVHALEAYVSIMASEFTDGQALQALKLLKENLPSAYVNGAKDPVARERVHS
GATIAGIAFANAFLGVCHSMAHKLGAAFHIPHGLSNALLICNVIRYNANDNPTKQTAFSQ
YDRPKSRHRYGEIAIALGLD---GVNTAARIDRLLEWLEGLKRELDIPASIREA-GVSEA
DFLAKVDNIAVEAFDDQCTGANPRFPLVSELKTILLDSYYGRAFSEAHEEDEVVTLSVAT
ANAAE-----------------
>gi|152970748|ref|YP_001335857.1| bifunctional acetaldehyde-CoA/alcohol
dehydrogenase [Klebsiella pneumoniae subsp. pneumoniae MGH 78578]
-------------------MAVTNIA----------------------------------
---------------------------------------------------------ELN
ALVERVKKAQREYA-SFTQEQVDKIFRAAALAA--ADARIPLAKMAVAESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGVLSEDDTFGTITIAEPIGIICGIVPTTNPTSTAIFKSLIS
LKTRNAIIFSPHPRAKEATNKAADIVLQAAIAAGAPKDLIGWIDQPSVELSNALMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDETADIKRAVASVLMSKTFDNGVIC
ASEQSVVVVDSVYDAVRERF-ASHGGYLL-QGKELKAVQDIIL-------KNGAL-----
NAAIVGQPAAKIAELAGFT--VPA-TTKILIGE-VTNVDESEPFAHEKLSPTLAMYRAKD
FEDAVAKAEKLVAMGGIGHTSCLYTDQDNQPARVAYFGQMMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALDEVI-TDGHKRALIVTDRFLFNNGYADQITSVLKAAGVETEVFFEVEADPTLTIV
RKGADLANSFKPDVIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKMVAITTTSGTGSEVTPFAVVTDDATGQKYPLADYALTPDMAIVDANLVMDMPKS
LCAFGGLDAVTHALEAYVSVLASEFSDGQALQALKLLKEYLPASYHEGSKNPVARERVHS
AATIAGIAFANAFLGVCHSMAHKLGSQFHIPHGLANALLICNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLGLSAP-GDRTAAKIEKLLAWLESIKAELGIPKSIREA-GVQEA
DFLAHVDKLSEDAFDDQCTGANPRYPLISELKQILLDTYYGREFVEGEAGAKAEVAPVKA
EKKAKKSA--------------
>gi|59711525|ref|YP_204301.1| fused acetaldehyde-CoA dehydrogenase/iron-dependent
alcohol dehydrogenase/pyruvate-formate lyase deactivase [Vibrio fischeri ES114]
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------MGIVEDKVI
KNHFASEFIYNKYKDEKTCGILEEDDNLGTMTIAEPVGIICGIVPTTNPTSTAIFKSLIS
LKTRNGIIFSPHPRAKNSTNDAAKLVLDAAVAAGAPKDIIGWIDQPSVELSNALMKHDGI
ALILATGGPGMVKAAYS-SGKPAIGVGAGNVPVVIDDTADVKRAVASVLMSKTFDNGVVC
ASEQAVIVMDEVYDEVKERF-ASHKGYVL-SKAEADKVRKVLL-------IDGNL-----
NANIVGQPATAIAEMAGVK--VPA-DTKILVGEGIGEVSYDDEFAHEKLSPTLGMFRASS
FENAVDQAVKMVEIGGIGHTSGLYTNQDVNADRIRYFGDKLKTARILVNIPTTHG--GIG
DLYNFNVAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIAMSDLE---GKKRAFLVTDRFLFNNGYADDVVQLLKAQGIEVQTFFDVEADPTLSVV
EKGAEAMKSFQPDVILALGGGSPMDAAKIMWVMYEHPETHFAELAMRFMDIRKRIYKFPK
MGKKAELVCITTTSGTGSEVTPFAVVTDDKTGAKYPLADYEITPNMAIVDANLVMNMPKS
LTAFGGYDAVTHALEAYVSVLANEYSDGQALQALKMLKEYLPSSYKNGANDPIAREKVHN
AATIAGIAFANAFLGVCHSMAHKIGAEFHLPHGLANALLISNVVRYNANDNPTKQTAFSQ
YDRPQARRRYAEVADHLGLSQA-GDRTAQKIERLLTWLEELKKDLDIPLSIKDA-GVNEA
DFIAKLDELSVEAFDDQCTGANPRYPLITELKEVLTTSYYGKPFVEGETFEGTTVIKKTE
EPKAKKAKK-------------
>gi|161614933|ref|YP_001588898.1| bifunctional acetaldehyde-CoA/alcohol
dehydrogenase [Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7]
MTFAAAFCGGASLFPFEVSMSINSIE----------------------------------
---------------------------------------------------------ELN
ALVARVKKAQRQYA-SFTQQQVDKIFRAAALAA--ADARIPLAKMAVAESGMGIVEDKVI
KNHFASEYIYNTYKDEKTCGVLSEDDTFGTITIAEPVGIICGIVPTTNPTSTAIFKSLIS
LKTRNAIIFSPHPRAKEATNKAADIVLQAAIAAGAPKDLIGWIDQPSVDLSNALMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDETADIKRAVASILMSKTFDNGVIC
ASEQSVVVVDSVYDAVRERF-AKCGAVIL-NKKERKAVGGVLL-------KNGAL-----
NAAIVGQSAATIAEIAGIF--VPE-NSKVLIGE-VSATDASEPFAHEKLSPTLAMYRAKD
FADAVDKAEQLVAMGGIGHTSCLYTDQDNQPERVAYFGQMMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALDEVI-TDGHKRALIVTDRFLFNNGYADQITSVLKAAGVETEVFFEVEADPTLSVV
RKGAELANSFKPDVIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKMIAVTTTSGTGSEVTPFAVVTDDATGQKYPLADYALTPDMAIVDANLVMDMPKS
LCAFGGLDAVTHALEAYVSVLASEFSDGQALQALKLLKENLPASYHEGSKNPVARERVHS
AATIAGIAFANAFLGVCHSMAHKLGSQFHIPHGLANALLICNVIRYNANDNPTKQTAFSQ
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YDRPQARRRYAEIADHLGLSAP-GDRTAAKIEKLLAWLESIKAELGIPKSIREA-GVQEA
DFLAHVDKLSEDAFDDQCTGANPRYPLVSELRQLLLASFYGEAFAEQ-------------
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>gi|206580610|ref|YP_002237946.1| aldehyde-alcohol dehydrogenase [Klebsiella
pneumoniae 342]
-------------------MAVTNIA----------------------------------
---------------------------------------------------------ELN
ALVERVKKAQREYA-SFTQEQVDKIFRAAALAA--ADARIPLAKMAVAESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGVLSEDDTFGTITIAEPIGIICGIVPTTNPTSTAIFKSLIS
LKTRNAIIFSPHPRAKEATNKAADIVLQAAIAAGAPKDLIGWIDQPSVELSNALMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDETADIKRAVASVLMSKTFDNGVIC
ASEQSVVVVDSVYDAVRERF-ASHGGYLL-QGKELKAVQDIIL-------KNGAL-----
NAAIVGQPAAKIAELAGFT--VPA-TTKILIGE-VTNVDESEPFAHEKLSPTLAMYRAKD
FEDAVTKAEKLVAMGGIGHTSCLYTDQDNQPARVAYFGQMMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALDEVI-TDGHKRALIVTDRFLFNNGYADQITSVLKAAGVETEVFFEVEADPTLTIV
RKGADLANSFKPDVIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKMVAITTTSGTGSEVTPFAVVTDDATGQKYPLADYALTPDMAIVDANLVMDMPKS
LCAFGGLDAVTHALEAYVSVLASEFSDGQALQALKLLKEYLPASYHEGSKNPVARERVHS
AATIAGIAFANAFLGVCHSMAHKLGSQFHIPHGLANALLICNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLGLSAP-GDRTAAKIEKLLAWLESIKAELGIPKSIREA-GVQEA
DFLANVDKLSEDAFDDQCTGANPRYPLISELKQILLDTYYGREFVEGETAAKTDAAPVKA
EKKAKKSA--------------
>gi|158333640|ref|YP_001514812.1| bifunctional acetaldehyde-CoA/alcohol
dehydrogenase [Acaryochloris marina MBIC11017]
------------MMTTQTQPQVTDIP----------------------------------
---------------------------------------------------------SLE
DLIARVKQAQEVYA-TYTQEQVDHIFKQVAIAA--NAERIPLAKQAVAETGMGVIEDKVI
KNHFASEYIYNKYKHEKTCGVVSADAHYGIQKVAEPLGIVAGIIPTTNPTSTAIFKALLC
LKTRNAIIFSPHPRAKHCTVRAVEIIRDAALQAGAPPDIVGWIDEPTLDLSQALMQHADI
KLILATGGPGMVKAAYS-SGHPSLGVGAGNTPAVIDETADIQVAVSSILLSKTFDNGMIC
ASEQSVVVTEAVYEQVKQEF-RKRGAYFL-TSEEKDKVAQTIL-------KNGKL-----
NPAIVGQPISELATLAGIE--GPQ-DHKVLIGE-VSTIGSSEPFAYEKLSPILAMYRAAD
FTDAVDQAKQLVNFGGRGHTSVLYTAASNC-DRIRIFETELATARVLINTPSSQG--AIG
DLYNFKLDPSLTLGCGTWGGNSISGNVNVQHLLNIKTVTERRENMLWFRVPPKIYFKYGC
IPVALRDLA---EKKRAFIITDRPLFDLGLTKEITETLDQLGIEHHLFFDVEPDPDLSTV
KRGLDVINTFQPDVIIALGGGSPMDAAKVMWLMYEHPEVEFDGLAMRFMDIRKRVYELPP
LGNKAILVAVPTTSGTGSEVTPFAVVTDDRVGIKYPLADYALTPTMAIVDPELVLNMPKK
LTAYGGVDALTHALEAYVSVLATEFTDGLALEAISLLMTYLPRAYHQGSADPEAREKVHY
AATIAGLAFANAFLGICHSLAHKLGSTFHVPHGLANALMISHVIRYNATDAPFKQAIFPQ
YEYPQAKGRYAAIADSLNLR---GTTADEKVERLITAIENLKQELDIPSSIREVLSVDEQ
TFFEHLDLMSEQAFDDQCTGANPRYPLIRDLKALYLEAYQNSSQATTLATEIALEAAAHN
QALLGKNINFTSIENS------
>gi|50121254|ref|YP_050421.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Pectobacterium atrosepticum SCRI1043]
-------------------MAVTNVA----------------------------------
---------------------------------------------------------ELN
ALVERVKKAQQEFA-TYTQEQVDKIFRAAALAA--SDARIPLAKMAVAESGMGIVEDKVI
KNHFASEYIYNAYQDEKTCGVLSTDDTFGTITIAEPIGLICGIVPTTNPTSTAIFKALIS
LKTRNGIIFSPHPRAKNATNKAADIVLQAAIAAGAPKDIIGWIDQPSVDLSNQLMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDETADIKRAVASILMSKTFDNGVIC
ASEQSVIVVDSAYDAVRERF-ATHGGYML-KGKELHAVQGILL-------KNGSL-----
NADIVGQPAPKIAEMAGIT--VPA-NTKVLIGE-VTAVDESEPFAHEKLSPTLAMYRAKD
FNDAVIKAEKLVAMGGIGHTSCLYTDQDNQPERVNHFGNMMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALEEVA-SDGAKRAFIVTDRFLFNNGYVDQVTSVLKQHGLETEVFFEVEADPTLSIV
RKGAEQMHSFKPDVIIALGGGSPMDAAKIMWVMYEHPTTHFEELALRFMDIRKRIYKFPK
MGVKAKMVAITTTSGTGSEVTPFAVVTDDATGQKYPLADYALTPDMAIVDANLVMNMPKS
LCAFGGLDAVTHSLEAYVSVLANEYSDGQALQALKLLKENLPDSYRDGAKNPVARERVHN
AATIAGIAFANAFLGVCHSMAHKLGSEFHIPHGLANAMLISNVIRYNANDNPTKQTTFSQ
YDRPQARRRYAEIADHLRLTAP-SDRTAQKIEKLLNWLEEIKTELGIPASIREA-GVQEA
DFLAKVDKLSEDAFDDQCTGANPRYPLISELKQILLDTYYGRKFSEEVKTETVEPVAKAA
KTGKKAAH--------------
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>gi|218699946|ref|YP_002407575.1| fused acetaldehyde-CoA dehydrogenase ;
iron-dependent alcohol dehydrogenase ; pyruvate-formate lyase deactivase
[Escherichia coli IAI39]
-------------------MAVTNVA----------------------------------
---------------------------------------------------------ELN
ALVERVKKAQREYA-SFTQEQVDKIFRAAALAA--ADARIPLAKMAVAESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGVLSEDDTFGTITIAEPIGIICGIVPTTNPTSTAIFKSLIS
LKTRNAIIFSPHPRAKDATNKAADIVLQAAIAAGAPKDLIGWIDQPSVELSNALMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDETADIKRAVASVLMSKTFDNGVIC
ASEQSVVVVDSVYDAVRERF-ATHGGYLL-QGKELKAVQDVIL-------KNGAL-----
NAAIVGQPAYKIAELAGFS--VPE-NTKILIGE-VTVVDESEPFAHEKLSPTLAMYRAKD
FEDAVEKAEKLVAMGGIGHTSCLYTDQDNQPARVSYFGQKMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALDEVI-TDGHKRALIVTDRFLFNNGYADQITSVLKAAGVETEVFFEVEADPTLSIV
RKGAELANSFKPDVIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKMIAVTTTSGTGSEVTPFAVVTDDATGQKYPLADYALTPDMAIVDANLVMDMPKS
LCAFGGLDAVTHAMEAYVSVLASEFSDGQALQALKLLKEYLPASYHEGSKNPVARERVHS
AATIAGIAFANAFLGVCHSMAHKLGSQFHIPHGLANALLICNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLGLSAP-GDRTAAKIEKLLAWLETLKAELGIPKSIREA-GVQEA
DFLANVDKLSEDAFDDQCTGANPRYPLISELKQILLDTYYGRDYVEGETAAKKEAAPAKV
EKKAKKSA--------------
>gi|215486475|ref|YP_002328906.1| fused acetaldehyde-CoA
dehydrogenase/iron-dependent alcohol dehydrogenase/pyruvate-formate lyase deactivase
[Escherichia coli O127:H6 str. E2348/69]
-------------------MAVTNVA----------------------------------
---------------------------------------------------------ELN
ALVERVKKAQREYA-SFTQEQVDKIFRAAALAA--ADARIPLAKMAVAESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGVLSEDDTFGTITIAEPIGIICGIVPTTNPTSTAIFKSLIS
LKTRNAIIFSPHPRAKDATNKAADIVLQAAIAAGAPKDLIGWIDQPSVELSNALMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDETADIKRAVASVLMSKTFDNGVIC
ASEQSVVVVDSVYDAVRERF-ATHGGYLL-QGKELKAVQDVIL-------KNGAL-----
NAAIVGQPAYKIAELAGFS--VPE-NTKILIGE-VTVVDESEPFAHEKLSPTLAMYRAKD
FEDAVEKAEKLVAMGGIGHTSCLYTDQDNQPARVSYFGQKMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALDEVI-TDGHKRALIVTDRFLFNNGYADQITSVLKAAGVETEVFFEVEADPTLSIV
RKGAELANSFKPDVIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKMIAVTTTSGTGSEVTPFAVVTDDTTGQKYPLADYALTPDMAIVDANLVMDMPKS
LCAFGGLDAVTHAMEAYVSVLASEFSDGQALQALKLLKEYLPVSYHEGSKNPVARERVHS
AATIAGIAFANAFLGVCHSMAHKLGSQFHIPHGLANALLICNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLGLSAP-GDRTAAKIEKLLAWLETLKAELGIPKSIREA-GVQEA
DFLANVDKLSEDAFDDQCTGANPRYPLISELKQILLDTYYGRDYVEGETAAKKEAAPAKA
EKKAKKSA--------------
>gi|157370944|ref|YP_001478933.1| bifunctional acetaldehyde-CoA/alcohol
dehydrogenase [Serratia proteamaculans 568]
-------------------MAVTNVA----------------------------------
---------------------------------------------------------ELN
ELVARVKKAQREYA-NFTQEQVDKIFRAAALAA--ADARIPLAKLAVEESGMGIVEDKVI
KNHFASEFIYNAYKDEKTCGILAEDHTFGTITIAEPIGLICGIVPTTNPTSTAIFKALIS
LKTRNGIIFSPHPRAKNATNKAADIVLQAAIAAGAPKDIVGWIDQPTVELSNQLMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVVDETADIKRVVASILMSKTFDSGVIC
ASEQSVIVVDSIYDAVRERF-ASHGGYML-QGKELKAVQDIIL-------KNGGL-----
NAAIVGQSAPKIAEMAGIK--VPA-STKVLIGE-VKLVDETEPFAHEKLSPTLAMYRAKD
FADAVSKAEKLVAMGGIGHTSCLYTDQDNQPERVAFFGDKMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALEEVA-TDGAKRAFIVTDRYLFNNGYADQITSVLKSHGIETEVFFEVEADPTLSIV
RKGAEQMNSFKPDVIIALGGGSPMDAAKIMWVLYEHPETHFEDLALRFMDIRKRIYKFPK
MGVKAKMIAVTTTSGTGSEVTPFAVVTDDVTGQKYPLADYALTPDMAIVDANLVMNMPKS
LCAFGGLDAVTHALEAYVSVLANEYSDGQALQALKLLKEYLPASYKEGAKNPVARERVHN
AATIAGIAFANAFLGVCHSMAHKLGSEFHIPHGLANAMLISNVIRYNANDNPTKQTAFSQ
YDRPQARRRYGEIADHLGLSAP-GDRTAQKIEKLLTWLDEIKAELGIPASIREA-GVTEA
DFLAKVDKLSEDAFDDQCTGANPRYPLIAELKQIMLDTFYGRKFSEAEDEEVLVAPAAAK
AEKKSKK---------------
>gi|82544308|ref|YP_408255.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
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[Shigella boydii Sb227]
-------------------MAVTNVA----------------------------------
---------------------------------------------------------ELN
ALVERVKKAQREYA-SFTQEQVDKIFRAAALAA--ADARIPLAKMAVAESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGILSEDDTFGTITIAEPIGIICGIVPTTNPTSTAIFKSLIS
LKTRNAIIFSPHPRAKDATNKAADIVLQAAIAAGAPKDLIGWIDQPSVELSNALMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDETADIKRAVASVLMSKTFDNGVIC
ASEQSVVVVDSVYDAVRERF-ATHGGYLL-QGKELKAVQDVIL-------KNGAL-----
NAAIVGQPAYKIAELAGFS--VPE-NTKILIGE-VTVVDESEPFAHEKLSPTLAMYRAKD
FEDAVEKAEKLVAMGGIGHTSCLYTDQDNQPARVSYFGQKMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALDEVI-TDGHKRALIVTDRFLFNNGYADQITSVLKAAGVETEVFFEVEADPTLSIV
RKGAELANSFKPDVIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKMIAVTTTSGTGSEVTPFAVVTDDATGQKYPLADYALTPDMAIVDANLVMDMPKS
LCAFGGLDAVTHAMEAYVSVLASEFSDGQALQALKLLKEYLPASYHEGSKNPVARERVHS
AATIAGIAFANAFLGVCHSMAHKLGSQFHIPHGLANALLICNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLGLSAP-GDRTAAKIEKLLAWLETLKAELGIPKSIREA-GVQEA
DFLANVDKLSEDAFDDQCTGANPRYPLISELKQILLDTYYGRDYVEGETAAKKEAAPAKA
EKKAKKSA--------------
>gi|24112636|ref|NP_707146.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Shigella flexneri 2a str. 301]
-------------------MAVTNVA----------------------------------
---------------------------------------------------------ELN
ALVERVKKAQREYA-SFTQEQVDKIFRAAALAA--ADARIPLAKMAVAESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGVLSEDDTFGTITIAEPIGIICGIVPTTNPTSTAIFKSLIS
LKTRNAIIFSPHPRAKDATNKAADIVLQAAIAAGAPKDLIGWIDQPSVELSNALMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDETADIKRAVASVLMSKTFDNGVIC
ASEQSVVVVDSVYDAVRERF-ATHGGYLL-QGKELKAVQDVIL-------KNGAL-----
NAAIVGQPAYKIAELAGFS--VPE-NTKILIGE-VTVVDESEPFAHEKLSPTLAMYRAKD
FEDAVEKAEKLVAMGGIGHTSCLYTDQDNQPARVSYFGQKMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALDEVI-TDGHKRALIVTDRFLFNNGYADQITSVLKAAGVETEVFFEVEADPTLSIV
RKGAELANSFKPDVIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKMIAVTTTSGTGSEVTPFAVVTDDATGQKYPLADYALTPDMAIVDANLVMDMPKS
LCAFGGLDAVTHAMEAYVSVLASEFSDGQALQALKLLKEYLPASYHEGSKNPVARERVHS
AATIAGIAFANAFLGVCHSMAHKLGSQFHIPHGLANALLICNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLGLSAP-GDRTAAKIEKLLAWLETLKAELGIPKSIREA-GVQEA
DFLANVDKLSEDAFDDQCTGANPRYPLISELKQILLDTYYGRDYVEDETAAKKEAAPAKA
EKKAKKSA--------------
>gi|15801467|ref|NP_287484.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Escherichia coli O157:H7 EDL933]
-------------------MAVTNVA----------------------------------
---------------------------------------------------------ELN
ALVERVKKAQREYA-SFTQEQVDKIFRAAALAA--ADARIPLAKMAVAESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGVLSEDDTFGTITIAEPIGIICGIVPTTNPTSTAIFKSLIS
LKTRNAIIFSPHPRAKDATNKAADIVLQAAIAAGAPKDLIGWIDQPSVELSNALMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDETADIKRAVASVLMSKTFDNGVIC
ASEQSVVVVDSVYDAVRERF-ATHGGYLL-QGKELKAVQDVIL-------KNGAL-----
NAAIVGQPAYKIAELAGFS--VPE-NTKILIGE-VTVVDESEPFAHEKLSPTLAMYRAKD
FEDAVEKAEKLVAMGGIGHTSCLYTDQDNQPARVSYFGQKMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALDEVI-TDGHKRALIVTDRFLFNNGYADQITSVLKAAGVETEVFFEVEADPTLSIV
RKGAELANSFKPDVIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKMIAVTTTSGTGSEVTPFAVVTDDATGQKYPLADYALTPDMAIVDANLVMDMPKS
LCAFGGLDAVTHAMEAYVSVLASEFSDGQALQALKLLKEYLPASYHEGSKNPVARERVHS
AXTIAGIAFANAFLGVCHSMAHKLGSQFHIPHGLANALLICNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLGLSAP-GDRTAAKIEKLLAWLETLKAELGIPKSIREA-GVQEA
DFLANVDKLSEDAFDDQCTGANPRYPLISELKQILLDTYYGRDYVEGETAAKKEAAPAKA
EKKAKKSA--------------
>gi|91210463|ref|YP_540449.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Escherichia coli UTI89]
-------------------MAVTNVA----------------------------------
---------------------------------------------------------ELN
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ALVERVKKAQREYA-SFTQEQVDKIFRAAALAA--ADARIPLAKMAVAESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGVLSEDDTFGTITIAEPIGIICGIVPTTNPTSTAIFKSLIS
LKTRNAIIFSPHPRAKDATNKAADIVLQAAIAAGAPKDLIGWIDQPSVELSNALMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDETADIKRAVASVLMSKTFDNGVIC
ASEQSVVVVDSVYDAVRERF-ATHGGYLL-QGKELKAVQDVIL-------KNGAL-----
NAAIVGQPAYKIAELAGFS--VPE-NTKILIGE-VTVVDESEPFAHEKLSPTLAMYRAKD
FEDAVEKAEKLVAMGGIGHTSCLYTDQDNQPARVSYFGQKMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALDEVI-TDGHKRALIVTDRFLFNNGYADQITSVLKAAGVETEVFFEVEADPTLSIV
RKGAELANSFKPDVIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKMIAVTTTSGTGSEVTPFAVVTDDTTGQKYPLADYALTPDMAIVDANLVMDMPKS
LCAFGGLDAVTHAMEAYVSVLASEFSDGQALQALKLLKEYLPASYHEGSKNPVARERVHS
AATIAGIAFANAFLGVCHSMAHKLGSQFHIPHGLANALLICNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLGLSAP-GDRTAAKIEKLLAWLETLKAELGIPKSIREA-GVQEA
DFLANVDKLSEDAFDDQCTGANPRYPLISELKQILLDTYYGRDYVEGETAAKKEAAPAKA
EKKAKKSA--------------
>gi|157155679|ref|YP_001462491.1| bifunctional acetaldehyde-CoA/alcohol
dehydrogenase [Escherichia coli E24377A]
-------------------MAVTNVA----------------------------------
---------------------------------------------------------ELN
ALVERVKKAQREYA-SFTQEQVDKIFRAAALAA--ADARIPLAKMAVAESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGVLSEDDTFGTITIAEPIGIICGIVPTTNPTSTAIFKSLIS
LKTRNAIIFSPHPRAKDATNKAADIVLQAAIAAGAPKDLIGWIDQPSVELSNALMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDETADIKRAVASVLMSKTFDNGVIC
ASEQSVVVVDSVYDAVRERF-ATHGGYLL-QGKELKAVQDVIL-------KNGAL-----
NAAIVGQPAYKIAELAGFS--VPE-NTKILIGE-VTVVDESEPFAHEKLSPTLAMYRAKD
FEDAVEKAEKLVAMGGIGHTSCLYTDQDNQPARVSYFGQKMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALDEVI-TDGHKRALIVTDRFLFNNGYADQITSVLKAAGVETEVFFEVEADPTLSIV
RKGAELANSFKPDVIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKMIAVTTTSGTGSEVTPFAVVTDDATGQKYPLADYALTPDMAIVDANLVMDMPKS
LCAFGGLDAVTHAMEAYVSVLASEFSDGQALQALKLLKEYLPASYHEGSKNPVARERVHS
AATIAGIAFANAFLGVCHSMAHKLGSQFHIPHGLANALLICNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLGLSAP-GDRTAAKIEKLLAWLETLKAELGIPKSIREA-GVQEA
DFLANVDKLSEDAFDDQCTGANPRYPLISELKQILLDTYYGRDYVEGETAAKKEAAPAKA
EKKAKKPLNQ------------
>gi|15830995|ref|NP_309768.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Escherichia coli O157:H7 str. Sakai]
-------------------MAVTNVA----------------------------------
---------------------------------------------------------ELN
ALVERVKKAQREYA-SFTQEQVDKIFRAAALAA--ADARIPLAKMAVAESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGVLSEDDTFGTITIAEPIGIICGIVPTTNPTSTAIFKSLIS
LKTRNAIIFSPHPRAKDATNKAADIVLQAAIAAGAPKDLIGWIDQPSVELSNALMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDETADIKRAVASVLMSKTFDNGVIC
ASEQSVVVVDSVYDAVRERF-ATHGGYLL-QGKELKAVQDVIL-------KNGAL-----
NAAIVGQPAYKIAELAGFS--VPE-NTKILIGE-VTVVDESEPFAHEKLSPTLAMYRAKD
FEDAVEKAEKLVAMGGIGHTSCLYTDQDNQPARVSYFGQKMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALDEVI-TDGHKRALIVTDRFLFNNGYADQITSVLKAAGVETEVFFEVEADPTLSIV
RKGAELANSFKPDVIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKMIAVTTTSGTGSEVTPFAVVTDDATGQKYPLADYALTPDMAIVDANLVMDMPKS
LCAFGGLDAVTHAMEAYVSVLASEFSDGQALQALKLLKEYLPASYHEGSKNPVARERVHS
AATIAGIAFANAFLGVCHSMAHKLGSQFHIPHGLANALLICNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLGLSAP-GDRTAAKIEKLLAWLETLKAELGIPKSIREA-GVQEA
DFLANVDKLSEDAFDDQCTGANPRYPLISELKQILLDTYYGRDYVEGETAAKKEAAPAKA
EKKAKKSA--------------
>gi|24373696|ref|NP_717739.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Shewanella oneidensis MR-1]
-------------------MTVTNAQ----------------------------------
---------------------------------------------------------KLD
LMVERVARAQAEYA-SFSQAQVDAIFRAAALAA--ADARISLAKMAAAETRMGVIEDKVI
KNHFASEYIYNKYKDEKTCGILSEDPTFGTITIAEPVGIICGIVPTTNPTSTAIFKALIS
LKTRNAIIFSPHPRAKVSTTTAAKLVLDAAIAAGAPKDIIGWIDEPSVALSNQLMTHPKV
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NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPIVIDETADIKRAVSSILMSKTFDNGVVC
ASEQAVIVVDSIYEQVKERF-ATHGGYLL-NAAQTEAMQQVIL-------KNGGL-----
NADIVGQSAATIAQMAGIE--VPH-TTKVLIGE-VTDISETEAFAHEKLSPLLGMYRAAD
FNDAVDKAETLVALGGIGHTSGLYTDQDTQTERVKSFGFRMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPSHLINKKTVAKRAENMLWHKLPSSIYFRRGS
LPIALEELS---DKKRALIVTDPFLFNQGYCDETLKILKAQGLETEVFYEVEADPTLATV
RQGAKVANSFKPDVIIALGGGSPMDAAKIIWVMYEHPDVDFADLALRFMDIRKRIYKFPK
MGVKATMVAIPTTSGTGSEVTPFAVVTDEQTGKKYPIADYQLTPNMAIVDPNLVMDMPKS
LTAFGGIDAITHALEAYVSVMANEYSDGQALQALDLLCKYLPDAYQLGAASPIAREKVHN
GATIAGIAFANAFLGICHSMAHKLGAEFHLAHGLANALLISNVIRFNATDLPTKQAAFSQ
YDRPKALCRYAAIADHLALG---GNSDAQKVEKLLEKIEQLKKTLGIPASIQEA-GVNEA
DFLAKLDMLAEDAFDDQCTGANPRYPLISELKQLLLDSYYGRPFTEQ-------------
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>gi|26247570|ref|NP_753610.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Escherichia coli CFT073]
-------------------MAVTNVA----------------------------------
---------------------------------------------------------ELN
ALVERVKKAQREYA-SFTQEQVDKIFRAAALAA--ADARIPLAKMAVAESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGVLSEDDTFGTITIAEPIGIICGIVPTTNPTSTAIFKSLIS
LKTRNAIIFSPHPRAKDATNKAADIVLQAAIAAGAPKDLIGWIDQPSVELSNALMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDETADIKRAVASVLMSKTFDNGVIC
ASEQSVVVVDSVYDAVRERF-ATHGGYLL-QGKELKAVQDVIL-------KNGAL-----
NAAIVGQPAYKIAELAGFS--VPE-NTKILIGE-VIVVDESEPFAHEKLSPTLAMYRAKD
FEDAVEKAEKLVAMGGIGHTSCLYTDQDNQPARVSYFGQKMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALDEVI-TDGHKRALIVTDRFLFNNGYADQITSVLKAAGVETEVFFEVEADPTLSIV
RKGAELANSFKPDVIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKMIAVTTTSGTGSEVTPFAVVTDDTTGQKYPLADYALTPDMAIVDANLVMDMPKS
LCAFGGLDAVTHAMEAYVSVLASEFSDGQALQALKLLKEYLPASYHEGSKNPVARERVHS
AATIAGIAFANAFLGVCHSMAHKLGSQFHIPHGLANALLICNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLGLSAP-GDRTAAKIEKLLAWLETLKAELGIPKSIREA-GVQEA
DFLANVDKLSEDAFDDQCTGANPRYPLISELKQILLDTYYGRDYVEGETAAKKEAAPAKA
EKKAKKSA--------------
>gi|15004739|ref|NP_149199.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Clostridium acetobutylicum ATCC 824]
-------------------MKVTNQK----------------------------------
---------------------------------------------------------ELK
QKLNELREAQKKFA-TYTQEQVDKIFKQCAIAA--AKERINLAKLAVEETGIGLVEDKII
KNHFAAEYIYNKYKNEKTCGIIDHDDSLGITKVAEPIGIVAAIVPTTNPTSTAIFKSLIS
LKTRNAIFFSPHPRAKKSTIAAAKLILDAAVKAGAPKNIIGWIDEPSIELSQDLMSEADI
--ILATGGPSMVKAAYS-SGKPAIGVGAGNTPAIIDESADIDMAVSSIILSKTYDNGVIC
ASEQSILVMNSIYEKVKEEF-VKRGSYIL-NQNEIAKIKETMF-------KNGAI-----
NADIVGKSAYIIAKMAGIE--VPQ-TTKILIGE-VQSVEKSELFSHEKLSPVLAMYKVKD
FDEALKKAQRLIELGGSGHTSSLYIDSQNNKDKVKEFGLAMKTSRTFINMPSSQG--ASG
DLYNFAIAPSFTLGCGTWGGNSVSQNVEPKHLLNIKSVAERRENMLWFKVPQKIYFKYGC
LRFALKELK-DMNKKRAFIVTDKDLFKLGYVNKITKVLDEIDIKYSIFTDIKSDPTIDSV
KKGAKEMLNFEPDTIISIGGGSPMDAAKVMHLLYEYPEAEIENLAINFMDIRKRICNFPK
LGTKAISVAIPTTAGTGSEATPFAVITNDETGMKYPLTSYELTPNMAIIDTELMLNMPRK
LTAATGIDALVHAIEAYVSVMATDYTDELALRAIKMIFKYLPRAYKNGTNDIEAREKMAH
ASNIAGMAFANAFLGVCHSMAHKLGAMHHVPHGIACAVLIEEVIKYNATDCPTKQTAFPQ
YKSPNAKRKYAEIAEYLNLK---GTSDTEKVTALIEAISKLKIDLSIPQNISAA-GINKK
DFYNTLDKMSELAFDDQCTTANPRYPLISELKDIYIKSF---------------------
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>gi|209695322|ref|YP_002263251.1| aldehyde-alcohol dehydrogenase [Aliivibrio
salmonicida LFI1238]
-------------------MPVTNLA----------------------------------
---------------------------------------------------------ELD
ALVARVKAAQKEFA-SFSQEQVDTIFRAASLAA--STARIELAKMAAEESGMGIMEDKVI
KNHFASEFIYNKYKDELTCGIIDRNDEGGTITIAEPLGIVCAIVPTTNPTSTAIFKALIC
LKTRNGCIFSPHPRAKNATNYAAKVVLEAAIKAGAPKDIIGWIDQPSVELSNALMKHEHI
NMILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDETADIKRAVSSILMSKTFDNGVIC
ASEQAAIVVESIYDEVKARF-AKYGAVIL-SKEDANKVRKVLL-------IDGAL-----
NANIVGQPAYKIAELANVK--VPT-STKILIGE-GLEASWDDEFAHEKLSPTLGLFKAKD
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FEDAVRQAGIVLDIGGVGHTSVLYTDQDNNEERIAYFGDKMKTARILVNTPASQG--GIG
DLYNFELAPSLTLGCGSWGGNAISENVGPKHLINKKIVAKRAENMLWHKLPKSIYFRRGC
LPIAMSDLE---GKKRALIVTDRFLFNNGYIDDLRSILKEKGMEVEVFHEVEADPTLAVV
KAGAEACASYQPDVILAVGGGSPMDAAKIMWVMYEHPETDFEDLSMRFMDIRKRIYKFPK
MGQKAELVCITTTSGTGSEVTPFAVVTDEKTGQKYPLADYELTPNMAVVDANLVMDMPKS
LCAFGGYDAVTHALEAYVSVLANEYSDGHALQSLKMLKEYLPSSYANGKKDPIAREKVHN
AATIAGMSFAQSFLGVCHSMAHKLGAEFHIPHGLANALLISNTVRFNATNNPTKQAAFSQ
YDRPKARARYAEIAEHLGYR---DGNTETKVNALLNWLEELKIALDIPLSIQAA-GVNEA
EFMAKVDKLAEDAFDDQCTGANPRYPLIKELKEVLIASYYGTAYADVMDAPEVKEVVKAK
KAKK------------------
>gi|161503136|ref|YP_001570248.1| bifunctional acetaldehyde-CoA/alcohol
dehydrogenase [Salmonella enterica subsp. arizonae serovar 62:z4,z23:--]
-------------------MAVTNVA----------------------------------
---------------------------------------------------------ELN
ALVERVKKAQREYA-SFTQEQVDKIFRAAALAA--ADARIPLAKMAVAESGMGIIEDKVI
KNHFASEYIYNAYKDEKTCGVLSEDDTFGTITIAEPIGIICGIVPTTNPTSTAIFKSLIS
LKTRNAIIFSPHPRAKEATNKAADIVLQAAIAAGAPKDLIGWIDQPSVELSNALMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDETADIKRAVASVLMSKTFDNGVIC
ASEQSVVVVDSVYDAVRERF-ASHGGYML-QGQELKAVQNVIL-------KNGAL-----
NAAIVGQPAYKIAELAGFS--VPE-TTKILIGE-VTVVDESEPFAHEKLSPTLAMYRAKD
FEEAVEKAEKLVAMGGIGHTSCLYTDQDNQQDRVNYFGQKMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALDEVI-TDGHKRALIVTDRFLFNNGYADQITSVLKAAGVETEVFFEVEADPTLSVV
RKGAELANSFKPDVIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKMIAVTTTSGTGSEVTPFAVVTDDATGQKYPLADYALTPDMAIVDANLVMDMPKS
LCAFGGLDAVTHALEAYVSVLASEFSDGQALQALKLLKENLPASYHEGSKNPVARERVHS
AATIAGIAFANAFLGVCHSMAHKLGSQFHIPHGLANALLICNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLGLSAP-GDRTAAKIEKLLAWLESIKAELGIPKSIREA-GVQEA
DFLANVDKLSEDAFDDQCTGANPRYPLISELKQILLDTYYGRDFTEGEVAAKKDVVATPK
AEKKAKKSA-------------
>gi|123442494|ref|YP_001006472.1| bifunctional acetaldehyde-CoA/alcohol
dehydrogenase [Yersinia enterocolitica subsp. enterocolitica 8081]
-------------------MAVTNVA----------------------------------
---------------------------------------------------------ELN
ELVARVKKAQREYA-NFTQEQVDKIFRAAALAA--ADARIPLAKLAVEESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGILEEDKTFGTITIAEPIGLICGIVPTTNPTSTAIFKALIS
LKTRNGIVFSPHPRAKDATNKAADIVLQAAIAAGAPADIIGWIDAPTVELSNQLMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVVDETADIKRVVASILMSKTFDNGVIC
ASEQSIIVVDSVYDAVRERF-ASHGGYLL-QGKELKAVQDIIL-------KNGGL-----
NAAIVGQPATKIAEMAGIK--VPA-NTKILIGE-VKVVDESEPFAHEKLSPTLAMYRAKS
FEDAVEKAEKLVEMGGIGHTSCLYTDQDNQPARVKYFGDKMKTARILINTPASHG--GIG
DLYNFKVAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALEEVA-TDGAKRAFIVTDRYLFNNGYADQITSVLKSHGIETEVFFEVEADPTLSIV
RKGAEQMNSFKPDVIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKMIAVTTTSGTGSEVTPFAVVTDDATGQKYPLADYALTPDMAIVDANLVMNMPKS
LCAFGGLDAVTHALEAYVSVLANEYSDGQALQALKLLKEFLPASYHEGAKNPVARERVHN
AATIAGIAFANAFLGVCHSMAHKLGSEFHIPHGLANAMLISNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLGLSAP-GDRTAQKIQKLLAWLDEIKADLGIPASIREA-GVQEA
DFLAKVDKLSEDAFDDQCTGANPRYPLISELKQILMDTYYGREFSEELDREEVAVATSAP
KAEKKAKK--------------
>gi|110802422|ref|YP_699787.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Clostridium perfringens SM101]
-------------------MKVTNVD----------------------------------
---------------------------------------------------------ELM
LRLEKVRAAQKEFS-KFSQEQVDEIFRQAAVAA--NNERIRLAKMAVEESGMGIVEDKVI
KNHFAAEYIYNKYKNEKTCGVIEKDESFGITKIAEPIGVVAAIVPTTNPTSTAIFKALIS
LKTRNAVFFSPHPRAKNSTIEAARVVLEAAVKAGAPKDIIGWIDEPSVEMSQVLMAEADI
--ILATGGPGMVKAAYS-SGKPAIGVGAGNTPAIIDETAHLKMAVNSILLSKTFDNGVIC
ASEQTVLVVDKVYDEVRKEF-ADRGAYFL-KDKEIDKVRKTIL-------INGNL-----
NANIVGQSAWKIADMAGVK--VPK-DTKVLIGE-VESVELEEPFSHEKLSPVLGMYRVAN
FEEALVKAERLVELGGFGHTSVLYTDTMKSQDRVKKFGATMKTGRTIINMPSTQG--AIG
DIYNFKLAPSLTLGCGSWGGNSVSENVGPKHLINVKSVAERRENMLWFRVPEKVYFKYGA
LGVALRELK-DLNKKKVFIVTDNVLASLGYVDKITNVLEEIGVDFRVFSEVTPDPTLECA
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KKGAEAMRSYQPDTIIALGGGSPMDAAKIMWVMYEHPEVAFEDLAMRFMDIRKRVYPFPT
MGQKAMMISVPTSAGTGSEVTPFAVITDEESGVKYPLADYELTPDMAIIDAELMMNMPKG
LTAASGIDALTHALEAYVSVLASEYTNGLALEAIRLIFKYLPQAYAEGTTNIKAREKMAH
ASTMAGMAFANAFLGVCHSMAHKLGSEHHIAHGVANGILIDHVIRFNAVDNPRKQAAFPQ
YKYPNAKWRYTVIADYLGLG---GKNEEEKVNNLIKAIDNLKKTVGIPATIADC-GVSKE
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>gi|110798574|ref|YP_697219.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Clostridium perfringens ATCC 13124]
-------------------MKVTNVD----------------------------------
---------------------------------------------------------ELM
LRLEKVRAAQKEFS-KFSQEQVDEIFRQAAVAA--NNERIRLAKMAVEESGMGIVEDKVI
KNHFAAEYIYNKYKDEKTCGVIEKDESFGITKIAEPIGVVAAIVPTTNPTSTAIFKALIS
LKTRNAVFFSPHPRAKNSTIEAARVVLEAAVKAGAPKDIIGWIDEPSVEMSQVLMAEADI
--ILATGGPGMVKAAYS-SGKPAIGVGAGNTPAIIDETAHLKMAVNSILLSKTFDNGVIC
ASEQTVLVVDKVYDEVRKEF-ADRGAYFL-KDKEIDKVRKTIL-------INGNL-----
NANIVGQSAWKIADMAGVK--VPK-DTKVLIGE-VESVELEEPFSHEKLSPVLGMYRVAN
FEEALVKAERLVELGGFGHTSVLYTDTMKSQDRVQKFGATMKTGRTIINMPSTQG--AIG
DIYNFKLAPSLTLGCGSWGGNSVSENVGPKHLMNVKSVAERRENMLWFRVPEKVYFKYGA
LGVALRELK-DLNKKKVFIVTDNVLASLGYVDKITSVLEEIGVDFRVFSEVTPDPTLAYA
KKGAEAMRSYQPDAIIALGGGSPMDAAKIMWVMYEHPEVAFEDLAMRFMDIRKRVYPFPT
MGQKAMMISVPTSAGTGSEVTPFAVITDEESGVKYPLADYELTPDMAIIDAELMMNMPKG
LTAASGIDALTHALEAYVSVLASEYTNGLALEAIRLIFKYLPQAYAEGTTNIKAREKMAH
ASTMAGMAFANAFLGVCHSMAHKLGSEHHIAHGVANGILIDHVIRFNAVDNPRKQAAFPQ
YKYPNAKWRYAVIADYLGLG---GKNEEEKVNNLIKAIDNLKKTVGIPATIADC-GVSKE
SFYATLEKMSEDAFDDQCTGANPRYPLISEIKQMYINAFEGKKDRV--------------
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>gi|22125915|ref|NP_669338.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Yersinia pestis KIM]
-------------------MAVTNVA----------------------------------
---------------------------------------------------------ELN
ELVARVKKAQREYA-NFSQEQVDKIFRAAALAA--ADARIPLAKLAVTESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGILCEDKTFGTITIAEPIGLICGIVPTTNPTSTAIFKALIS
LKTRNGIIFSPHPRAKDATNKAADIVLQAAIAAGAPADIIGWIDAPTVELSNQLMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVVDETADIKRVVASILMSKTFDNGVIC
ASEQSIIVVDSVYDAVRERF-ASHGGYLL-QGKELKAVQDIIL-------KNGGL-----
NAAIVGQPATKIAEMAGIK--VPS-NTKILIGE-VKVVDESEPFAHEKLSPTLAMYRAKN
FEEAVEKAEKLVEMGGIGHTSCLYTDQDNQTARVKYFGDKMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALEEVA-TDGAKRAFIVTDRYLFNNGYADQVTSVLKSHGIETEVFFEVEAAPTLSIV
RKGAEQMNSFKPDVIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKLVAITTTSGTGSEVTPFAVVTDDATGQKYPLADYALTPDMAIVDANLVMNMPKS
LCAFGGLDAVTHALEAYVSVLANEYSDGQALQALKLLKEFLPASYNEGAKNPVARERVHN
AATIAGIAFANAFLGVCHSMAHKLGSEFHIPHGLANAMLISNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLGLSAP-GDRTAQKIQKLLAWLDEIKAELGIPASIREA-GVQEA
DFLAKVDKLSEDAFDDQCTGANPRYPLISELKQILMDTYYGREYVEEFDREEEVAAATAP
KAEKKTKK--------------
>gi|37526388|ref|NP_929732.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Photorhabdus luminescens subsp. laumondii TTO1]
-------------------MTVTHVT----------------------------------
---------------------------------------------------------ELN
ELVARVKKAQREFA-NFSQEQVDKIFRAAALAA--ADARIPLAKLAVAESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGILSEDKTFGTITIAEPIGLICGIVPTTNPTSTAIFKALIS
LKTRNGIILSPHPRAKKATTKAAELVLSAAVAAGAPKDIIGWIDEPSVELSNALMHHQDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDESADIKRAVASILMSKTFDNGVIC
ASEQSVIVVDEIYDQVRKRF-FTHGGYLL-QGKELKAVQDIIL-------KNGSL-----
NAEIVGQSATKIAEMAGIN--VPE-KTKILIGE-VSLTDEAEPFAHEKLSPLLAMYRGNS
FEDAVEKAEKLVEMGGIGHTSCLYTDQDNQAARIKYFGDKMKTARILVNTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINTKTVAKRAENMLWHKLPKSIYFRRGS
LPVALEEVA-TDGAKRAFIVTDRFLFNHGYADQVTDVLKSHGIETEVFFEVEADPTLSTV
RKGAEQMHSFKPDIIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYRFPK
MGVKAKMVAITTTSGTGSEVTPFAVVTDDATGQKYPLADYELTPNIAIVDANLVMDMPKS
LCAFGGLDAITHALEAYVSVLANEYSDGQALQALKLLKEFLPTSYHEGATNPVARERVHN
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AATIAGIAFANAFLGVCHSMAHKLGSEFHIPHGLANALLICNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLGLSAT-GDHTVTKIEKLLAWLKELKSELGIPTSIREA-GVQEA
DFLAKIDKLSEDAFDDQCTGANPRYPLISELKQLLLDSYYGREFTETVATEKSQ------
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>gi|18311513|ref|NP_563447.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Clostridium perfringens str. 13]
-------------------MKVTNVD----------------------------------
---------------------------------------------------------ELM
LRLEKVRAAQKEFS-KFSQEQVDEIFRQAAVAA--NNERIRLAKMAVEESGMGIVEDKVI
KNHFAAEYIYNKYKDEKTCGVIEKDESFGITKIAEPIGVVAAIVPTTNPTSTAIFKALIS
LKTRNAVFFSPHPRAKNSTIEAARVVLEAAVKAGAPKDIIGWIDEPSVEMSQVLMAEADI
--ILATGGPGMVKAAYS-SGKPAIGVGAGNTPAIIDETAHLKMAVNSILLSKTFDNGVIC
ASEQTVLVVDKVYDEVRKEF-ADRGAYFL-KDKEIDKVRKTIL-------INGNL-----
NANIVGQSAWKIADMAGVK--VPK-DTKVLIGE-VESVELEEPFSHEKLSPVLGMYRVAN
FEEALVKAERLVELGGFGHTSVLYTDTMKSQDRVQKFGATMKTGRTIINMPSTQG--AIG
DIYNFKLAPSLTLGCGSWGGNSVSENVGPKHLMNVKSVAERRENMLWFRVPEKVYFKYGA
LGVALRELK-DLNKKKVFIVTDNVLASLGYVDKITSVLEEIGVDFRVFSEVTPDPTLACA
KKGAEAMRSYQPDAIIALGGGSPMDAAKIMWVMYEHPEVAFEDLAMRFMDIRKRVYPFPT
MGQKAMMISVPTSAGTGSEVTPFAVITDEESGVKYPLADYELTPDMAIIDAELMMNMPKG
LTAASGIDALTHALEAYVSVLASEYTNGLALEAIRLIFKYLPQAYAEGTTNIKAREKMAH
ASTMAGMAFANAFLGVCHSMAHKLGSEHHIAHGVANGILIDHVIRFNAVDNPRKQAAFPQ
YKYPNAKWRYAVIADYLGLG---GKNEEEKVNNLIKAIDNLKKTVGIPATIADC-GVSKE
SFYATLEKMSEDAFDDQCTGANPRYPLISEIKQMYINAFEGKKDRV--------------
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>gi|45441777|ref|NP_993316.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Yersinia pestis biovar Microtus str. 91001]
-------------------MAVTNVA----------------------------------
---------------------------------------------------------ELN
ELVARVKKAQREYA-NFSQEQVDKIFRAAALAA--ADARIPLAKLAVTESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGILCEDKTFGTITIAEPIGLICGIVPTTNPTSTAIFKALIS
LKTRNGIIFSPHPRAKDATNKAADIVLQAAIAAGAPADIIGWIDAPTVELSNQLMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVVDETADIKRVVASILMSKTFDNGVIC
ASEQSIIVVDSVYDAVRERF-ASHGGYLL-QGKELKAVQDIIL-------KNGGL-----
NAAIVGQPATKIAEMAGIK--VPS-NTKILIGE-VKVVDESEPFAHEKLSPTLAMYRAKN
FEEAVEKAEKLVEMGGIGHTSCLYTDQDNQTARVKYFGDKMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALEEVA-TDGAKRAFIVTDRYLFNNGYADQVTSVLKSHGIETEVFFEVEADPTLSIV
RKGAEQMNSFKPDVIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKLVAITTTSGTGSEVTPFAVVTDDATGQKYPLADYALTPDMAIVDANLVMNMPKS
LCAFGGLDAVTHALEAYVSVLANEYSDGQALQALKLLKEFLPASYNEGAKNPVARERVHN
AATIAGIAFANAFLGVCHSMAHKLGSEFHIPHGLANAMLISNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLGLSAP-GDRTAQKIQKLLAWLDEIKAELGIPASIREA-GVQEA
DFLAKVDKLSEDAFDDQCTGANPRYPLISELKQILMDTYYGREYVEEFDREEEVAAATAP
KAEKKTKK--------------
>gi|218549066|ref|YP_002382857.1| fused acetaldehyde-CoA dehydrogenase ;
iron-dependent alcohol dehydrogenase ; pyruvate-formate lyase deactivase
[Escherichia fergusonii ATCC 35469]
-------------------MAVTNVA----------------------------------
---------------------------------------------------------ELN
ALVERVKKAQREYA-SFTQEQVDKIFRAAALAA--ADARIPLAKMAVAESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGVLSEDDTFGTITIAEPIGIICGIVPTTNPTSTAIFKSLIS
LKTRNAIIFSPHPRAKDATNKAADIVLQAAIAAGAPKDLIGWIDQPSVELSNALMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDETADIKRAVASVLMSKTFDNGVIC
ASEQSVVVVDSVYDAVRERF-ATHGGYIL-QGKELKAVQDVIL-------KNGAL-----
NAAIVGQPAYKIAELAGFT--VPQ-NTKILIGE-VTAVDESEPFAHEKLSPTLAMYRAKD
FEDAVEKAEKLVAMGGIGHTSCLYTDQDNQPARVTYFGQKMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALDEVI-TDGHKRALIVTDRFLFNNGYADQITSVLKAAGVETEVFFEVEADPTLSVV
RKGAELANSFKPDVIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKMIAVTTTSGTGSEVTPFAVVTDDATGQKYPLADYALTPDMAIVDANLVMDMPKS
LCAFGGLDAVTHALEAYVSVLASEFSDGQALQALKLLKENLPASYNEGSKNPVARERVHS
AATIAGIAFANAFLGVCHSMAHKLGSQFHIPHGLANALLICNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLGLSAP-GDRTAAKIEKLLAWLESLKAELGIPKSIREA-GVQEA
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DFLANVDKLSEDAFDDQCTGANPRYPLISELKQILLDTYYGRDFVEGAAVNQEAAPAPKA
EKKAKKSA--------------
>gi|148378348|ref|YP_001252889.1| bifunctional acetaldehyde-CoA/alcohol
dehydrogenase [Clostridium botulinum A str. ATCC 3502]
-------------------MKITTTE----------------------------------
---------------------------------------------------------ELI
RKIEKIKEAQKIYS-TYSQDKVDKIFKAAAIAA--NKERIKLAKMAVEETGMGIVEDKVI
KNHFASEYIYNKYKDEKTCGVIEKDEAFGLTKIAEPIGVIAAIVPTTNPTSTAIFKALIA
LKTRNGIIFSPHPRAKKSTIMAAKIVLDAAVQAGAPKEIIGWIDEPTLELSNAVMSNS--
NLVLATGGPGMVKAAYS-SGKPAIGVGPGNVPAIIHETADIKMAVSSVVLSKTFDNGMIC
ASEQSVIVMNSIYEEVKKEF-VIRGAYVL-NKEEIEKVKKIIL-------VNGNV-----
NAKIVGQTPQKIGEMAGIQ--VPD-WAKLLVGE-VQSVELEEPFSHEKLSPVLAMYKVKT
YEEALTKAERLVELGGFGHTSSLYINTVKCKEEVEKFSNNMKTGRTIINMPSAQG--GIG
DIYNFKLAPSLTLGCGSWGGNSVSENVGPKHLLNIKNVAERRENMLWFRVPEKVYFKYGC
LPIALKELK-RMNKKKAFIVTDKVLYELGVAKKATDVLDEIGINYKVFFDVAPDPTLETA
KKGAKEMVDFNPDTIIAIGGGSAMDAAKIMWVMYEHPEVEFEDLAMRFMDIRKRVYEFPH
MGDKAMMISVATSAGTGSEVTPFAVITDEKTGVKYPLADYELTPDMAIVDADLMLNMPKG
LTAASGIDALTHAVEAYVSVMASEYTDGLCLEAIKTIFEYLPKAYKEGAQDIEAREKMAH
ASTIAGMAFANAFLGVCHSMAHKLGSMHHVPHGIANALLINETIKFNSEDMPRKQTAFPQ
YKYPNAKAKYANIADYLSLG---GKTPEEKVELLIKAIDKLKAEVNIPTSIEEA-GVSKD
KFFKTLDEMSEQAFDDQCTGANPRYPLISEIKEMYTNVFSTKK-----------------
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>gi|153940830|ref|YP_001389712.1| bifunctional acetaldehyde-CoA/alcohol
dehydrogenase [Clostridium botulinum F str. Langeland]
-------------------MKITTTE----------------------------------
---------------------------------------------------------ELI
RKIEKIKEAQKIYS-TYSQDKVDKIFKAAAIAA--NKERIKLAKMAVEETGMGIVEDKVI
KNHFASEYIYNKYKDEKTCGVIEKDEAFGLTKIAEPIGVIAAIVPTTNPTSTAIFKALIA
LKTRNGIIFSPHPRAKKSTIMAAKIVLDAAVQAGAPKEIIGWIDEPTLELSNAVMSNS--
NLVLATGGPGMVKAAYS-SGKPAIGVGPGNVPAIIHETADIKMAVSSVVLSKTFDNGMIC
ASEQSVIVMNSIYEEVKKEF-VIRGAYVL-NKEEIEKVKKIIL-------VNGNV-----
NAKIVGQTPQKIGEMAGIK--VPD-WAKLLVGE-VQSVELEEPFSHEKLSPVLAMYKVKT
YEEALTKAERLVELGGFGHTSSLYINTIKCKEEVEKFSNNMKTGRTIINMPSAQG--GIG
DIYNFKLAPSLTLGCGSWGGNSVSENVGPKHLLNIKNVAERRENMLWFRVPEKVYFKYGC
LPIALKELK-RMNKKKAFIVTDKVLYELGVAKKATDVLDEIGINYKVFFDVAPDPTLETA
KKGAKEMVDFNPDTIIAIGGGSAMDAAKIMWVMYEHPEVEFEDLAMRFMDIRKRVYEFPH
MGDKAMMISVATSAGTGSEVTPFAVITDEKTGVKYPLADYELTPDMAIVDADLMLNMPKG
LTAASGIDALTHAVEAYVSVMASEYTDGLCLEAIKTIFEYLPKAYKEGAQDIEAREKMAH
ASTIAGMAFANAFLGVCHSMAHKLGSMHHVPHGIANALLINETIKFNSEDMPRKQTAFPQ
YKYPNAKAKYANIADYLSLG---GKTPEEKVELLIKAIDKLKAEVNIPTSIEEA-GVSKD
KFFKTLDEMSEQAFDDQCTGANPRYPLISEIKEMYTNVFSTKK-----------------
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>gi|160875070|ref|YP_001554386.1| bifunctional acetaldehyde-CoA/alcohol
dehydrogenase [Shewanella baltica OS195]
-------------------MTVTNAQ----------------------------------
---------------------------------------------------------ELD
LMVERVAKAQAEYA-TFSQAQVDKIFRAAALAA--ADARISLAKMAAAETRMGVVEDKVI
KNHFASEYIYNKYKDEKTCGILSEDVTFGTITIAEPVGIICGIVPTTNPTSTAIFKALIS
LKTRNAIIFSPHPRAKVSTTTAAKLVLDAAIAAGAPKDIIGWIDEPSVALSNQLMTHPRI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPIVIDETADIKRAVSSILMSKTFDNGVVC
ASEQAVIVVDSIYEQVKERF-ISHGGYML-SKNETAAMQQVIL-------KNGGL-----
NADIVGQSAASIAQMAGFE--VPH-WTKVLIGE-VTDICDSEAFAHEKLSPLLGMYRAID
FNDAMDKAEALVALGGIGHTSGLYTDQDTQTERVHAFGFRMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPSHLINKKTVAKRAENMLWHKLPASIYFRRGS
LPIALEELS---DKKRALIITDRFLFNHGYCDETMRILKAQGLETEIFYDVEADPTLAIV
RQGAKVAQSFKPDVIIALGGGSPMDAAKIIWVMYEHPDVDFADLALRFMDIRKRIYKFPK
MGTKAMMVAIPTTSGTGSEVTPFAVVTDEITGKKYPIADYQLTPNMAIVDPNLVMDMPKS
LTAFGGIDAVTHALEAYVSVMANEYSDGQALQALDLLCKYLPDAYNLGSQSPVAREKVHN
GATIAGIAFANAFLGICHSMAHKLGAEFHLAHGLANALLINNVIRFNATDLPTKQAAFSQ
YDRPKALCRYAAIADHLKLG---GKTDEEKVEKLLEKITHLKKTIGIPASIQEA-GVNEA
DFLAKLDELAEDAFDDQCTGANPRYPLINELKQLFLDSYYGRDYSDNN------------
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>gi|62180314|ref|YP_216731.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
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[Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
-------------------MAVTNVA----------------------------------
---------------------------------------------------------ELN
ALVERVKKAQREYA-SFTQEQVDKIFRAAALAA--ADARIPLAKMAVAESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGVLSEDDTFGTITIAEPIGIICGIVPTTNPTSTAIFKSLIS
LKTRNAIIFSPHPRAKEATNKAADIVLQAAIAAGAPKDLIGWIDQPSVELSNALMRHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDETADIKRAVASVLMSKTFDNGVIC
ASEQSVVVVDSVYDAVRERF-ASHGGYML-QGQELKAVQNVIL-------KNGAL-----
NAAIVGQPAYKIAELAGFS--VPE-TTKILIGE-VTVVDESEPFAHEKLSPTLAMYRAKD
FEEAVEKAEKLVAMGGIGHTSCLYTDQDNQPERVAYFGQMMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALDEVI-TDGHKRALIVTDRFLFNNGYADQITSVLKAAGVETEVFFEVEADPTLSVV
RKGAELANSFKPDVIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKMIAVTTTSGTGSEVTPFAVVTDDATGQKYPLADYALTPDMAIVDANLVMDMPKS
LCAFGGLDAVTHALEAYVSVLASEFSDGQALQALKLLKENLPASYHEGSKNPVARERVHS
AATIAGIAFANAFLGVCHSMAHKLGSQFHIPHGLANALLICNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLGLSAP-GDRTAAKIEKLLAWLESIKAELGIPKSIREA-GVQEA
DFLAHVDKLSEDAFDDQCTGANPRYPLISELKQILLDTYYGRDFTEGEVAAKKDVVAAPK
AEKKTKKSA-------------
>gi|16765093|ref|NP_460708.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Salmonella typhimurium LT2]
-------------------MAVTNVA----------------------------------
---------------------------------------------------------ELN
ALVERVKKAQREYA-SFTQEQVDKIFRAAALAA--ADARIPLAKMAVAESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGVLSEDDTFGTITIAEPIGIICGIVPTTNPTSTAIFKSLIS
LKTRNAIIFSPHPRAKEATNKAADIVLQAAIAAGAPKDLIGWIDQPSVELSNALMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDETADIKRAVASVLMSKTFDNGVIC
ASEQSVVVVDSVYDAVRERF-ASHGGYML-QGQELKAVQNVIL-------KNGAL-----
NAAIVGQPAYKIAELAGFS--VPE-TTKILIGE-VTVVDESEPFAHEKLSPTLAMYRAKD
FEEAVEKAEKLVAMGGIGHTSCLYTDQDNQPERVAYFGQMMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALDEVI-TDGHKRALIVTDRFLFNNGYADQITSVLKAAGVETEVFFEVEADPTLSVV
RKGAELANSFKPDVIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKMIAVTTTSGTGSEVTPFAVVTDDATGQKYPLADYALTPDMAIVDANLVMDMPKS
LCAFGGLDAVTHALEAYVSVLASEFSDGQALQALKLLKENLPASYHEGSKNPVARERVHS
AATIAGIAFANAFLGVCHSMAHKLGSQFHIPHGLANALLICNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLGLSAP-GDRTAAKIEKLLAWLESIKAELGIPKSIREA-GVQEA
DFLAHVDKLSEDAFDDQCTGANPRYPLISELKQILLDTYYGRDFTEGEVAAKKDVVAAPK
AEKKAKKSA-------------
>gi|16760134|ref|NP_455751.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Salmonella enterica subsp. enterica serovar Typhi str. CT18]
-------------------MAVTNVA----------------------------------
---------------------------------------------------------ELN
ALVERVKKAQREYA-SFTQEQVDKIFRAAALAA--ADARIPLAKMAVAESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGVLSEDDTFGTITIAEPIGIICGIVPTTNPTSTAIFKSLIS
LKTRNAIIFSPHPRAKEATNKAADIVLQAAIAAGAPKDLIGWIDQPSVELSNALMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDETADIKRAVASVLMSKTFDNGVIC
ASEQSVVVVDSVYDAVRERF-ASHGGYML-QGQELKAVQNVIL-------KNGAL-----
NAAIVGQPAYKIAELAGFS--VPE-TTKILIGE-VTVVDESEPFAHEKLSPTLAMYRAKD
FEEAVEKAEKLVAMGGIGHTSCLYTDQDNQPERVAYFGQMMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALDEVI-TDGHKRALIVTDRFLFNNGYADQITSVLKAAGVETEVFFEVEADPTLSVV
RKGAELANSFKPDVIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKMIAVTTTSGTGSEVTPFAVVTDNATGQKYPLADYALTPDMAIVDANLVMDMPKS
LCAFGGLDAVTHALEAYVSVLASEFSDGQALQALKLLKENLPASYHEGSKNPVARERVHS
AATIAGIAFANAFLGVCHSMAHKLGSQFHIPHGLANALLICNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLGLSAP-GDRTAAKIEKLLAWLESIKAELGIPKSIREA-GVQEA
DFLAHVDKLSEDAFDDQCTGANPRYPLISELKQILLDTYYGRDFTEGEVAAKKDVVAAPK
AEKKAKKSA-------------
>gi|161613759|ref|YP_001587724.1| bifunctional acetaldehyde-CoA/alcohol
dehydrogenase [Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7]
-------------------MAVTNVA----------------------------------
---------------------------------------------------------ELN
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ALVERVKKAQREYA-SFTQEQVDKIFRAAALAA--ADARIPLAKMAVAESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGVLSEDDTFGTITIAEPVGIICGIVPTTNPTSTAIFKSLIS
LKTRNAIIFSPHPRAKEATNKAADIVLQAAIAAGAPKDLIGWIDQPSVELSNALMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDETADIKRAVASVLMSKTFDNGVIC
ASEQSVVVVDSVYDAVRERF-ASHGGYML-QGQELKAVQNVIL-------KNGAL-----
NAAIVGQPAYKIAELAGFS--VPE-TTKILIGE-VTVVDESEPFAHEKLSPTLAMYRAKD
FEEAVEKAEKLVAMGGIGHTSCLYTDQDNQPERVAYFGQMMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALDEVI-TDGHKRALIVTDRFLFNNGYADQITSVLKAAGVETEVFFEVEADPTLSVV
RKGAELANSFKPDVIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKMIAVTTTSGTGSEVTPFAVVTDDATGQKYPLADYALTPDMAIVDANLVMDMPKS
LCAFGGLDAVTHALEAYVSVLASEFSDGQALQALKLLKENLPASYHEGSKNPVARERVHS
AATIAGIAFANAFLGVCHSMAHKLGSQFHIPHGLANALLICNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLGLSAP-GDRTAAKIEKLLAWLESIKAELGIPKSIREA-GVQEA
DFLAHVDKLSEDAFDDQCTGANPRYPLISELKQILLDTYYGRDFTEGEVAAKKDVVAAPK
AEKKAKKSA-------------
>gi|218887410|ref|YP_002436731.1| iron-containing alcohol dehydrogenase
[Desulfovibrio vulgaris str. 'Miyazaki F']
--------MSKKPNAQGAKPATTPDA-----------------ISLNDISPSSIAPNSI-
---------------------------------------------------------TVD
DIVTRVNEAQRAFA-NFTQQQVDAIFHAAAAAA--TAQRIHLARMAVQETGMGILEDKVI
KNHFASEYIYNKYKDDKTCGVIRDDPAYGYREVAAPIGVIAGIIPTTNPTSTTIFKALLA
LKTRNGIIFAPHPRAAKSTVEAARIVHEAAVAAGAPRGIIGWVEAPTPDLTRQLMQHRGV
ALILATGGPGMVHAAYS-SGKPAIGVGAGNTPVVVDASANVKMAVNSIILSKTFDNGMIC
ASEQAVIVEDAAADAVKAEF-AARGCHFA-SPQEAEALAGVVF-------TDGRL-----
NAAIVGRSAAEIAAMAGIT--VPP-TTKILIAE-RDAIDPLDPFAHEKLSPVLGFYRAPD
FAAAVDMAQRLVELGGAGHTSVLYTNEANR-ERIVHFQNVLTTGRTLVNMPSSQG--AIG
DVYNFELAPSLTLGCGSWGDNSVSENIGVKHLMNVKTVAERRENMLWFRVPPKIYFKMGA
LRLALEDMR---DRKRAFIVTDRTMEDLGHVGKVTAVLEKLGIQFRVFSDVKPDPDLSGT
YAALDSIRAFRPDMFIALGGGSPMDAAKIMWLMYEQPDLKFEEISLRFMDIRKRVHAFPA
LGKKAVMVAVPTTSGTGSEVTPFAVITDDATGMKYPIADYELTPDMAIVDPEFVMDMPKT
LTAHSGLDALTHAVEAFTSTYANNFSDGNALEAVRLVFKYLRRAYNDGARDVMAREKMHY
AGTIAGMAFANAFLGVCHSMAHKLGAAFHMPHGLANALLLSHVIEYNATDTPTKQGLMPQ
YRYPFVKGRYARIADMLGLTEGCGDDRDRKVARLVQAIEQLKADLNVPGSLREA-GIAEA
DFLERVDLLAEQAFDDQCTGGNPRYPLIAEIRELYLKAYYGAPLASLASPPPAKAG----
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>gi|188533723|ref|YP_001907520.1| Aldehyde-alcohol dehydrogenase [Erwinia
tasmaniensis Et1/99]
-------------------MTVTNVA----------------------------------
---------------------------------------------------------ELN
ALVERVKQAQRIYA-GFTQEQVDKIFRSAALAA--ADARIPLAKMAVAESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGILESDDTFGTITIAEPVGLICAIVPTTNPTSTAIFKALIA
LKTRNAVIFSPHPRAKDATNQAAKIVLQAAIEAGAPADIIGWIDQPSVELSNQLMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVIDEYADIKRAVASILMSKTFDNGVIC
ASEQSVIVVESIYDAVRERF-ATHGGYVL-QGRELQAVQDVIL-------KNGAL-----
NAAIVGQPAAKIAELAGID--VPE-RTKILIGE-VQRTDESEPFAHEKLSPMLAMYRAKD
FSDALMKAEKLVAMGGIGHTSCLYTDQDNQQDRVHAFGSRMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGA
LPIALEEVA-DEGAKRAFIVTDRFLFNQGYADQIIKVLKARGVETEVFSEVAADPTLSIV
RQGAEKMHSFKPDVIIALGGGSPMDAAKIMWVLYEHPETHFADLALRFMDIRKRIYRFPK
MGIKAKLVAVTTTSGTGSEVTPFAVVTDDATGQKYPLADYALTPDMAIVDANLVMDMPKS
LCAFGGMDAITHALEAYVSVLANEYSDGQALQALKLLKENLPSSYSQGAKNPLARERVHN
AATIAGIAFANAFLGVCHSMAHKLGSEFHLPHGLANALLIGNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLHLSAT-SDRTAQKIEKLLAWLESLKTELGIPASIREA-GVQEA
DFLAKLDKLTEDALDDQCTGANPRFPLISELKQVLLDSFYGRDFYENRVNPPEAATLRVV
AKKGDKNLKGLNQA--------
>gi|170761297|ref|YP_001785682.1| aldehyde-alcohol dehydrogenase [Clostridium
botulinum A3 str. Loch Maree]
-------------------MKITTTE----------------------------------
---------------------------------------------------------ELI
RKIEKIKEAQKIYS-TYSQDKVDKIFKAAAIAA--NKERIKLAKMAVEETGMGIVEDKVI
KNHFASEYIYNKYKDEKTCGVIEKDEAFGLTKIAEPIGVIAAIVPTTNPTSTAIFKALIA
LKTRNGIIFSPHPRAKKSTIMAAKIVLDAAVQAGAPKEIIGWIDEPTLELSNAVMSNS--
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NLVLATGGPGMVKAAYS-SGKPAIGVGPGNVPAIIHETADIKMAVSSVVLSKTFDNGMIC
ASEQSVIVMNSIYEEVKKEF-VIRGAYVL-NKEEIEKVKKIIL-------INGNV-----
NAKIVGQTPQKIGEMAGVQ--VPD-WAKLLVGE-VQSVELEEPFSHEKLSPVLAMYKVKT
YEEASAKAERLVELGGFGHTSSLYINTIKCKEEVEKFSNNMKTGRTIINMPSAQG--GIG
DIYNFKLAPSLTLGCGSWGGNSVSENVGPKHLLNIKNVAERRENMLWFRVPEKVYFKYGC
LPIALKELK-RMNKKKAFIVTDKVLYELGVAKKATDVLDEIGINYKVFFDVAPDPTLETA
KKGAKEMVDFNPDTIIAIGGGSAMDAAKIMWVMYEHPEVEFEDLAMRFMDIRKRVYEFPH
MGDKAMMISVATSAGTGSEVTPFAVITDEKTGVKYPLADYELTPDMAIVDADLMLNMPKG
LTAASGIDALTHAVEAYVSVMASEYTDGLCLEAIKTIFEYLPKAYKEGAQDIEAREKMAH
ASTIAGMAFANAFLGVCHSMAHKLGSMHHVPHGIANALLINETIKFNSEDMPRKQTAFPQ
YKYPNAKAKYANIADYLSLG---GKTPEEKVELLIKAIDKLKAEVNIPTSIEEA-GVSKD
KFFKTLDEMSEQAFDDQCTGANPRYPLISEIKQMYTNVFSTKK-----------------
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>gi|146311950|ref|YP_001177024.1| bifunctional acetaldehyde-CoA/alcohol
dehydrogenase [Enterobacter sp. 638]
-------------------MAVTNIA----------------------------------
---------------------------------------------------------ELN
ALVERVKKAQREYA-NFTQEQVDKIFRAAALAA--ADARIPLAKMAVAESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGVLDEDHTFGTITIAEPIGIICGIVPTTNPTSTAIFKSLIS
LKTRNAIIFSPHPRAKDATNKAADIVLQAAIAAGAPKDLIGWIDQPSVELSNALMHHPDI
NMILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVVDETADIKRVVASILMSKTFDNGVIC
ASEQSVIVVDSAYNAVRERF-ATHGGYML-QGKELKAVQDIIL-------KNGAL-----
NAAIVGQPAAKIAELAGFT--VPS-DTKILIGE-VSVVDESEPFAHEKLSPTLAMYRAKS
FEDAVMKAEKLVEMGGIGHTSCLYTDQDNQPERVKYFGDKMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGS
LPIALDEVI-TDGHKRALIVTDRFLFNNGYADQITSVLKAAGVETEVFFEVEADPTLTVV
RKGAELANSFKPDVIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKMIAVTTTSGTGSEVTPFAVVTDDATGQKYPLADYALTPDMAIVDANLVMDMPKS
LCAFGGLDAVTHALEAYVSVLASEFSDGQALQALKLLKENLPASYNEGSKNPVARERVHN
AATIAGIAFANAFLGVCHSMAHKLGSQFHIPHGLANALLISNVIRYNANDNPTKQTAFSQ
YDRPQARRRYAEIADHLGLSAP-GDRTAAKIEKLLAWLDSIKAELGIPKSIREA-GVQEA
DFLAHVDKLSEDAFDDQCTGANPRYPLISELKQILLDTFYGREFSENDTAAVKIDAPVKA
DKKVKKNA--------------
>gi|15004865|ref|NP_149325.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Clostridium acetobutylicum ATCC 824]
-------------------MKVTTVK----------------------------------
---------------------------------------------------------ELD
EKLKVIKEAQKKFS-CYSQEMVDEIFRNAAMAA--IDARIELAKAAVLETGMGLVEDKVI
KNHFAGEYIYNKYKDEKTCGIIERNEPYGITKIAEPIGVVAAIIPVTNPTSTTIFKSLIS
LKTRNGIFFSPHPRAKKSTILAAKTILDAAVKSGAPENIIGWIDEPSIELTQYLMQKADI
TL--ATGGPSLVKSAYS-SGKPAIGVGPGNTPVIIDESAHIKMAVSSIILSKTYDNGVIC
ASEQSVIVLKSIYNKVKDEF-QERGAYII-KKNELDKVREVIF-------KDGSV-----
NPKIVGQSAYTIAAMAGIK--VPK-TTRILIGE-VTSLGEEEPFAHEKLSPVLAMYEADN
FDDALKKAVTLINLGGLGHTSGIYADEIKARDKIDRFSSAMKTVRTFVNIPTSQG--ASG
DLYNFRIPPSFTLGCGFWGGNSVSENVGPKHLLNIKTVAERRENMLWFRVPHKVYFKFGC
LQFALKDLK-DLKKKRAFIVTDSDPYNLNYVDSIIKILEHLDIDFKVFNKVGREADLKTI
KKATEEMSSFMPDTIIALGGTPEMSSAKLMWVLYEHPEVKFEDLAIKFMDIRKRIYTFPK
LGKKAMLVAITTSAGSGSEVTPFALVTDNNTGNKYMLADYEMTPNMAIVDAELMMKMPKG
LTAYSGIDALVNSIEAYTSVYASEYTNGLALEAIRLIFKYLPEAYKNGRTNEKAREKMAH
ASTMAGMASANAFLGLCHSMAIKLSSEHNIPSGIANALLIEEVIKFNAVDNPVKQAPCPQ
YKYPNTIFRYARIADYIKLG---GNTDEEKVDLLINKIHELKKALNIPTSIKDA-GVLEE
NFYSSLDRISELALDDQCTGANPRFPLTSEIKEMYINCFKKQP-----------------
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>gi|220931059|ref|YP_002507967.1| iron-containing alcohol dehydrogenase
[Halothermothrix orenii H 168]
------------MAKAVLEKSVDKAT-----------------KEKKEIRKGL-------
-----------------------------------------------------KIEDSIN
KLVERANEAARKFK-DYDQEQVDRIVKKMALAA--NDKHIELAKMAHRETGMGVYEDKIT
KNLFASEYVYNYLRDKKTAGILNKNIEENYIEVAEPIGVVAALTPVTNPTSTTIFKALIC
MKTRNPVIFSFHPRAMKCSIEAARILKEAAIKAGAPENCISWIEEPSIEATNYLMKHPEV
DLILATGGSGMVKAAYS-SGKPALGVGPGNVPCYIEKTANIKQAVSDLILSKTFDNGMIC
ASEQAVVVDKEIAAEVKKFM-QENGCYFV-SKKESEKLARVAV-----DQERGAM-----
NPAVVGQPARKIAKMAGIK--VPD-DTKILVAE-LKGVGENYPLSREKLSPILGWYVVKD
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YREGIKRCEEITEFGGLGHSSVLHSNDE---KVIDEFSRRLRTGRLIINSPSSQG--AIG
DMYNF-NVPSLTLGCGSMGKNSTTDNVNVDNLINKKRVAMRKERMKWVKVPPRIYFEYGS
LRY-LSGVR----GERAFIITDKTMSQLGFIDKVEEHLSVAGVQTRVFDSVEPDPSVETV
LNGCQEMNEFKPDIIIALGGGSPMDAAKGMWLFYEHPETRFEDLKMKFNDIRKRVYKFPR
LGKKATFIAVPTTSGTGSEVTAFSVITDKKRNIKYPLADYELTPDIAIIDPELVLTVPQS
VTADTGLDVLTHAIEAYVSVMASDYTDALAEKAIKLVFEYLPRAYKNG-NDREARKKMHN
ASCIAGMAFTNAFLGLNHSMAHILGGKFHIPHGRANAILLPHVIRYNA-GKPSKLASFPQ
YDYPRAGERYAEIARILGLP---ASTTEEGVESLVKAITDLMRELNIPLSLEEA-GVNHN
KFEKELEDMADIAHNDQCTGTNPRMPLVNEIKEIYRQAYKGVSIKDKKKVRNA-------
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>gi|217973538|ref|YP_002358289.1| iron-containing alcohol dehydrogenase [Shewanella
baltica OS223]
-------------------MTVTNAQ----------------------------------
---------------------------------------------------------ELD
LMVERVAKAQAEYA-TFSQAQVDNIFRAAALAA--ADARISLAKMAAVETRMGVVEDKVI
KNHFASEYIYNKYKDEKTCGILSEDVTFGTITIAEPVGIICGIVPTTNPTSTAIFKALIS
LKTRNAIIFSPHPRAKVSTTTAAKLVLDAAIAAGAPKDIIGWIDEPSVALSNQLMTHPKV
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPIVIDETADIKRAVSSILMSKTFDNGVVC
ASEQAVIVVDSIYEQVKERF-ISHGGYML-SKDETAAMQNVIL-------KNGGL-----
NADIVGQSAASIAQMAGFE--VPH-WTKVLIGE-VTDICDSEAFAHEKLSPLLGMYRAID
FNDAMDKAEALVALGGIGHTSGLYTDQDTQTERVHAFGFRMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPSHLINKKTVAKRAENMLWHKLPASIYFRRGS
LPIALEELS---DKKRALIITDRFLFNHGYCDETMRILKAQGLETEIFYDVEADPTLAIV
RQGAKVAQSFKPDVIIALGGGSPMDAAKIIWVMYEHPDVDFADLALRFMDIRKRIYKFPK
MGTKAMMVAIPTTSGTGSEVTPFAVVTDEITGKKYPIADYQLTPNMAIVDPNLVMDMPKS
LTAFGGIDAVTHALEAYVSVMANEYSDGQALQALDLLCKYLPDAYNLGSQSPVAREKVHN
GATIAGIAFANAFLGICHSMAHKLGAEFHLAHGLANALLINNVIRFNATDLPTKQAAFSQ
YDRPKALCRYAAIADHLKLG---GKTDEEKVEKLLEKITHLKTTIGIPASIQEA-GVNEA
DFLAKLDELAEDAFDDQCTGANPRYPLINELKQLFLDSYYGRDYSDNN------------
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>gi|153000473|ref|YP_001366154.1| bifunctional acetaldehyde-CoA/alcohol
dehydrogenase [Shewanella baltica OS185]
-------------------MTVTNAQ----------------------------------
---------------------------------------------------------ELD
LMVERVAKAQAEYA-TFSQAQVDKIFRAAALAA--ADARISLAKMAAAETRMGVVEDKVI
KNHFASEYIYNKYKDEKTCGILSEDVTFGTITIAEPVGIICGIVPTTNPTSTAIFKALIS
LKTRNAIIFSPHPRAKVSTTTAAKLVLDAAIAAGAPKDIIGWIDEPSVALSNQLMTHPKV
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPIVIDETADIKRAVSSILMSKTFDNGVVC
ASEQAVIVVDSIYEQVKERF-ISHGGYML-SKDETAAMQHVIL-------KNGGL-----
NADIVGQSAASIAQMAGFE--VPH-WTKVLIGE-VTDICDSEAFAHEKLSPLLGMYRAID
FNDAMDKAEALVALGGIGHTSGLYTDQDTQTERVHAFGFRMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPSHLINKKTVAKRAENMLWHKLPASIYFRRGS
LPIALEELS---DKKRALIITDRFLFNHGYCDETMRILKAQGLETEIFYDVEADPTLAIV
RQGAKVAQSFKPDVIIALGGGSPMDAAKIIWVMYEHPDVDFADLALRFMDIRKRIYKFPK
MGTKAMMVAIPTTSGTGSEVTPFAVVTDEITGKKYPIADYQLTPNMAIVDPNLVMDMPKS
LTAFGGIDAVTHALEAYVSVMANEYSDGQALQALDLLCKYLPDAYNLGSQSPVAREKVHN
GATIAGIAFANAFLGICHSMAHKLGAEFHLAHGLANALLINNVIRFNATDLPTKQAAFSQ
YDRPKALCRYAAIADHLKLG---GKTDEEKVEKLLEKITHLKKTIGIPASIQEA-GVNEA
DFLAKLDELAEDAFDDQCTGANPRYPLINELKQLFLDSYYGRDYSDNN------------
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>gi|34496592|ref|NP_900807.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Chromobacterium violaceum ATCC 12472]
-------------------MAVSNQI----------------------------------
---------------------------------------------------------ELD
ALVARVKKAQTAFA-QFTQEQVDHIFRCAALAA--ADARIPLARMAVAETGMGVMEDKVI
KNHFASEYIYNKYKDEKTCGVLSEDDTFGTITIAEPIGVLCGIVPTTNPTSTAIFKALIS
LKTRNGIIFSPHPRARRSTCEAARLVLEAAVAAGAPQDIIGWIDEPSVALSNQLMHHPDV
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPAVIDETADIKRAVASILMSKTFDNGVVC
ASEQSVIIVDEIYDAVRERF-SKHGGYIL-KGSEAEAVRKVIL-------QDGSL-----
NAAIVGQSAAKIAAMAGIE--VPP-TTKVLIGE-VTEVSEKEAFAHEKLSPTLAMYRAKD
FLDACDKAAALVTMGGIGHTSALYTDQDLQEERVRYFGDKMKTARILINTPSSQG--GIG
DLYNFSLAPSLTLGCGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGC
LPVALEDLA---GKKRCLIVTGQYLFENGFVDEPIRLLKKMGLEVETFFEVPADPTLAVV
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RKGAELAHAFKPDVIMAIGGGSPMDAAKIMWVMYEHPEVHFADLALRFMDIRKRIYQFPK
LGQKAMMVAVPTTSGTGSEVTPFAVVTDEVTGVKYPIADYELTPNMAIVDANLVMSMPKS
LTAFGGIDAVTHALEAYVSVMANEYSDPQALQALKLLKEYLPSSYLNGANDPKAREQVHN
AATIAGVAFANAFLGVCHSMAHKIGAEFGLAHGLANALLISNVIRYNAADVPTKQTAFSQ
YDRPKSVARYAEIARHLGLE---ASRDHQRVEKLIEWVDELKKTLGIPASIQAA-GVAES
DFLAKVDEVAEAAFDDQCTGANPRYPLISELKQLLLDSFYGRPYKEAWERDEAAVEDKPA
KGKSKAKA--------------
>gi|85059350|ref|YP_455052.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Sodalis glossinidius str. 'morsitans']
-------------------MAVTNVA----------------------------------
---------------------------------------------------------ELN
TLVAQVRKAQREYA-NFTQEQVDKIFRAAALAA--ADARIPLAKMAVAESGMGIVEDKVI
KNHFASEYIYNAYKDEKTCGILAEDDTFGTISIAEPIGLICGIVPTTNPTSTAIFKALIS
LKTRNGIIFSPHPRAKNATNKAADIVLQAAIAAGAPRDIIGWIDEPSVELSNQLMHHPDI
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPVVVDETADIKRVVASILMSKTFDNGVIC
ASEQSVVVVDALYDQVRERF-ASHGGCML-RGQELKAVSDIIL-------KNGGL-----
NAAIVGQPAAKIAEMAGLL--VPG-NTKVLIGE-VSKVDESEPFAHEKLSPTLAMYRARD
FEDAVDIAEKLVAMGGIGHTSCLYTNQDNQGERVKFFGDKMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPKHLINTKTVAKRAENMMWHKLPKSIYFRRGS
LPIALEEVA-SDGAKRAFIVTDRYLFNNRYADQITSVLKKHGIETEVFFEVEADPTLSIV
RKGAMQMNSFKPDTIIALGGGSPMDAAKIMWVMYEHPETHFEELALRFMDIRKRIYKFPK
MGVKAKMIAITTTSGTGSEVTPFAVVTDDATGQKYPLADYALVPDMAIVDANLVMNMPKS
LCAFGGLDAVTHALEAYVSIMATEFSDGQALQALKLLKEYLPASYHDGTKNPVARERVHN
AATIAGIAFANAFLGVCHSMAHKLGSEFHIPHGLANAMLVSNVIRYNANDNPTKQAAFSQ
YDRPQARRRYAEIADHLGLSAA-GDRTAQKIEKLLQWLDEIKLELGIPTSIRKA-GVQEA
DFLAKVDKLSEDAFDDQCTSANPRYPLIAELKQILLDTYYGRKFVEPFDNAVEAATAPAP
VGDVKASVQAPKSEKKAEKVTS
>gi|126174148|ref|YP_001050297.1| bifunctional acetaldehyde-CoA/alcohol
dehydrogenase [Shewanella baltica OS155]
-------------------MTVTNAQ----------------------------------
---------------------------------------------------------ELD
LMVERVAKAQAEYA-TFSQAQVDKIFRAAALAA--ADARISLAKMAAAETRMGVVEDKVI
KNHFASEYIYNKYKDEKTCGILSEDVTFGTITIAEPVGIICGIVPTTNPTSTAIFKALIS
LKTRNAIIFSPHPRAKVSTTTAAKLVLDAAIAAGAPKDIIGWIDEPSVALSNQLMTHPKV
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPIVIDETADIKRAVSSILMSKTFDNGVVC
ASEQAVIVVDSIYEQVKERF-ISHGGYML-SKDETAAMQHVIL-------KNGGL-----
NADIVGQSAASIAQMAGFE--VPH-WTKVLIGE-VTDICDSEAFAHEKLSPLLGMYRAID
FNDAMDKAEALVALGGIGHTSGLYTDQDTQTERVHAFGFRMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPSHLINKKTVAKRAENMLWHKLPASIYFRRGS
LPIALEELS---DKKRALIITDRFLFNHGYCDETMRILKAQGLETEIFYDVEADPTLAIV
RQGAKVAQSFKPDVIIALGGGSPMDAAKIIWVMYEHPDVDFADLALRFMDIRKRIYKFPK
MGTKAMMVAIPTTSGTGSEVTPFAVVTDEITGKKYPIADYQLTPNMAIVDPNLVMDMPKS
LTAFGGIDAVTHALEAYVSVMANEYSDGQALQALDLLCKYLPDAYNLGSQSPVAREKVHN
GATIAGIAFANAFLGICHSMAHKLGAEFHLAHGLANALLINNVIRFNATDLPTKQAAFSQ
YDRPKALCRYAAIADHLKLG---GKTDEEKVEKLLEKITHLKKTIGIPASIQEA-GVNEA
DFLAKLDELAEDAFDDQCTGANPRYLLINELKQLFLDSYYGRDYSDNN------------
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>gi|220930559|ref|YP_002507468.1| iron-containing alcohol dehydrogenase [Clostridium
cellulolyticum H10]
--------------MTKKNMVVNSVD----------------------------------
---------------------------------------------------------TLL
VKLAEIRKAQKEYS-TFTQEQVDKIFLAASLAA--NKKRIPLSKMAQAETGMGVIEDKVI
KNHYAAEYIYNAYKDTQTCGVIERDEAFGITKIAEPLGVVAAIVPTTNPTSTAIFKALIA
LKTRNGIIFSPHPRAKKCTIEAANVILEAAVAAGAPKGIIGWIDEPSIELSERVMKEADI
--ILATGGPGMVKAAYS-SGKPAIGVGPGNVPAIIDESADIKTAVSSIIVSKTFDNGMIC
ASEQSVIVLDKIYNEVRKEF-ILRGAYML-NKEETQKVREVIL-------VNGAL-----
NAKIVGQTASTIAKLAGFE--VPA-ETKVLVGE-VESVELSEAFAHEKLSPVLAMYKAKT
FDDAVSKAERLIADGGFGHTASLYIDTVNSKDKLDKFTAAMKTCRILINTPSAQG--GIG
DLYNFKLAPSLTLGCGSWGGNSVSENVGVKHLINIKTVAERRENMLWFRAPEKVYFKKGC
LGVALRELKTEMNKQRAFIVTDSFLYNNGYTKAVTNLLDDMNIKHHTFFDVAPDPTLACA
KLGAEAMRDFKPDVIIAIGGGSAMDAGKIMWTLYEHPEVDFQDLAMRFMDIRKRVYTFPK
IGEKAYFVAIPTSAGTGSEVTPFAVITDEQSGVKYPLADYELMPKMAIVDADLMMNMPKG
LTAASGIDALTHAVEAYASMLLTDYTKGLALQATKNIFEYLPSAYENGAKDPIAREKMAD
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ASTMAGMAFANSFLGICHSMAHKLGAFHHLPHGVANALLITEVMKFNIAEAPTKMGAFSQ
YKYPEILKRYAEVASFIGIT---GSTDEEKFKKLIAKIDELKAKVGLPKTIKEA-GVDEE
KFLATLDEMVEQAFDDQCTGANPRYPLLSEIKDMYLKVYYGK------------------
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>gi|114563069|ref|YP_750582.1| bifunctional acetaldehyde-CoA/alcohol dehydrogenase
[Shewanella frigidimarina NCIMB 400]
-------------------MTVTNTQ----------------------------------
---------------------------------------------------------ELD
LLVERVAKAQAEFA-NFSQEKVDTIFRAAALAA--ADARISLAKMAVTETGMGVLEDKVI
KNHFASEYIYNKYKDEKTCGILSEDLTFGTITIAEPVGIICGIVPTTNPTSTAIFKALIS
LKTRNGIIFSPHPRAKNSTTTAARIVLDAAVAAGAPKDIIGWIDQPSVALSNQLMTHAKV
NLILATGGPGMVKAAYS-SGKPAIGVGAGNTPIVIDETADIKRAVSSILMSKTFDNGVVC
ASEQAVIVVDSIYKQVKERF-ISHGGHIL-SKAETAAMQSVIL-------KNGGL-----
NADIVGQSAVSIAAMAGFE--VPS-TTKVLIGE-VTDINDAEAFAHEKLSPLLGMYKAKD
FNEAMDKAEALVTLGGIGHTSGLYTDQDTQDERVKAFGFRMKTARILINTPASQG--GIG
DLYNFKLAPSLTLGCGSWGGNSISENVGPSHLINKKMVAKRAENMLWHKLPSSIYFRRGS
LPIALEELS---DKKRALIITDKFLFNNGYCNETLKILKAQGLETEVFYEVEADPTLAIV
RQGAKVAQSFQPDVIIALGGGSPMDAAKIIWVMYEHPEVDFADLALRFMDIRKRIYKFPK
MGVKAQMVAIPTTSGTGSEVTPFAVVTDEVTGKKYPIADYQLTPNMAIVDPNLVMDMPKS
LTAFGGIDAVTHALEAYVSVMANEYSDGQALQALDLLFKYLPDSYEFGAKAPVAREKVHN
GATIAGIAFANAFLGVCHSMAHKLGAEFHLAHGLANALLISNVIRFNATDMPTKQAAFSQ
YDRPKALCRYAAIADYLKLG---GKTDAQKVEKLIEKIEQLKTTIGIPASIQDA-GVNEA
DFIAKLDELAEDAFDDQCTGANPRYPLIKELKQVLLDSFYGRAYKD--------------
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%%  EutB [targeting tail not implicated]

>gi++|16765778|ref|NP_461393.1| ethanolamine ammonia-lyase heavy chain [Salmonella
typhimurium LT2]
------------------------------------------------MKLKTTLFGNVY
QF------------------------------------KDVKEVLAKANELRSGD-----
VLAGVAAASSQERVAAKQVLSEMTVADIRNN-------PVIAYEEDCVTRLIQDDVNETA
YNRIKNWSISELREYVLSDET---SVDDIAFTRKGLTSEVVAAVAKICSNADLIYGGKKM
PVIKKANTTIGIPGTFSCRLQPNDTRDDVQSIAAQIYEGLSFGAGDAVIGVNPVTDDVEN
LTRVLDTVYGVIDKFNIP--TQGCVLAHVTTQIEAIRRG-APGGLIFQSICGSEKGLKEF
GVELAMLDEARAVGAEFNRIA----------GENCLYFETGQGSALSAGANFG-----AD
QVTMEARNYGLARHYDPFL--------------VNTVVGFIGPEYLYNDRQIIRAGLEDH
FMGKLSGISMGCDCCYTNHADADQNLNENLMILLATAGCNYIMGMPLGDDIMLNYQTTAF
HDTATVRQLLNLRPSPEFERWLETMGIMA--NGRLTKRAGDPSL--FF------------
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
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>gi++|198245031|ref|YP_002216528.1| ethanolamine ammonia-lyase, large subunit
[Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853]
------------------------------------------------MKLKTTLFGNVY
QF------------------------------------KDVKEVLAKANELRSGD-----
VLAGVAAASSQERVAAKQVLSEMTVADIRNN-------PVIAYEEDCVTRLIQDDVNETA
YNRIKNWSISELREYVLSDET---SVDDIAFIRKGLTSEVVAAVAKICSNADLIYGGKKM
PVIKKANTTIGIPGTFSCRLQPNDTRDDVQSIAAQIYEGLSFGAGDAVIGVNPVTDDVEN
LTRVLDTVYGVIDKFNIP--TQGCVLAHVTTQIEAIRRG-APGGLIFQSICGSEKGLKEF
GVELAMLDEARAVGAEFNRIA----------GENCLYFETGQGSALSAGANFG-----AD
QVTMEARNYGLARHYDPFL--------------VNTVVGFIGPEYLYNDRQIIRAGLEDH
FMGKLSGISMGCDCCYTNHADADQNLNENLMILLATAGCNYIMGMPLGDDIMLNYQTTAF
HDTATVRQLLNLRPSPEFERWLETMGIMA--NGRLTKRAGDPSL--FF------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
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>gi++|16761376|ref|NP_456993.1| ethanolamine ammonia-lyase heavy chain [Salmonella
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enterica subsp. enterica serovar Typhi str. CT18]
------------------------------------------------MKLKTTLFGNVY
QF------------------------------------KDVKEVLAKANELRSGD-----
VLAGVAAASSQERVAAKQVLSEMTVADIRNN-------PVIAYEEDCVTRLIQDDVNETA
YNRIKNWSISELREYVLSDET---SVDDIAFTRKGLTSEVVAAVAKICSNADLIYGGKKM
PVIKKANTTIGIPGTFSCRLQPNDTRDDVQSIAAQIYEGLSFGAGDAVIGVNPVTDDVEN
LTRVLDTVYGVIDKFNIP--TQGCVLAHVTTQIEAIRRG-APGGLIFQSICGSEKGLKEF
GVELAMLDEARAVGAEFNRIA----------GENCLYFETGQGSALSAGANFG-----AD
QVTMEARNYGLARYYDPFL--------------VNTVVGFIGPEYLYNDRQIIRAGLEDH
FMGKLSGISMGCDCCYTNHADADQNLNENLMILLATAGCNYIMGMPLGDDIMLNYQTTAF
HDTATVRQLLNLRPSPEFERWLETMGIMA--NGRLTKRAGDPSL--FF------------
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>gi++|161502392|ref|YP_001569504.1| hypothetical protein SARI_00426 [Salmonella
enterica subsp. arizonae serovar 62:z4,z23:--]
------------------------------------------------MKLKTTLFGNVY
QF------------------------------------KDVKEVLAKANELRSGD-----
VLAGVAAASSQERVAAKQVLSEMTVADIRNN-------PVIAYEEDCVTRLIQDDVNETA
YNRIKNWSISELREYVLSDET---SVDDIAFTRKGLSSEVVAAVAKICSNADLIYGGKKM
PVIKKANTTIGIPGTFSCRLQPNDTRDDVQSIAAQIYEGLSFGSGDAVIGVNPVTDDVEN
LTRVLDTVYGVIDKFNIP--TQGCVLAHVTTQIEAIRRG-APGGLIFQSICGSEKGLKEF
GVELAMLDEARAVGAEFNRIA----------GENCLYFETGQGSALSAGANFG-----AD
QVTMEARNYGLARHYDPFL--------------VNTVVGFIGPEYLYNDRQIIRAGLEDH
FMGKLSGISMGCDCCYTNHADADQNLNENLMILLATAGCNYIMGMPLGDDIMLNYQTTAF
HDTATVRQLLNLRPSPEFERWLETMGIMA--NGRLTKRAGDPSL--FF------------
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>gi++|205353563|ref|YP_002227364.1| ethanolamine ammonia-lyase heavy chain
[Salmonella enterica subsp. enterica serovar Gallinarum str. 287/91]
------------------------------------------------MKLKTTLFGNVY
QF------------------------------------KDVKEVLAKANELRSGD-----
VLAGVAAASSQERVAAKQVLSEMTVADIRNN-------PVIAYEEDCVTRLIQDDVNETA
YNRIKNWSISELREYVLSDET---SVDDIAFTRKGLTSEVVAAVAKICSNADLIYGGKKM
PVIKKANTTIGIPGTFSCRLQPNDTRDDVQSIAAQIYEGLSFGAGDAVIGVNPVTDDVEN
LTRVLDTVYGVIDKFNIP--TQGCVLAHVTTQIEAIRRG-APGGLIFQSICGSEKGLKEF
GVELAMLDEARAVGAEFNRIA----------GENCLYFETGQGSALSAGANFG-----AD
QVTMEARNYGLARHYDPFL--------------VNTVVGFIGPEYLYNDRQIIRAGLEDH
FMGKLSGISMGGDCCYTNHADADQNLNENLMILLATAGCNYIMGMPLGDDIMLNYQTTAF
HDTATVRQLLNLRPSPEFERWLETMGIMA--NGRLTKRAGDPSL--FF------------
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>gi++|15802972|ref|NP_289002.1| ethanolamine ammonia-lyase, heavy chain [Escherichia
coli O157:H7 EDL933]
------------------------------------------------MKLKTTLFGNVY
QF------------------------------------KDVKEVLAKANELRSGD-----
VLAGVAAASSQERVAAKQVLSEMTVADIRNN-------PVIAYEDDCVTRLIQDDVNETA
YNQIKNWSISELREYVLSDET---SVDDIAFTRKGLTSEVVAAVAKICSNADLIYGAKKM
PVIKKANTTIGIPGTFSARLQPNDTRDDVQSIAAQIYEGLSFGVGDAVIGVNPVTDDVEN
LSRVLDTIYGVIDKFNIP--TQGCVLAHVTTQIEAIRRG-APGGLIFQSICGSEKGLKEF
GVELAMLDEARAVGAEFNRIA----------GENCLYFETGQGSALSAGANFG-----AD
QVTMEARNYGLARHYDPFI--------------VNTVVGFIGPEYLYNDRQIIRAGLEDH
FMGKLSGISMGCDCCYTNHADADQNLNENLMILLATAGCNYIMGMPLGDDIMLNYQTTAF
HDTATVRQLLNLRPSPEFERWLESMGIMA--NGRLTKRAGDPSL--FF------------
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>gi++|26248817|ref|NP_754857.1| ethanolamine ammonia-lyase heavy chain [Escherichia
coli CFT073]
------------------------------------------------MKLKTTLFGNVY
QF------------------------------------KDVKEVLAKANELRSGD-----
VLAGVAAASSQERVAAKQVLSEMTVADIRNN-------PVIAYEDDCVTRLIQDDVNETA
YNQIKNWSISELREYVLSDEI---SVDDIAFTRKGLTSEVVAAVAKICSNADLIYGAKKM
PVIKKANTTIGIPGTFSARLQPNDTRDDVQSIAAQIYEGLSFGVGDAVIGVNPVTDDVEN
LSRVLDTIYGVIDKFNIP--TQGCVLAHVTTQIEAIRRG-APGGLIFQSICGSEKGLKEF
GVELAMLDEARAVGAEFNRIA----------GENCLYFETGQGSALSAGANFG-----AD
QVTMEARNYGLARHYDPFI--------------VNTVVGFIGPEYLYNDRQIIRAGLEDH
FMGKLSGISMGCDCCYTNHADADQNLNENLMILLATAGCNYIMGMPLGDDIMLNYQTTAF
HDTATVRQLLNLRPSPEFERWLESMGIMA--NGRLTKRAGDPSL--FF------------
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>gi++|218696076|ref|YP_002403743.1| ethanolamine ammonia-lyase, large subunit, heavy
chain [Escherichia coli 55989]
------------------------------------------------MKLKTTLFGNVY
QF------------------------------------KDVKEVLAKANELCSGD-----
VLAGVAAASSQERVAAKQVLSEMTVADIRNN-------PVIAYEDDCVTRLIQDDVNETA
YNQIKNWSISELREYVLSDET---SVDDIAFTRKGLTSEVVAAVAKICSNADLIYGAKKM
PVIKKANTTIGIPGTFSARLQPNDTRDDVQSIAAQIYEGLSFGVGDAVIGVNPVTDDVEN
LSRVLDTIYGVIDKFNIP--TQGCVLAHVTTQIEAIRRG-APGGLIFQSICGSEKGLKEF
GVELAMLDEARAVGAEFNRIA----------GENCLYFETGQGSALSAGANFG-----AD
QVTMEARNYGLARHYDPFI--------------VNTVVGFIGPEYLYNDRQIIRAGLEDH
FMGKLSGISMGCDCCYTNHADADQNLNENLMILLATAGCNYIMGMPLGDDIMLNYQTTAF
HDTATVRQLLNLRPSPEFERWLESMGIMA--NGRLTKRAGDPSL--FF------------
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>gi++|91211779|ref|YP_541765.1| regulatory subunit of ethanolamine ammonia-lyase
[Escherichia coli UTI89]
------------------------------------------------MKLKTTLFGNVY
QF------------------------------------KDVKEVLAKANELRSGD-----
VLAGVAAASSQERVAAKQVLSEMTVADIRNN-------PVIAYEDDCVTRLIQDDVNETA
YNQIKNWSISELREYVLSDET---SVDDIAFTRKGLTSEVVAAVAKICSNADLIYGAKKM
PVIKKANTTIGIPGTFSARLQPNDTRDDVQSIAAQIYEGLSFGVGDAVIGVNPVTDDVEN
LSRVLDTIYGVIDKFNIP--TQGCVLAHVTTQIEAIRRG-APGGLIFQSICGSEKGLKEF
GVELAMLAEARAVGAEFNRIA----------GENCLYFETGQGSALSAGANFG-----AD
QVTMEARNYGLARHYDPFI--------------VNTVVGFIGPEYLYNDRQIIRAGLEDH
FMGKLSGISMGCDCCYTNHADADQNLNENLMILLATAGCNYIMGMPLGDDIMLNYQTTAF
HDTATVRQLLNLRPSPEFERWLESMGIMA--NGRLTKRAGDPSL--FF------------
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>gi++|209919922|ref|YP_002294006.1| ethanolamine ammonia-lyase heavy chain
[Escherichia coli SE11]
------------------------------------------------MKLKTTLFGNVY
QF------------------------------------KDVKEVLAKANELRSGD-----
VLAGVAAASSQERVAAKQVLSEMTVADIRNN-------PVIAYEDDCVTRLIQDDVNETA
YNQIKNWSISELREYVLSDET---SVDDIAFTRKGLTSEVVAAVAKICSNADLIYGAKKM
PVIKKANTTIGIPGTFSARLQPNDTRDDVQSIAAQIYEGLSFGVGDAVIGVNPVTDDVEN
LSRVLDTIYGVIDKFNIP--TQGCVLAHVTTQIEAIRRG-APGGLIFQSICGSEKGLKEF
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GVELAMLDEARAVCAEFNRIA----------GENCLYFETGQGSALSAGANFG-----AD
QVTMEARNYGLARHYDPFI--------------VNTVVGFIGPEYLYNDRQIIRAGLEDH
FMGKLSGISMGCDCCYTNHADADQNLNENLMILLATAGCNYIMGMPLGDDIMLNYQTTAF
HDTATVRQLLNLRPSPEFERWLENMGIMA--NGRLTKRAGDPSL--FF------------
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>gi++|218690576|ref|YP_002398788.1| ethanolamine ammonia-lyase, large subunit, heavy
chain [Escherichia coli ED1a]
------------------------------------------------MKLKTTLFGNVY
QF------------------------------------KDVKEVLAKANELRSGD-----
VLAGVAAASSQERVAAKQVLSEMTVADIRNN-------PVIAYEDDCVTRLIQDDVNETA
YNQIKNWSISELREYVLSDEI---SVDDIAFTRKGLTSEVVAAVAKICSNADLIYGAKKM
PVIKKANTTIGIPGTFSARLQPNDTRDDVQSIAAQIYEGLSFGVGDAVIGVNPVTDDVEN
LSRVLDTIYGVIDKFNIP--TQGCVLAHVTTQIEAIRRG-APGGLIFQSICGSEKGLKEF
GVELAMLDEARAVGAEFNRIA----------GENCLYFETGQGSALSAGANFG-----AD
QVTMEARNYGLARHYDPFI--------------VNTVVGFIGPEYLYNDRQIICAGLEDH
FMGKLSGISMGCDCCYTNHADADQNLNENLMILLATAGCNYIMGMPLGDDIMLNYQTTAF
HDTATVRQLLNLRPSPEFERWLESMGIMA--NGRLTKRAGDPSL--FF------------
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>gi++|152971315|ref|YP_001336424.1| ethanolamine ammonia-lyase, heavy chain
[Klebsiella pneumoniae subsp. pneumoniae MGH 78578]
------------------------------------------------MKLKTTLFGNVY
QF------------------------------------KDVKEVLAKANELRSGD-----
VLAGVAAESSQQRVAAKQVLSDMTVADIRNN-------PVIPYEEDCVTRLIQDDVNETA
YQRIKHWTISDLREYVLNDEV---TSDDIAFVRKGLTSEVVAAVAKICSNADLIYGGKKM
PVIKKANTTIGLPGTFSCRLQPNDTRDDVQSIAAQIYEGLSFGAGDAVIGVNPVTDDVEN
LSRVLDTVYGVIDKFNIP--TQGCVLAHVTTQIEAIRRG-APGGLIFQSICGSEKGLKEF
GVELAMLDEARAVGAEFNRIA----------GENCLYFETGQGSALSAGANFG-----AD
QVTMEARNYGLARHYDPFL--------------VNTVVGFIGPEYLYNDRQIIRAGLEDH
FMGKLSGISMGCDCCYTNHADADQNLNENLMILLATAGCNYIMGMPLGDDIMLNYQTTAF
HDTATVRQLLGLRPSPEFERWLETMGIMA--NGRLTKRAGDPSL--FF------------
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>gi++|206580690|ref|YP_002237213.1| ethanolamine ammonia-lyase, large subunit
[Klebsiella pneumoniae 342]
------------------------------------------------MKLKTTLFGNVY
QF------------------------------------KDVKEVLAKANELRSGD-----
VLAGVAAESSQQRVAAKQVLSDMTVADIRNN-------PVIPYEEDCVTRLIQDDVNETA
YQRIKHWTISDLREHVLNDEV---TSDDIAFVRKGLTSEVVAAVAKICSNADLIYGGKKM
PVIKKANTTIGLPGTFSCRLQPNDTRDDVQSIAAQIYEGLSFGAGDAVIGVNPVTDDVEN
LSRVLDTVYGVIDKFSIP--TQGCVLAHVTTQIEAIRRG-APGGLIFQSICGSEKGLKEF
GVELAMLDEARAVGAEFNRIA----------GENCLYFETGQGSALSAGANFG-----AD
QVTMEARNYGLARHYDPFL--------------VNTVVGFIGPEYLYNDRQIIRAGLEDH
FMGKLSGISMGCDCCYTNHADADQNLNENLMILLATAGCNYIMGMPLGDDIMLNYQTTAF
HDTATVRQLLGLRPSPEFEGWLERMGIMA--NGRLTKRAGDPSL--FF------------
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>gi++|82544902|ref|YP_408849.1| ethanolamine ammonia-lyase, heavy chain [Shigella
boydii Sb227]
---------MQNELQTALFQAFDTLNLQRVKTFSVPPVTLCGPGSVSSCGQQAQTRGLKH
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LFVMADSFLHQAGMTAGLTRSLAVKGIAMTLWPCPVGEPCITDVCAAVAQLRESGCDGVI
AFGGGSVLDAAKAVALLVTNPDSTLAEMSETSVLQPRLPLIAYEDDCVTRLIQDDVNETA
YNQIKNWSISELREYVLSDET---SVDDIAFTRKGLTSEVVAAVAKICSNADLIYGAKKM
PVIKKANTTIGIPGTFSARLQPNDTRDDVQSIAAQIYEGLSFGVGDAVIGVNPVTDDVEN
LSRVLDTIYGVIDKFNIP--TQGCVLAHVTTQIEAIRRG-APGGLIFQSICGSEKGLKEF
GVELAMLDEARAVGAEFNRIA----------GENCLYFETGQGSALSAGANFG-----AD
QVTMEARNYGLARHYDPFI--------------VNTVVGFIGPEYLYNDRQIIRAGLEDH
FMGKLSGISMGCDCCYTNHADADQNLNENLMILLATAGCNYIMGMPLGDDIMLNYQTTAF
HDTATVRQLLNLRPSPEFERWLESMGIMA--NGRLTKRAGDPSL--FF------------
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>gi++|120554166|ref|YP_958517.1| ethanolamine ammonia lyase large subunit
[Marinobacter aquaeolei VT8]
------------------------------------------------MNLKTTLFGKVY
QF------------------------------------RDVKDVLAKANELRSGD-----
VLAGVAAETAQERVAAKQVLSEMRLETLREN-------PIVPYEEDAITRVIQDAVNKAA
YEDIRHWTVSELREYILSDVP---TREDYERMRRGLTSEMVAAVCKICSNGDLMVGAKKL
YVISKANCTVGIPGRFSSRLQPNDTRDDIDSIMVQVYEGLSYGCGDAVIGINPVTESVEN
TIRILNAVKEATDKWNIP--TQGCVLAHISNQMAALEKG-APGGLLFQSLSGTEKGLNEF
GVTVELLDEAYEMGKHYCKLA----------GSNMMYFETGQGTALSANAHHG-----AD
QVTIEARNYGLAKRYKPHL--------------LNTVVGFIGPEYLFNHQQITRAALEDH
FMGKLTGISMGCDACYTNHADTDQNSNENLTTLLAAAGCNYVMSLPLGDDIMLNYQTTGF
HDVVTARQLLSYRPAPEFEAWMETMGLME--NGKLTARAGDPSI--FF--D---------
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>gi++|116872549|ref|YP_849330.1| ethanolamine ammonia lyase large subunit [Listeria
welshimeri serovar 6b str. SLCC5334]
------------------------------------------------MILKTNLFGHTY
QF------------------------------------KSITDVLAKANEEKSGD-----
RLAGVAAESAEERVAAKVVLSKMTLGDLRNN-------PVVPYETDEVTRIIQDQVNERI
HDSIKNWTVEELREWILDHKT---TDADIKRVSRGLTSEIIAAVTKLMSNLDLIYGAKKI
RVIAHANTTIGLPGTFSARLQPNHPTDDPDGILASLMEGLTYGIGDAVIGLNPVDDSTDS
VVRLLNKFEEFRSKWDVP--TQTCVLAHVKTQMEAMRRG-APTGLVFQSIAGSEKGNTAF
GFDGATIEEARQLALQSGAAT----------GPNVMYFETGQGSELSSDAHFG-----VD
QVTMEARCYGFAKKFDPFL--------------VNTVVGFIGPEYLYDSKQVIRAGLEDH
FMGKLTGISMGCDVCYTNHMKADQNDVENLSVLLTAAGCNFIMGIPHGDDVMLNYQTTGY
HETATLRELFGLKPIKEFDQWMEKMGFSE--NGKLTSRAGDASI--FL--K---------
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>gi++|16800208|ref|NP_470476.1| hypothetical protein lin1139 [Listeria innocua
Clip11262]
------------------------------------------------MILKTNLFGHTY
QF------------------------------------KSITDVLAKANEEKSGD-----
RLAGVAAESAEERVAAKVVLSKMTLGDLRNN-------PVVPYETDEVTRIIQDQVNERI
HDSIKNWTVEELREWILDHKT---TDADIKRVARGLTSEIIAAVTKLMSNLDLIYGAKKI
RVIAHANTTIGLPGTFSARLQPNHPTDDPDGILASLMEGLTYGIGDAVIGLNPVDDSTDS
VVRLLNKFEEFRSKWDVP--TQTCVLAHVKTQMEAMRRG-APTGLVFQSIAGSEKGNTAF
GFDGATIEEARQLALQSGAAT----------GPNVMYFETGQGSELSSDAHFG-----VD
QVTMEARCYGFAKKFDPFL--------------VNTVVGFIGPEYLYDSKQVIRAGLEDH
FMGKLTGISMGCDVCYTNHMKADQNDVENLSVLLTAAGCNFIMGIPHGDDVMLNYQTTGY
HETATLRELFGLKPIKEFDQWMEKMGFSE--NGKLTSRAGDASI--FL--K---------
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>gi++|28211785|ref|NP_782729.1| ethanolamine ammonia-lyase heavy chain [Clostridium
tetani E88]
---------------------------------------------MRKVILKTKLFGKIY
QF------------------------------------KDVKEVLAKANEEKSGD-----
KLAGVAANSAQERIAAKVVLSNLTVADLRNN-------PVVPYETDEITRIIQDSVNEKI
YGEVKNWTISELREWILNENT---TGAQIKRISRGLTSEVIAGVAKLMSNLDLIYGANKI
KITAHCNTTIGENGRLSARLQPNHPTDDVDGIVASLLEGLSFGIGDALIGLNPVDDTTGS
VVRVLKKFEEIKQKYEIP--TQNCVLAHVTTQMEAIKKG-APTDLIFQSIAGSEKGNAAF
GITADLIEEARQLALTEGTAA----------GPNVMYFETGQGSELSAEAHFG-----AD
QVTMEARCYGFAKKYEPFV--------------VNTVVGFIGPEYLYDSKEVIRAGLEDH
FMGKLTGISMGCDVCYTNHMKADQNDAENLAVLLSTAGCNYFMGIPHGDDVMLNYQTTGY
HETASLRELLNKRPIVEFEGWLEKWGFMK--DGKLTSKAGDASV--FL--KK--------
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>gi++|29376187|ref|NP_815341.1| ethanolamine ammonia-lyase large subunit
[Enterococcus faecalis V583]
------------------------------------------------MILKTKLFGKVY
QF------------------------------------TSVKEVLAKANEEKSGD-----
KLAGVAANSAEERVAAKVVLSELSLNDLFNN-------PVVDYDEDEVTRIIIDQVNMRI
FESIKHWTVAELREFILSSET---TDFDIKRISRGLTSEMIAAVCKLMSNMDLIVGAKKI
NIEKTANTTIGRPGTFSNRLQPNHPTDNVDGIMASVMEGLSYGAGDALIGLNPVDDSTES
VKRILNKFEEFRSEWEIP--TQTCVLAHVTTQMEAMRQG-APTGLVFQSIAGSEKGNTAF
GLNAEILAEAQDLALHSGQAA----------GPNVMYFETGQGSELSSEANFG-----AD
QVTMEARCYGLAKKFDPYI--------------VNTVVGFIGPEYLYDSKQVIRAGLEDH
FMGKLTGISMGCDVCYTNHMKADQNDMENLAMLLATAGCTYIMGIPHGDDVMLNYQTTGF
HETATIRETLGLRPIKEFEEWMEKMGLME--NGKLTSRAGDASV--FI--K---------
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>gi++|16803215|ref|NP_464700.1| hypothetical protein lmo1175 [Listeria monocytogenes
EGD-e]
------------------------------------------------MILKTNLFGHTY
QF------------------------------------KSITDVLAKANEEKSGD-----
RLAGVAAESAEERVAAKVVLSKMTLGDLRNN-------PVVPYETDEVTRIIQDQVNDRI
HDSIKNWTVEELREWILDHKT---TDADIKRVARGLTSEIIAAVTKLMSNLDLIYGAKKI
RVIAHANTTIGLPGTFSARLQPNHPTDDPDGILASLMEGLTYGIGDAVIGLNPVDDSTDS
VVRLLNKFEEFRSKWDVP--TQTCVLAHVKTQMEAMRRG-APTGLVFQSIAGSEKGNTAF
GFDGATIEEARQLALQSGAAT----------GPNVMYFETGQGSELSSDAHFG-----VD
QVTMEARCYGFAKKFDPFL--------------VNTVVGFIGPEYLYDSKQVIRAGLEDH
FMGKLTGISMGCDVCYTNHMKADQNDVENLSVLLTAAGCNFIMGIPHGDDVMLNYQTTGY
HETATLRELFGLKPIKEFDQWMEKMGFSE--NGKLTSRAGDASI--FL--K---------
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>gi++|150388098|ref|YP_001318147.1| ethanolamine ammonia lyase large subunit
[Alkaliphilus metalliredigens QYMF]
------------------------------------------------MILKSKLFGTVY
QF------------------------------------KSLNEVMAKANEERSGD-----
KLAGLAAESVTEMVAAKEVLSNITLKDIRNN-------PAVPYETDEVTRVIQDGVNEKI
YKEIQNWTVSELREWILSNET---TGSDIKRIGRGLTSEMVAAVTKLMSNLDLVYGAKKI
IVTAHCNTTIGESGTLAYRLQPNHTTDNIEGIKVSLYEGLSYGVGDAVLGLNPVNDTVNS
VKNVLNLFEEVKQKWQIP--TQTCVLAHITTQMEAIRQG-APSDMIFQSIAGTEKGNEAF
GLNDSLLSEARELVLKEGTST----------GPNVMYFETGQGSELSSDAHMG-----VD
QVTLEARCYGLAKKHSPFL--------------VNTVVGFIGPEYLYNSKQVMRAGLEDH
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FMGKLSGIPMGVDVCYTNHMKADQNDIENLSVLLASAGCNFLIGTPAGDDIMLNYQSSSF
HDAATLRELLNLTPIPEFQKWLEKMGISE--NGRLSKRAGDASI--FF--SK--------
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>gi++|125717383|ref|YP_001034516.1| ethanolamine ammonia-lyase large subunit,
putative [Streptococcus sanguinis SK36]
------------------------------------------------MILKTKLFGRLY
EF------------------------------------KSVKEVLAKANEYKSGD-----
QLAGVAAESAEERVAAKVVLAQLKLSDLFNN-------PVVPYEEDEVTRIIIDDVNLRT
YEKIKNWTVEELREWILDNKT---KNVDIQWLSRGLTSEMVAAVAKLMTNLDLIVAANKI
VITKHANTTIGMPGTFSSRLQPNHTTDDPDGIMASTMEGFAYGCGDALLGLNPVDDSVES
TKRVLHKFNDFIEEYKIP--TQHCVLAHVTTQIEAMNQG-APTGLVFQSIAGSEKGNEAF
GFDAKIIQEAWDTALKVGTAA----------GPNVMYFETGQGSELSSDAHHG-----AD
QVTMEARCYGFAKRFDPFL--------------VNTVVGFIGPEYLYDSKQVIRAGLEDH
FMGKLTGISMGCDICYTNHMKADQNDAENLLVLLGAANVNYIMAIPHGDDIMLNYQTTGY
HETATMRSLLNKRPIKEFEEWMEKMGLME--DGHLTEIGGDGSI--FM--KSN-------
------------------------------------------------------------
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>gi++|158319837|ref|YP_001512344.1| ethanolamine ammonia lyase large subunit
[Alkaliphilus oremlandii OhILAs]
------------------------------------------------MILKTKLFGKTY
QF------------------------------------SSVMEVMGKANEEKSGD-----
NLAGVAAESAEERVAAKVVLSQLKLSDLFNN-------PAVPYEKDEVTRIIIDHVNLKT
YERIKNWTVAELREWILNSNT---TNYDIHRISNGLTAEMVAAVAKIMSNLDLIVGAQKI
VVTKTANTTIGVPGTFSTRLQPNHTTDNVDGIMATVMEGLSMGAGDAVIGLNPVDDTTES
VKRILHKFNDFINKWEIP--TQHVVLAHVATQMEAMEQG-APTGLVFQSIAGSEKGNAAF
GISAKMLSEAKDMALKLGTAV----------GPNVMYFETGQGSELSSDAHNG-----VD
QLTMEARCYGFAKHFDPFL--------------VNTVVGFIGPEYLYDSKQVIRAGLEDH
FMGKLTGISMGCDVCYTNHMKADQNDAENLTVLLATAGVNFIMGIPNGDDIMLNYQTTGF
HEGASIRQLLNKRTIKEFDQWLEKMGFSE--NGRLTSKAGDASV--FL--KG--------
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>gi++|18309880|ref|NP_561814.1| ethanolamine ammonia lyase heavy chain [Clostridium
perfringens str. 13]
------------------------------------------------MILKTKLFGKVY
AF------------------------------------KSLNEVMAKANEEKSGD-----
RLAGLAAESSEERVAAKVVLSNITLEDLRNN-------PAVPYEIDEVTRIIQDDVNEKI
YNEIKHWTVSEFREWILDENT---TGADIRRISRGLTSEMVAAVAKLMSNMDLIYGARKI
KVTAHCNTTIGEKGTLSARLQPNHPTDDPDGIMASLLEGLTFGVGDAVLGLNPVDDSVES
VTKVLKRFDEIKRKFKIP--TQTCVLAHVTTQMEAIRQG-APTDLIFQSIAGSEKGNEAF
GFNAATIEEARQLALKQGTAT----------GPNVMYFETGQGSELSSDAHHG-----VD
QVTMEARCYGFAKRFQPFL--------------VNTVVGFIGPEYLYDSKQVIRAGLEDH
FMGKLTGIPMGCDACYTNHMKADQNDIENLAVLLTTAGCTYFMGIPHGDDVMLNYQTTGY
HETAALREMFGLTAIKEFQDWLVEMGFVD-ENGKLTKKAGDASV--LL--G---------
------------------------------------------------------------
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>gi++|160880778|ref|YP_001559746.1| ethanolamine ammonia lyase large subunit
[Clostridium phytofermentans ISDg]
------------------------------------------------MILKAQLFGHTY
EF------------------------------------KSLMDVMAKANEEKSGD-----
TLAGIAAESAEQRVAAKVVLSNITLEQLRNN-------PAVPYEIDEVTRIIQDDVNEKI
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YNEIKHWTVAEFREWILDENT---TGADIRRVSRGITSEMVAAVAKLMSNMDLVYGARKI
RVTAHCNTTIGEPGTLSCRLQPNHPTDDPDGIMASLLEGLTYGAGDALLGLNPVDDSTES
VMRVLKRFDEIKHKFNIP--TQTCVLAHVTTQMDAIRKG-APSDLIFQSIAGSEKGNEAF
GFTAAILEEARQLALTEGTAE----------GPNVMYFETGQGSELSSEAHHG-----VD
QVTMEARCYGFAKRFNPFV--------------VNTVVGFIGPEYLYDGRQVNRAGLEDH
FMGKLTGISMGCDACYTNHMKADQNTIEDLSVLLTTAGCNYFMGIPHGDDVMLNYQTTGY
HETAALREMFGLTAIKPFHEWMIHMGFID-EKGKLTKLAGDASV--LF------------
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>gi++|126699523|ref|YP_001088420.1| putative ethanolamine/propanediol ammonia-lyase
heavy chain [Clostridium difficile 630]
------------------------------------------------MILNTKLFGRTY
QF------------------------------------KGLYDVMAKANEEKSGD-----
KLAGLAAESAEERIAAKVVLSHIKLEDIRNN-------PAVAYEEDEVTRIIQDAVNEKV
YEEIKNWTVSELREWLLDSNT---TSLDIRRISRGLTSEMIAAVAKLMSNMDLVYAAKKI
KVTAHCNTTIGEQGTLSARLQPNHPTDDPDGILASLLEGLTFGIGDAVLGLNPVDDSVES
VTKVLKRFEEVKQKYQIP--TQTCVLAHVTTQMEAIRNG-APADLIFQSIAGSEKGNEAF
GFNGDTIEEARQLALKHGTAT----------GPNVMYFETGQGSELSSEAHHG-----ID
QVTMEARCYGFAKKYEPFL--------------VNTVVGFIGPEYLYDAREVVRAGLEDH
FMGKLHGLPMGVDVCYTNHMKADQNDMENLAILLTTAGCTYFMGIPHGDDVMLNYQTTGY
HETASLREMFGLTAIKEFDAWMEKMGFSK--DGKLTELAGDASI--LL--G---------
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>gi++|119718253|ref|YP_925218.1| ethanolamine ammonia-lyase heavy chain
[Nocardioides sp. JS614]
------------------------------------------------MQLAATLFGTRY
QF------------------------------------RDIKDLLAKANEEKSGD-----
RLAGVAADSAAERMAARFVLSEVTLETLRAN-------PAVPYEEDEVTRVIDDGVNEAV
YAEIKGMQVGELREWLLADTT---TGEMIRRLSNGLTAEMVAAVTKLMSNLDLMLAASKI
KIVKHANNTIGLRGTLASRCQPNNQTDSVEGIRAAVYEGLSFGSGDSVIGINPSDDSLGS
VSRLLEMTHEVITRWEIP--TQNCVLAHVSTQMEAMRHG-APVGLVFQSLAGSQKGNESF
GIDVGMLDEAYALAKRYSVAT----------GPNYMYFETGQGSELSADAHHG-----AD
QVVMEARCYGLAKRYDPFQ--------------LNTVVGFIGPEYLYDSTQITRAGLEDH
FMGKLTGISMGADVCYTNHARSTQNELENLAVLLGAAGVNFIMGIPMGDDSMLSYQSSSF
HDAPSLRQLLGLRPLPEFEAWMEGLGLLR--DGRLTEKAGDASF--FL--SR--------
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>gi++|51893201|ref|YP_075892.1| ethanolamine ammonia-lyase, heavy chain
[Symbiobacterium thermophilum IAM 14863]
------------------------------------------------MILKTTLRGQVY
QF------------------------------------RSVKEVLAKANELRSGD-----
VLAGIAAETEAERVAAKHVLANLTLEDLRNN-------PVIPYEEDEVTRVIQDAVNEHV
YRQIKGWTVAELREYILSDKA---DAQEIQRISRGLTSEMVAAVAKLCSNLDLIYGASKM
HNVVQCNTTIGLPGTLAMRLQPNDPVDSIDGIMPQIMEGLSYGIGDAVIGINPVNDDPES
VSRLLWAVYEFMEKWRIP--TQQCVLAHVTTQMRCIRDG-APVGLVFQSIAGSEKAMEAF
GVSVEMLDEALELVRKYGSAK----------GPNLMYFETGQGSELSADAHHG-----AD
QVTLEARCYGLAKRYQPLL--------------VNTVVGFIGPEYLYDAKQVIRAGLEDV
FMGKLTGISMGCDVCYTNHMKADQHDIENLAVLLTAAGVNYFIGVPMGDDPMLNYQCGAF
HDGAAPWRITRSRP----------------------------------------------
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>gi++|19703431|ref|NP_602993.1| ethanolamine ammonia-lyase heavy chain
[Fusobacterium nucleatum subsp. nucleatum ATCC 25586]
------------------------------------------------MILSVELFDHVY
NF------------------------------------SSLKEVMAKANEKKSGD-----
TLAGIAASSSKERVAAKVVLSKITLKDLKEN-------PAVPYEEDEVTRIIIDDLNLQI
YDEIKDWTVSDLREWLLSEEA---TPSKINWIRRGLTSEMIAAVAKLMSNMDLIVAAKKI
EVRAHCNTTIGGYDTLAVRLQPNHTTDDPDGIMISTLEGLSYGIGDAVIGLNPVDDSVDS
VMAVMERFHKIKTEYQIP--TQTCVLAHVTTQMEAIKRG-AKVDMIFQSIAGSEKGNEAF
GITGAMIEEARQLGLKYGTAA----------GPNIMYFETGQGSELSSDAHNG-----AD
QVTMEARCYGFAKRFQPFL--------------VNTVVGFIGPEYLYDSKQVIRAGLEDH
FMGKLHGLPMGVDVCYTNHMKAEQSDVEILATLLTAAGCNYFMGVPAGDDIMLNYQTTGF
HDNQSLRELFGKQPIKEFKEWLVKYGFMT-EDGKLTEKAGDPSV--FL--K---------
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>gi++|89897708|ref|YP_521195.1| hypothetical protein DSY4962 [Desulfitobacterium
hafniense Y51]
------------------------------------------------MILKAKVYHKVF
AF------------------------------------KDLKEVLAKANEEKSGD-----
VLAGIGATSASERVAAKLVLSNLTLEDLYNH-------PVLPYEEDEVTRVIYDGLNLRI
YQEMKGWTVGQLREYILDHGT---TGSHLNHISRGLTSEMIAAVAKLMSNMDLVYGSKKM
RHQAHCNTTIGIPGTLAFRCQPNHPTDSVEGVMASLKEGLSYGSGDAVIGINPVEDNVDT
LSRLLETVKEFMQQWEIP--TQNCVLAHITTQMKAITKG-VPIDLVFQSIAGTQKANEAF
GISKELIDEAFALIQRNGTAT----------GPNLMYFETGQGSEISLAAHHG-----VD
MMTLESRTYGFGRHYRPFL--------------LNNVSGFIGPETIYSGREVIRADLEDL
FMGKLHGLPMGIAPCYTNHMKADQNDQEIATLLCAMAGANYFMGLPGGDDVMLSYQDTSY
HDDAATREILGLRPLPEFEKWLEKMGIME--NGQLTERAGDPSV--FD--K---------
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>gi++|169827647|ref|YP_001697805.1| ethanolamine ammonia-lyase heavy chain
[Lysinibacillus sphaericus C3-41]
----------------------------------------------MNVNLSVIFGGEKY
NF------------------------------------KSLKDVMAKANEEKSGD-----
QLAGIAAETVQQRIAAKAVLSELLVKDIREN-------PLVPQENDEVSRIIEGDINEQI
YGEIKNWSIEQLREYILSNDT---GDRELKRLSKGMNSEVIAAVTKLMSNLDLVHAANKV
EILSTCNITIGQKGTLSSRLQPNHPTDNIDGIIASLKEGLSYGIGDAVIGINPVDDSVES
VKKVLTATKEFINDWSIP--TQNCVLAHITTQMKAIKQG-APADMIFQSIAGTEIANRSF
GISADLIREAEELIKKQGTGT----------GPNLFYFETGQGSELSAEAHMG-----ID
QVTLESRNYGFARHFNPYI--------------VNTVVGFIGPEYLYNNKQVIRAGLEDH
FMGKMHGIPMGVDICYTNHIKADQNDVEDLSVLLTAAGVNFIIAAPMGDDVMLNYQSMSF
HDVATLLQTFGKKPAPEYLAWLEKMGIYE--NGRLSARAGDLSI--FE--R---------
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>gi|37526860|ref|NP_930204.1| ethanolamine ammonia-lyase heavy chain [Photorhabdus
luminescens subsp. laumondii TTO1]
------------------------------------------------MKLKTQLFGKTY
QF------------------------------------KDVKQVLAMANELRSGD-----
VLAGVAAESSQQRVAAKHVLSEMTIADIRMN-------PIIPYEEDCVTRIIQDDINEIA
YAGIKNWSIGELREYILSDDT---RVDDIAFLRKGISSEVVAAVAKISSNADLIYGAKKM
PVIKKANTTIGTPGTFSARLQPNDTRDDVQSILAQIYEGLSFGVGDAVIGVNPVTDDVEN
LTRVLDTLYEVIDKFSIP--TQGCVLAHVTTQIEAIKRG-APGGLIFQSICGSEKGLKEF
GVELAMLDEARAVGAEYCRLA----------GDNCLYLETGQGSALSAGAHFG-----AD
QVTMEARNYGLARHYDPFL--------------VNTVVGFIGPEYLYNDRQIIRAGLEDH
FMGKLSGVSMGCDCCYTNHADSDQNQNENLMILLATAGCNFIMGMPLGDDIMLNYQTSAF
HDTATIRHLLNLRPSPEFERWLEQMGLMA--NGRLTSRAGDASF--FF------------
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>gi|15895975|ref|NP_349324.1| ethanolamine ammonia lyase large subunit [Clostridium
acetobutylicum ATCC 824]
------------------------------------------------MNLKTTLFNTTY
KF------------------------------------KDIKDVLAKANEKKSGD-----
EMAGIAASGARERVAAKTVLADITLEELRNN-------PVVSYEKDEITRVIQDSVDEEQ
YKKIKALTVGEFREFLLEN-----DEDKIKEIRDGLTSEMIAAVTKLMSNMDLVYAAQKI
CNTAKCNTTIGRRGTFSSRLQPNHPTDNPQGIMASLIDGISYGVGDAVIGLNPVADTIES
VSDVLKVFNDFTRKWRIP--TQNCVLAHITTQMEALKNG-VPIDLMFQSIAGSEIANKDF
GISVALLDEAYELMKTKKSSK----------GPNFMYFETGQGTELSSEGNNR-----AD
QLVMEARCYGLAKRYKPFL--------------VNTVVGFIGPEYLYDGKQVIRAGLEDH
FMGKLTGLSMGVDTCYTNHMKADQNDLENLAMLLLAANCNYLMGIPCGDDVMLMYQSSSY
HDIATLREISDKRPIKEFEKRMEELGIMK--NGKLTRNAGDPSI--FM------------
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>gi|186474779|ref|YP_001856249.1| ethanolamine ammonia lyase large subunit
[Burkholderia phymatum STM815]
------------------------------------------------MSYMETIGSRTY
RF------------------------------------ADLKSLMAKASPLRSGD-----
QLAGIAAASEEERVAAKMALADVPLRTFLNE-------ALIPYESDEVTRLVIDTHSPEA
FAPIAHLTVGEFRNWLLSSET---DTDTLTRVTKGLTPEMVAAVSKLMRNQDLILAARKR
PVITRFRNTVGLPGHMSVRLQPNHPTDDVKGIAASMIDGLMYGCGDAMIGINPASDSLSA
ITNLLLMIDDFRTRYHVP--TQSCVLTHVTNTISAIEKG-APVDLVFQSIAGTEKANAGF
GISLALLQEAYEAALALKRGT---------VGDNVMYFETGQGSALSADAHHG-----VD
QQTCEVRAYAVARHFNPFL--------------VNTVVGFIGPEYLYDGKQITRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDNLLTLLGVAGINFIMGIPGADDVMLNYQSTSF
HDALYVREVLGLRRAPEFEEWLESMQITD-TRGALLNAPTGQPL--LE--GASE------
----WMGIA---------------------------------------------------
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>gi|91781403|ref|YP_556609.1| ethanolamine ammonia-lyase heavy chain [Burkholderia
xenovorans LB400]
------------------------------------------------MSYTETIGSRTY
RF------------------------------------ADLKTLMAKASPQRSGD-----
QLAGVAAASEEERVAAKMALAQVPLRTFLNE-------ALIPYESDEVTRLVIDDHSPQA
FAEIAHLTVGDFRNWLLSSTT---DADALTRIAAGLTPEMVAAVSKLMRNQDLIAAARKR
PVITRFRNTVGLPGHMSVRLQPNHPTDDVKGIAASMLDGLMYGCGDAMIGINPASDNLAA
ITRLLLMVDDFRQRYQVP--TQSCVLTHVTNTIAAIEKG-APVDLVFQSIAGTEKANAGF
GISLALLQEAYEAGLSLKRGT---------VGNNLMYFETGQGSALSADAHFG-----VD
QQTCEVRAYAVARKFNPFL--------------VNTVVGFIGPEYLYDGKQITRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDNLLTLLGVAGINFIMGIPGADDVMLNYQSTSF
HDALYVREVLGLRRAPEFEEWLESMQITD-ARGALLSASTQQPL--LE--GAPD------
----WMGIA---------------------------------------------------
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>gi|134294258|ref|YP_001117993.1| ethanolamine ammonia-lyase heavy chain
[Burkholderia vietnamiensis G4]
------------------------------------------------MSYTETIGPRTY
RF------------------------------------ADLKTLLAKASPLRSGD-----
QLAGVAAASEEERVAAKIALASVPLKAFLNE-------AVIPYEQDEVTRLIVDDHDAQA
FAEISHLTVGDFRNWLLSPAA---DGAALERIAPGLTPEMVAAVSKLMRNQDLIAAARKR
RVVTRFRNTVGLPGRMSVRLQPNHPTDDVKGIAASMLDGLMYGCGDAMIGINPATDSLAA
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IVKLLAMIDGFRERYGVP--TQSCVLTHVTNTIAAIDKG-APVDLVFQSIAGTEKANASF
GISLALLGEARAAALSLARGT---------VGNNVMYFETGQGSALSANAHFG-----VD
QQTCEVRAYAVARKFDPFL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDTLLTLLGAAGINFIMGIPGADDVMLNYQSTSF
HDQLYVREVLGLRRAPEFEEWLETMEIAD-AHGALRAANARVPL--LA--GAND------
----WMGISA--------------------------------------------------
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>gi|187922055|ref|YP_001893697.1| Ethanolamine ammonia lyase large subunit
[Burkholderia phytofirmans PsJN]
------------------------------------------------MSYTETIGTRTY
RF------------------------------------ADLKTLLAKASPQRSGD-----
QLAGVAAASEEERVAAKMALAQVPLRTFLNE-------ALIPYESDEVTRLVIDDHSPQA
FAEISHLTVGDFRNWLLSSTT---DADALTRISAGLTPEMVAAVSKLMRNQDLIAAARKR
PVITRFRNTVGLPGHMSVRLQPNHPTDDVKGIAASMLDGLMYGCGDAMIGINPASDNLAA
ITKLLLMIDDFRQRYQVP--TQSCVLTHVTNTIAAIEKG-APVDLVFQSIAGTEKANAGF
GISLALLQEAYEAGLSLKRGT---------VGNNLMYFETGQGSALSADAHFG-----VD
QQTCEVRAYAVARRFNPFL--------------VNTVVGFIGPEYLYDGKQITRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDNLLTLLGVAGINFIMGIPGADDVMLNYQSTSF
HDALYVRDVLGLRRAPEFEEWLESMQITD-ARGALLSASTQQPL--LE--GARD------
----WMGIA---------------------------------------------------
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>gi|115350175|ref|YP_772014.1| ethanolamine ammonia lyase large subunit
[Burkholderia ambifaria AMMD]
------------------------------------------------MAYTETIGPRTY
RF------------------------------------ADLKTLLAKASPLRSGD-----
QLAGVAAASEEERVAAKIALAGVPLKAFLNE-------ALIPYEHDEVTRLILDDHDAAA
FAEISHLTVGDFRNWLLSPVA---DGAALERIAPGLTPEMVAAVSKLMRNQDLIAAARKR
RVVTRFRNTVGLPGRMSVRLQPNHPTDDVKGIAASMLDGLMYGCGDAMIGINPATDSLAA
IVKLLAMIDGFRERYGVP--TQSCVLTHVTNTIAAIEKG-APVDLVFQSIAGTEKANASF
GISLALLGEAREAALSLGRGT---------VGNNLMYFETGQGSALSANAHFG-----VD
QQTCEVRAYAVARKFDPFL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDTLLTLLGAAGINFIMGIPGADDVMLNYQSTSF
HDQLYVREVLGLRRAPEFEEWLETMEIAD-AHGALRVASARVPL--LA--GAND------
----WMGISA--------------------------------------------------
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>gi|183221860|ref|YP_001839856.1| ethanolamine ammonia-lyase, heavy chain
(ethanolamine ammonia-lyase large subunit) [Leptospira biflexa serovar Patoc strain
'Patoc 1 (Paris)']
------------------------------------------------MSYQIVIGKKTY
QF------------------------------------QDLKQVLAKASPLRSGD-----
QLSGIAAADQKERIAAQMVLADIYLSDFLNV-------ELIPSDIDEVTRLILTSHDKVS
FQTISHLTVGGFRDFLLSETT---DAQVLESIRMALTPEMVAAVSKLMSNQDLILVSQKI
NIVTKFRNTIGLPGRLSVRLQPNHPTDDLKGIAASILDGLILGSGDAVIGINPATDHIPT
CITLLEMLDTIIQKYSIP--TQSCILTHVTTSMQVMQKG-APVDLVFQSIGGTEDLNKSF
GINLSMLGEAREMALSLKRGT---------IGDHVMYFETGQGSALSAGAHHG-----ID
QQTLEVRAYAVARKFSPLL--------------VNTVVGFIGPEYLYNGKQIIRAGLEDH
FCGKLMGLPMGVDICYTNHADADQDDMDTLLTLLGVAGCNFIMGIPGADDVMLSYQSTSF
HDALYLRQVLGLRPTPEFEQWLLDFGIFSKGKNFLPIENQMVAL--FE--NGMR------
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>gi|170731498|ref|YP_001763445.1| ethanolamine ammonia lyase large subunit
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[Burkholderia cenocepacia MC0-3]
------------------------------------------------MSYTETIGPRTY
RF------------------------------------ADLKTLLAKASPLRSGD-----
QLAGVAAASEEERVAAKIALAGVPLKAFLNE-------AVIPYEDDEVTRLIIDDHDAQA
FAEISHLTVGDFRNWLLSPAA---DGAALERIAPGLTPEMVAAVSKLMRNQDLIAAARKR
RVVTRFRNTVGLPGRMSVRLQPNHPTDDVKGIAASMLDGLMYGCGDAMIGINPATDSLAA
IVKLLAMIDGFRERYGVP--TQSCVLTHVTNTIAAIEKG-APVDLVFQSIAGTEKANASF
GISLALLAEAREAALALKRGT---------VGNNLMYFETGQGSALSANAHFG-----VD
QQTCEVRAYAVARKFEPFL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDTLLTLLGAAGINFIMGIPGADDVMLNYQSTSF
HDQLYVREVLGLRRAPEFEEWLETMEIAD-AHGALRAATARVPL--LA--GAND------
----WMGISA--------------------------------------------------
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>gi|172059195|ref|YP_001806847.1| ethanolamine ammonia lyase large subunit
[Burkholderia ambifaria MC40-6]
------------------------------------------------MAYTETIGPRTY
RF------------------------------------ADLKTLLAKASPLRSGD-----
QLAGVAAASEEERVAAKIALAGVPLKAFLNE-------ALIAYEYDEVTRLILDDHDAAA
FAEISHLTVGDFRNWLLSPVA---DGAALERIAPGLTPEMVAAVSKLMRNQDLIAAARKR
RVVTRFRNTVGLAGRMSVRLQPNHPTDDVKGIAASMLDGLMYGCGDAMIGINPATDSLAA
IVKLLAMIDGFRERYGVP--TQSCVLTHVTNTIAAIEKG-APVDLVFQSIAGTEKANASF
GISLALLGEAREAALSLGRGT---------VGNNLMYFETGQGSALSANAHFG-----VD
QQTCEVRAYAVARKFDPFL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDTLLTLLGAAGINFIMGIPGADDVMLNYQSTSF
HDQLYVREVLGLRRAPEFEEWLETMEIAD-AHGALRVASARVPL--LA--GAND------
----WMGISA--------------------------------------------------
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>gi|76809343|ref|YP_331557.1| ethanolamine ammonia-lyase, large subunit
[Burkholderia pseudomallei 1710b]
------------------------------------------------MRYTETIGSRTY
RF------------------------------------ADLKTLLAKASPLRSGD-----
QLAGVAAATEEERVAAKMALASAPLTAFLNE-------AVIPYEDDEVTRLVVDTHSRDA
FAEISHLTVGDFRNWLLSPAA---DAAALERIAPGLTPEMVAAVSKLMRNQDLIAAARKR
RVVTRFRNTVGLPGRMSVRLQPNHPTDDVKGIAASMLDGLMYGCGDAMIGINPATDSLAA
ITKLLAMIDAFRERYRVP--TQSCVLTHVTNTIAAIGKG-APVDLVFQSIAGTEKANASF
GISLALLAEAREAALALKRGT---------VGNNLMYFETGQGSALSANAHHG-----VD
QQTCEVRAYAVARAFEPFL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAQADQDDMDNLLTLLGAAGINFIMGIPGADDVMLNYQSTSF
HDQLYVREVLGLRRAPEFEEWLETMEITD-AHGALRAASARVPL--LA--GAND------
----WMGRCA--------------------------------------------------
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>gi|78064786|ref|YP_367555.1| ethanolamine ammonia-lyase heavy chain [Burkholderia
sp. 383]
------------------------------------------------MSYTETIGPRTY
RF------------------------------------ADLKTLLAKASPLRSGD-----
QLAGVAAASEEERVAAKIALAGVPLKAFLSE-------AVIPYEDDEVTRLIVDDHDAQA
FAEISHLTVGDFRNWLLSPAA---DCAALERIAPGLTPEMVAAVSKLMRNQDLIAAARKR
RVVTRFRNTVGLPGRMSVRLQPNHPTDDVKGIAASMLDGLMYGCGDAMIGINPATDSLAA
IVKLLAMIDGFRERYGVP--TQSCVLTHVTNTIAAVEKG-APVDLVFQSIAGTEKANASF
GISLALLGEAREAALSLKRGT---------VGNNLMYFETGQGSALSANAHFG-----VD
QQTCEVRAYAVARKFEPFL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADSDDMDTLLTLLGAAGINFIMGIPGADDVMLNYQSTSF
HDQLYVREVLGLRRAPEFEEWLETMEIAD-AHGALRAATSRVPL--LA--GAND------
----WMGISA--------------------------------------------------
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>gi|83719390|ref|YP_443774.1| ethanolamine ammonia-lyase, large subunit
[Burkholderia thailandensis E264]
------------------------------------------------MRYTETIGSRTY
RF------------------------------------ADLKTLLAKASPLRSGD-----
QLAGVAAATEEERVAAKMALASVPLAAFLNE-------AVIPYEDDEVTRLVVDTHSRDA
FAEISHLTVGDFRNWLLSPAA---DAAALERIASGLTPEMVAAVSKLMRNQDLIAAARKR
RVVTRFRNTVGLPGRMSVRLQPNHPTDDVKGIAASMLDGLMYGCGDAMIGINPATDSLAA
ITKLLAMIDAFRERYRVP--TQSCVLTHVTNTIAAIEKG-APVDLVFQSIAGTEKANASF
GISLALLAEARDAALALKRGT---------VGDNLMYFETGQGSALSANAHHS-----VD
QQTCEVRAYAVARVFEPFL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAQADQDDMDNLLTLLGAAGINFIMGIPGADDVMLNYQSTSF
HDQLYVREVLGLRRAPEFEEWLEAMEIAD-AHGALRAASARVPL--LA--GAND------
----WMGLSA--------------------------------------------------
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>gi|107024468|ref|YP_622795.1| ethanolamine ammonia lyase large subunit
[Burkholderia cenocepacia AU 1054]
------------------------------------------------MSYTETIGPRTY
RF------------------------------------ADLKTLLAKASPLRSGD-----
QLAGVAAASEEERVAAKIALAGVPLKAFLNE-------AVIPYEDDEVTRLIIDDHDAQA
FAEISHLTVGDFRNWLLSPAA---DGAALERIAPGLTPEMVAAVSKLMRNQDLIAAARKR
RVVTRFRNTVGLAGRMSVRLQPNHPTDDVKGIAASMLDGLMYGCGDAMIGINPATDSLAA
IVKLLAMIDGFRERYGVP--TQSCVLTHVTNTIAAIEKG-APVDLVFQSIAGTEKANASF
GISLALLGEAREAALALKRGT---------VGNNLMYFETGQGSALSANAHFG-----VD
QQTCEVRAYAVARKFEPFL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDTLLTLLGAAGINFIMGIPGADDVMLNYQSTSF
HDQLYVREVLGLRRAPEFEEWLETMEIAD-AHGALRAATARVPL--LA--GAND------
----WMGISA--------------------------------------------------
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>gi|53720981|ref|YP_109967.1| ethanolamine ammonia-lyase heavy chain [Burkholderia
pseudomallei K96243]
------------------------------------------------MRYTETIGSRTY
RF------------------------------------ADLKTLLAKASPLRSGD-----
QLAGVAASTEEERVAAKMALASAPLTAFLNE-------AVIPYEDDEVTRLVVDTHSRDA
FAEISHLTVGDFRNWLLSPAA---DAAALERIAPGLTPEMVAAVSKLMRNQDLIAAARKR
RVVTRFRNTVGLPGRMSVRLQPNHPTDDVKGIAASMLDGLMYGCGDAMIGINPATDSLAA
ITKLLAMIDAFRERYRVP--TQSCVLTHVTNTIAAIDKG-APVDLVFQSIAGTEKANASF
GISLALLAEAREAALALKRGT---------VGNNLMYFETGQGSALSANAHHG-----VD
QQTCEVRAYAVARAFEPFL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAQADQDDMDNLLTLLGAAGINFIMGIPGADDVMLNYQSTSF
HDQLYVREVLGLRRAPEFEEWLETMEITD-AHGALRAASARVPL--LA--GAND------
----WMGRCA--------------------------------------------------
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>gi|126455070|ref|YP_001068230.1| ethanolamine ammonia-lyase, large subunit
[Burkholderia pseudomallei 1106a]
------------------------------------------------MRYTETIGSRTY
RF------------------------------------ADLKTLLAKASPLRSGD-----
QLAGVAASTEEERVAAKMALASAPLTAFLNE-------AVIPYEDDEVTRLVVDTHSRDA
FAEISHLTVGDFRNWLLSPAA---DAAALERIAPGLTPEMVAAVSKLMRNQDLIAAARKR
RVVTRFRNTVGLPGRMSVRLQPNHPTDDVKGIAASMLDGLMYGCGDAMIGINPATDSLAA
ITKLLAMIDAFRERYRVP--TQSCVLTHVTNTIAAIGKG-APVDLVFQSIAGTEKANASF
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GISLALLAEAREAALALKRGT---------VGNNLMYFETGQGSALSANAHHG-----VD
QQTCEVRAYAVARAFEPFL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAQADQDDMDNLLTLLGAAGINFIMGIPGADDVMLNYQSTSF
HDQLYVREVLGLRRAPEFEEWLETMEITD-AHGALRAASARVPL--LA--GAND------
----WMGRCA--------------------------------------------------
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>gi|206558463|ref|YP_002229223.1| ethanolamine ammonia-lyase heavy chain
[Burkholderia cenocepacia J2315]
------------------------------------------------MSYTETIGPRTY
RF------------------------------------ADLKTLLAKASPLRSGD-----
QLAGVAAASEEERVAAKIALAGVPLKAFLNE-------AVIPYEDDEVTRLIIDDHDAQA
FADISHLTVGDFRNWLLSPAA---DGAALERIAPGLTPEMVAAVSKLMRNQDLIAAARKR
RVVTRFRNTVGLAGRMSVRLQPNHPTDDVKGIAASMLDGLMYGCGDAMIGINPATDSLAA
IVKLLAMIDGFRERYGVP--TQSCVLTHVTNTIAAIEKG-APVDLVFQSIAGTEKANASF
GISLALLGEAREAALALKRGT---------VGNNLMYFETGQGSALSANAHFG-----VD
QQTCEVRAYAVARKFEPFL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDTLLTLLGAAGINFIMGIPGADDVMLNYQSTSF
HDQLYVREVLGLRRAPEFEEWLETMEIAD-AHGALRAATARVPL--LA--GAND------
----WMGVSA--------------------------------------------------
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>gi|161523307|ref|YP_001578319.1| ethanolamine ammonia lyase large subunit
[Burkholderia multivorans ATCC 17616]
------------------------------------------------MSYTETIGSRTY
RF------------------------------------ADLKTLLAKASPLRSGD-----
QLAGVAAASEEERVAAKIALAGVPLRAFLNE-------AVIPYEADEVTRLIVDDHDAHA
FAEIAHLTVGDFRNWLLSPAA---DGAALERIAPGLTPEMVAAVSKLMRNQDLIAAARKR
RVVTRFRNTVGLPGRMSVRLQPNHPTDDVKGIAASMLDGLMYGCGDAMIGINPATDSLAA
IVKLLAMIDAFRERYRVP--TQSCVLTHVTNTIAAIEKG-APVDLVFQSIAGTEQANASF
GISLALLAEAREAALSLKRGT---------VGDNLMYFETGQGSALSANAHHG-----VD
QQTCEVRAYAVARKFEPFL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDNLLTLLGAAGINFIMGIPGADDVMLNYQSTSF
HDQLYVREVLGLRRAPEFEEWLETMEIAD-AHGVLRTATSRVPL--LA--GAND------
----WMGLSA--------------------------------------------------
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>gi|116622922|ref|YP_825078.1| ethanolamine ammonia-lyase heavy chain [Solibacter
usitatus Ellin6076]
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--------------------------------------MTLRELLGKASPARSGD-----
ELAGVAARTAEERVRAQMALADVPLKTILAD-------PVVPYESDEVTRLICDSHDAAA
FAPVAHLTVGGLRDWLLSEQA---ATPVLAALAPGITPEMAAAVSKLMRVQDLITVAAKC
RVVTRFRSTIGLAGRMSTRLQPNHPTDDLKGIAASILDGLSLGSGDAVIGVNPASDNVAG
LEAMLHMLDRIRERYQIP--TQTCVLAHVTTQMEAMRMG-APVDLVFQSIAGTEAANASF
GITLAMLDEAHAAARELNRGE------------NVMYFETGQGSALSANAHHG-----VD
QQTCEARAYAVARRYRPLL--------------VNTVVGFIGPEYLYNGKQIQRAGLEDH
FCGKLLGLPMGCDICYTNHAEADQDDMDTLLTLLAAAGCTYIMGVPGADDVMLNYQSTSF
HDALYVRQLLGLRPAPEFEAWLER-----------RPEIAAASW--LL--T---------
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>gi|126440450|ref|YP_001060932.1| ethanolamine ammonia-lyase, large subunit
[Burkholderia pseudomallei 668]
------------------------------------------------MRYTETIGSRTY
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RF------------------------------------ADLKTLLAKASPLRSGD-----
QLAGVAAATEEERVAAKMALASAPLTAFLNE-------AVIPYEDDEVTRLVVDTHSRDA
FAEISHLTVGDFRNWLLSPAA---DAAALERIAPGLTPEMVAAVSKLMRNQDLIAAARKR
RVVTRFRNTVGLPGRMSVRLQPNHPTDDVKGIAASMLDGLMYGCGDAMIGINPATDSLAA
ITKLLAMIDAFRERYRVP--TQSCVLTHVTNTIAAIDKG-APVDLVFQSIAGTEKANASF
GISLALLAEAREAALALKRGT---------VGNNLMYFETGQGSALSANAHHG-----VD
QQTCEVRAYAVARAFEPFL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAQADQDDMDTLLTLLGAAGINFIMGIPGADDVMLNYQSTSF
HDQLYVREVLGLRRAPEFEEWLETMEITD-AHGALRAASARVPL--LA--GAND------
----WMGRCA--------------------------------------------------
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>gi|120555851|ref|YP_960202.1| ethanolamine ammonia lyase large subunit
[Marinobacter aquaeolei VT8]
----------------------------------------------MSGQYTYRMGFQTM
DF------------------------------------RDLGTLMAKATPERSGD-----
HLAGVGAASAEERVLAQMCLADLPLKTFLTD-------ALIPYETDEVTRLIMDSHDATA
FAPVSHLTVGDFRNWLLSDNA---SPEMLARLRPGLTPEMVAAVSKLMRNQDLILVAQKC
QITTAFRNTVGLPGRLSTRLQPNHPTDDMAGIAASILDGLLYGNGDAVIGINPATDNVAQ
TKRLLTMVDEVIQRYDIP--TQSCVLTHVTNTLEAIEQG-APVDLVFQSIGGTEATNQSF
GFNLATLKEAQEAALSLKRGS---------VGQNVMYFETGQGSALSANAHHG-----LD
QQTCEARAYAVARHFDPLL--------------VNTVVGFIGPEYLYDGKQITRAGLEDH
FCGKLLGLPMGCDICYTNHAEADQNDMDNLLTLLGVAGCTFIMGIPGSDDIMLNYQTTSF
HDALYARRVLNLKPAPEFEQWLHAMQIFE-DSDPVSLNNDIPAA--FR--HSLS------
-GPRRRA-----------------------------------------------------
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>gi|109897749|ref|YP_661004.1| ethanolamine ammonia lyase large subunit
[Pseudoalteromonas atlantica T6c]
----------------------------------------------MSQGYRHTVGGTTY
QF------------------------------------TSLAQLMAKATPLRSGD-----
ILAGVAAETEQERVAAQFTLADVALTDFLNE-------ALVPYESDEVTRLIVDNHNKEA
FAPLAHLTIGDFRNWLLSDFA---TSEVLASVCAGITPEMAAAVCKIMRNQDLILVAKKC
QVTTAFRSTIGLPNRLSTRLQPNHPTDDINGIAASMLDGLLYGNGDAVIGINPATDNVTQ
ATHLLHLMDDVIQQYQIP--TQSCVLTHVTNTIECIEAD-APVDLVFQSIGGTQATNSSF
GFDLSTLAEAHAAALSLGRGT---------AGTNVMYFETGQGSALSANGHHG-----LD
QQTCEARAYAVARKFNPLL--------------VNTVVGFIGPEYLYDGKQITRAGLEDH
FCGKLLGLPMGCDVCYTNHAEADQNDMDNLLTLLGVAGCSFIMGIPGSDDIMLNYQTTSF
HDALYLRRVIGARPAPEFEMWLEKMNIMK-NDGQYILSDHVPDV--FA--RSLK------
----ALRGRS--------------------------------------------------
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>gi|34496640|ref|NP_900855.1| ethanolamine ammonia-lyase heavy chain
[Chromobacterium violaceum ATCC 12472]
------------------------------------------------MSHAIAIGPRTY
RF------------------------------------ADLKTLLARASPLRSGD-----
QLAGVAAASAEERVAAQMCLADLPLKVFLNQ-------AVIPYEEDEVTRLILDSHDQAA
FAAVSHLTVGGLRDWLLSDAA---TAETLAALAPGLTPEMAAAVSKLMRNQDLVLAARKC
RVVTAFRNTQGLPGRMGVRLQPNHPADDARAIAAATLDGLLYGAGDAVIGINPAGDSPDD
IRSLLTLLDEVRQRYAIP--TQSCVLTHVTSTLDLMRRG-APVDLVFQSIAGTQKANAGF
GVSLAVLDEAHQAARELKRGT---------VGDNVMYFETGQGSALSANAHWG-----VD
QQTCEARAYAVARRYSPLL--------------VNTVVGFIGPEYLYNGKQIIRAGLEDH
FCGKLLGLPMGCDICYTNHAEADQDDMDALLTLLGAAGVHFIIGVPGADDIMLGYQSTSF
HDALYLRNVLGLKRAPEFEDWLETMEITR--GGRLLPQDRRQRLLAMM--EGVA------
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>gi|171059482|ref|YP_001791831.1| ethanolamine ammonia lyase large subunit
[Leptothrix cholodnii SP-6]
------------------------------------------------MSYAHTIGSRRY
TF------------------------------------DDLRTLLARASPARSGD-----
RLAGVSAASAQERVAAQMALADLPLTTFLHE-------AVVPYEDDEVTRLIVDHHDAAA
FAPVSHLTVGDLRNWLLGDAA---DGASLAALAPGLTPEMVAAVSKLCRLQDLMLIAHKC
TVVTRFRGTIGLPGRLATRLQPNHPTDDSAGIAASLLDGLLHGSGDAVIGINPATDNLPQ
VMRILQMLDGVISRYGIP--TQSCVLTHVTNTLQAIERG-APVDLVFQSIGGTEATNRSF
GIDLAVLGEARAAALSLRRGAVFDDGHGSTMGDNVMYFETGQGSALSAGANHG-----CD
QQTIEARAYAVARHFKPLL--------------VNTVVGFIGPEYLFDGKQIIRAGLEDH
FCAKLLGLPMGCDVCYTNHAEADSDDMDALLTMLCAAGCSFIMGIPGSDDIMLNYQSTSF
HDALVMRQLMGRRAAPEFEAWLQRMGVFE-AGVRSRLADTLPAP--FA--SVLR------
----RLEAA---------------------------------------------------
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>gi|89899397|ref|YP_521868.1| ethanolamine ammonia lyase large subunit [Rhodoferax
ferrireducens T118]
---------------------------------------------MQTHQYTHSVGATTY
SF------------------------------------RDLKDLMAKATPERSGD-----
LLAGVAAHSAQERVVAQMALAEVPLKTFLTE-------VLVPYEDDEITRLIIDSHDATA
FAPVSHLTVGDFRNWLLGDEV---DSAVLTALAPGITPEMAAAVSKIMRNQDLILVAKKC
RVVTKFRNTIGLPGRMATRLQPNHPTDDATGIAASLLDGLLYGSGDAVIGINPATDNVPQ
VIKLVTMMSDIIQQYEIP--TQSCVLTHVTNTIEAINRG-APVDLVFQSIGGTEATNRSF
GVSLDLLGQARSAALSLKRGT---------VGDNVMYFETGQGSALSANAHHG-----VD
QQTCEARAYAVARHFKPLL--------------VNTVVGFIGPEYLFDGKQIIRAGLEDH
FCAKLLGLPMGCDVCYTNHAEADQNDMDVLLTLLGVAGCSFVMGIPGSDDIMLNYQTTSF
HDALYVRRVLGLKPAPEFEAWLQKMQIFS-RDAQFRLNPALPPA--FQ--RALL------
----RLA-----------------------------------------------------
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>gi|218886350|ref|YP_002435671.1| Ethanolamine ammonia lyase large subunit
[Desulfovibrio vulgaris str. 'Miyazaki F']
----------------------------------------------------------MN
VH------------------------------------SPLRELLAKASPLRSGD-----
VLAGVAAASDEERVRAQMLLADVPLKRFLDE-------AVIPYEDDEITRLIMDSHDAAA
FAPVRSYTVGQFRDWLLTGAA---DHASLAALAPGLTPEMVAAASKLMRLQDLVLVASRC
RVVTRFRNTIGLPGHFSARLQPNHPTDDARGILASTIDGLYYGSGDAVIGINPASDSLEN
IARLMHLLDELIARYEIP--TQGCVLTHVTSAMELIRRG-TPLDLCFQSIAGTEKANASF
GISLGLLDEAWQATLELQRGT---------LGDNVMYFETGQGSALSANAHHG-----VD
QQTVECRAYAVARRYRPLL--------------VNTVVGFIGPEYLYNGKQIIRAGLEDH
CCGKLLGLPMGVDICYTNHADADQDDMDALLTLLGTAGCNFIMGVPGADDIMLNYQSTSF
HDAAYLRKLLGRRPAPEFEAWLERMGIHD-RDGNLLAPGGALLG--LE--QRVR------
----QDA-----------------------------------------------------
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>gi|121605520|ref|YP_982849.1| ethanolamine ammonia lyase large subunit [Polaromonas
naphthalenivorans CJ2]
---------------------------------------------MKRHQYTHTAGCRTY
GF------------------------------------HDLKDLMAKATPARSGD-----
LLAGVAAHSAEERAVAQMALAEVPLATFLKE-------ALIPYERDEITRLIIDTHDAPA
FAPVSHLTVGDFRNWLLGDAV---DSEALAALAPGITPEMAAAVAKLMRNQDLILVAKKC
RVVTRFRNTLGLAGRLATRLQPNHPTDDASGIAASLLDGLLYGSGDAVIGINPATDNVPQ
VIRLVTMLNDIISQYAIP--TQSCVLTHVTNTIEAINRG-APVDLVFQSIGGTEATNRSF
GVSLDLLGEARSAALSLNRGT---------LGDNVMYFETGQGSALSANANFG-----ID
QQTCEARAYAVARQFKPLL--------------VNTVVGFIGPEYLFDGKQIIRAGLEDH
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FCAKLLGLPMGCDVCYTNHAEADQNDMDVLLTLLSVAGCNFVMGIPGSDDIMLNYQTTSF
HDALYARRVLGLRPAPEFEAWLQKMDIFS-KDAQFRLNPSLPPA--FH--KALL------
----RLP-----------------------------------------------------
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>gi|119944061|ref|YP_941741.1| ethanolamine ammonia lyase large subunit
[Psychromonas ingrahamii 37]
-----------------------------------------------MANYRYQLGSHVY
QF------------------------------------ASLADVMAKASPLRSGD-----
QLAGVAALSSEQRVVAQMLLADMPLKDFLQE-------MLIPYESDEITRLIIDEHDSGA
FAEIAHLTVGDFRNWLLKETT---TAVELARVRSGITPEMAAAVSKIMRNQDLILVAKKC
HIITQFRNTIGLSGHLSTRLQPNHPTDDVNGIAASLFDGLMYGNGDAVIGINPATDNVQQ
AVKLMKLMDDVIQHYEIP--TQSCVLTHVTNTIEAIELG-APVDLVFQSIGGTEATNQGF
GINLNVLNEAHQAALELKRGT---------VGNNLMYFETGQGSALSANGHHN-----ID
QQTCEARAYAVARKFNPLL--------------VNTVVGFIGPEYLFDGKQIIRAGLEDH
FCGKLLGLPMGCDICYTNHAYADQNDMDNLLTLLGVAECSFIMGIPGSDDIMLNYQTTSF
HDALYARQVLGLRPAPEFDQWLKKMNISS-ADNRFQLSDQLPAS--FA--HPLE------
----MIKEAL--------------------------------------------------
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>gi|146283993|ref|YP_001174146.1| ethanolamine ammonia-lyase large subunit
[Pseudomonas stutzeri A1501]
------------------------------------------------MTYSHSVGGTTW
RF------------------------------------DDLREVMAKASPARSGD-----
LLAGVAAGSDAERVAAQMCLADVPLRRFLEE-------ALIPYESDEVTRLIIDSHDAAA
FAPISHLTVGDFRNWLLGEEA---DESSLKALAPGLTPEMVAAVSKIMRVQDLILVAQKV
RVVTRFRNSIGLAGRMSTRLQPNHPTDDGAGIAASILDGLLYGNGDAVIGINPATDSTAG
ICELLKMLDAVISRYEIP--TQGCILTHVTTSIEAINRG-APLDLVFQSIAGTEAANASF
GINLSTLQEGYEAGLSQKRGT---------LGDNLMYFETGQGSALSANAHHG-----VD
QQTCEARAYAVARRYKPLL--------------VNTVVGFIGPEYLYNGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDMLLTLLGTAGINFIMGIPGSDDVMLNYQTTSF
HDALYVRQVLGLRPAPEFEEWLAKMQILRQDGNRLQLGRDLPEA--FR--RALE------
----QQA-----------------------------------------------------
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>gi|17547846|ref|NP_521248.1| putative ethanolamine ammonia-lyase heavy chain
protein [Ralstonia solanacearum GMI1000]
-----------------------------------------------MARFSHTLGHETY
RF------------------------------------DNLRDVLAKASPARSGD-----
ALAGIAAASAAERVAAQMALAEIPLRHFLDE-------AVIPYEADEVTRLIVDTHDAAA
FAPVSHLTVGDFRDWLLGDAA---DEAALAALAPGLTPEMAAAVSKLMRVQDLILVAQKT
RVVTRFRNTIGLRGRMATRLQPNHPTDDPAGIAASLLDGLMYGSGDAVIGVNPVSDSTAA
ICDLLGMLDAVIRRYDIP--TQACVLTHVTTTLEAIRRG-MPVDLVFQSIAGTEAANASF
GVSLALLHEARDAALGLQRGT---------VGDNVMYFETGQGSALSANAHHG-----VD
QQTCEARAYAVARRFRPLL--------------VNTVVGFIGPEYLYDGKQILRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDTLLTLLGAAGVNYIMGIPGSDDVMLNYQTTSF
HDALYVRRVLGLRPAPEFEDWLARMGICTAGDGRIALADGLPDP--FR--RAVA------
----QLA-----------------------------------------------------
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>gi|110639427|ref|YP_679636.1| ethanolamine ammonia-lyase heavy chain [Cytophaga
hutchinsonii ATCC 33406]
-------------------------------------------------MYKHTVSQHVF
TF------------------------------------DSLTELMAKASPLRSGD-----
QLAGIAAGSYQERIAAQMALADLPLTTFLQE-------PLIPYESDEVTRLIFDTHEHTA
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FTAIAHLTVGDFRNFLLSNNT---HTSQLTALQKAITPEMAAAVSKIMNVQDLILVSSKC
EIITRFRNTIGVKGCMSTRLQPNHPTDDLKAIMASVLDGLFYGSGDAVIGINPATDHIST
QVQLLKLIDAVREQYAIP--TQSCILSHITNTILAIEQG-APVDLVFQSIGGTEKTNSSF
GINLSLLQEGYEAALSLGRGT---------IGNNVMYFETGQGSSLSANAHYG-----ID
QQTLEARAYAVARAFNPLL--------------VNTVVGFIGPEYLFDGKQIIRAGLEDH
FCGKLMGLPMGCDICYTNHADADQDDMDALLTLLGVAGCNFIMGVPGSDDIMLNYQSTSF
HDALYIRKLLNVKPAPEFEEWLLKMGIMN-TQHEITV---------HR--IYCG------
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>gi|170719781|ref|YP_001747469.1| ethanolamine ammonia lyase large subunit
[Pseudomonas putida W619]
-----------------------------------------------MASFVHTVGHLVY
RF------------------------------------DSLKEVMAKASPARSGD-----
YLAGVAAVNDGERVAAQMALANIPLSHFLSE-------ALIPYEQDEVTRLIIDTHDAQA
FAPVSHLTVGGLRDWLLSDEA---NEDSLHALAPGLTPEMAAAVSKIMRVQDLVLVAQKI
RVVTRFRGTMGLRGRLSTRLQPNHPTDEPAGIAASILDGLLYGNGDAMIGINPATDSIAS
ICAMLEMLDAIIQRYDIP--TQACVLTHVTTSIEAINRG-VPLDLVFQSIAGTEAANAGF
GINLNVLQEGYEAGLSLKRGT---------LGQNLMYFETGQGSALSANAHHG-----VD
QQTCETRAYAVARHFKPFL--------------VNTVVGFIGPEYLYNGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDTLLTLLGVAGINFIMGIPGSDDIMLNYQTTSF
HDALYARQTLGLKPGPEFEAWLQRTGIFTQADGRVRFGDNLPPA--FR--QALA------
----QLA-----------------------------------------------------
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>gi|167647493|ref|YP_001685156.1| ethanolamine ammonia lyase large subunit
[Caulobacter sp. K31]
------------------------------------------------MAYSATLGSTTW
TF------------------------------------ETLADLLAKASPLRSGD-----
VLAGLAATSAQQNVAAKMALADLPLKTFLTQ-------ALVPYETDEVTRLILDGHDAAA
FAPVASLTVGEFRDWLLSEIA---TPAALARLAPGLTPEMVAAVSKLMRNQDLILAASKC
KVTTRFRDTIGLPGTMAVRLQPNHPTDDPAGITASILDGLLYGCGDAVIGINPASDSLTV
LGDLTRLMDDLIQRFEIP--TQSCVLTHVTTAIQLIERG-APVDLVFQSIAGTESANASF
GVTLALLKEGLDAGRSLNRGT---------VGDNVMYFETGQGSALSAGAHHG-----VD
QQTLEARAYGVARAFEPLL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGAPLGVDVCYTNHAEADQDDMDSLLTLLATAGVTFIMGVPGADDVMLNYQSTSF
HDALYVRELLGLKRAPEFEAWLQRLRIVG-ADGRLAPRAAGHPL--LT--AGVSG-----
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>gi|206577600|ref|YP_002240182.1| putative ethanolamine ammonia-lyase, large subunit
[Klebsiella pneumoniae 342]
-------------------------------------------------MYKTTLSGQVW
RF------------------------------------DSLKTLMAKASPARSGD-----
ALAGVIATSAEERMAAKMALAEVPLTDILDN-------PLIPYEQDEVTRLILDTHDAQG
FAALRHLTVGDFRDWLLDDAT---DTATLQRVARAITPEMAAAVSKLMRNQDLILAASKC
QVVTRFRNTIGLPGHLSVRLQPNHPTDDLKGIAASMLDGLLYGAGDAVIGINPASDSLPV
LAQLNVMLDDIIQRFAIP--TQSCILTHVTNTLQLIERG-APVDLVFQSVAGTEAANSGF
GINLAMLQEAREAALSLRRGT---------LGNNVMYFETGQGSCLSANAHHG-----VD
QQTCEARAYAVARHFEPLL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLMGLPIGCDVCYTNHAEADQDDMDTLLTLLCTAGLTFLIGVPGADDIMLNYQSTSF
HDALYARRLLGLKHAPEFADWLAKMQIID-PHGTLRLTDARHPL--LS--VLPQGASV--
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>gi|182677067|ref|YP_001831213.1| ethanolamine ammonia lyase large subunit
[Beijerinckia indica subsp. indica ATCC 9039]
------------------------------------------------MPYSSTIAGTHY
CF------------------------------------PDLRTLLARASPLRAGD-----
RLAGLTADTDAERVAARMTLADLPLKTFLNE-------PLIPYEQDEVTRLIVDTHDAEA
FAPVAAMTVGEFRDFLLSDAT---TTESLAKLAPGLTPEMAAAVSKLMRNQDLIAVARKI
SVITHFRTTIGLPGRLSVRLQPNHPSDDLAGIGASILDGLLYGCGDACIGINPATDSAAQ
ALTLLQRIEELRLRFDIP--IQACVLAHVTTTLDVIAQG-GPVDLVFQSIAGSEAANRAF
GVDLPLLDEAHAAVRGLNRAD---------ASANLLYFETGQGSALSSDAHYD-----VD
QQTMEARAYAVARRYSPLL--------------VNTVVGFIGPEYLYDGKEIIRAGLEDH
FCGKLLGLPMGVDVCYTNHAEADSDDMDNLMTLLGVAGCTYIMGVPGADDIMLGYQSTSY
HDALYLRSVLGLKPAPEFEAWLLKMGIMD-SQSRIRPALQAQKL--LA--AFP-------
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>gi|124267603|ref|YP_001021607.1| ethanolamine ammonia-lyase heavy chain
[Methylibium petroleiphilum PM1]
------------------------------------------------MAYAHSIGPRRY
SF------------------------------------DDLRTLMARASPARSGD-----
ELAGVAARSSEERAAAQIALAALPLKTFLND-------ALVPYEDDEVTRLILDSQDAAA
FAPIAHLTVGDLRDWLLSDAV---DGDTLRAAAPGLTPEMTAAVSKIMRNQDLILVARKC
RVRTRFRDTIGLPGRLSTRLQPNHPTDNAAGIAASTLDGLLYGSGDAVIGINPATDNVAQ
VTRLLQMLDAVIQRYEIP--TQSCVLTHVTNTLQCIERG-APVDLVFQSIGGTEATNRSF
GIDLALLAEAHDAALSLQRGA--LFSDDGQRGRNVMYFETGQGSALSAQAHHG-----CD
QQTIEARAYAVARRFEPLL--------------VNSVVGFIGPEYLYDGKQIIRAGLEDH
FCAKLLGLPMGCDICYTNHAEADQNDMDVLLTLLGVAGCSFIMGIPGSDDVMLNYQTTSF
HDALYARRVLGLRPAPEFERWLEAMRITE-PGAPDRLTDLMPPA--LA--RLLE------
----HPR-----------------------------------------------------
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>gi|167031604|ref|YP_001666835.1| ethanolamine ammonia lyase large subunit
[Pseudomonas putida GB-1]
-----------------------------------------------MASFVHTVGHLVY
RF------------------------------------DSLKDVMAKASPARSGD-----
YLAGVAASNDGERVAAQMALANIPLTHFLNE-------ALIPYEDDEVTRLIVDTHDAQA
FAPVSHLTVGGLRDWLLSEEA---NEDSLRALAPGLTPEMAAAVSKIMRVQDLVLVAQKI
RVVTRFRGTMGLRGRLSTRLQPNHPTDEPAGIAASILDGLLYGNGDAMIGINPATDSIAS
ICALLEMLDAIIQRYDIP--TQSCVLTHVTTSIEAINRG-VPLDLVFQSIAGTEAANAGF
GINLNVLQEGYEAGLSLKRGT---------LGQNLMYFETGQGSALSANAHHG-----VD
QQTCETRAYAVARHFKPFL--------------VNTVVGFIGPEYLYNGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDTLLTLLGVAGINFIMGIPGSDDIMLNYQTTSF
HDALYARQTLGLKPGPEFEAWLARTGIFTQADGRVRFGDNLPPA--FR--QALA------
----QLA-----------------------------------------------------
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>gi|26987281|ref|NP_742706.1| ethanolamine ammonia lyase large subunit [Pseudomonas
putida KT2440]
-----------------------------------------------MASFVHTVGHLVY
RF------------------------------------DSLKEVMAKASPARSGD-----
CLAGVAASNDAERVAAQMALANIPLTHFLNE-------ALIPYEADEVTRLIIDTHDAQA
FAPVSHLTVGGLRDWLLSEEA---NEDSLRALAPGLTPEMAAAVSKIMRVQDLVLVAQKI
RVVTRFRGTMGLRGRLSTRLQPNHPTDEPAGIAASILDGLLYGNGDAMIGINPATDSIAS
ICALLEMLDAIIQRYDIP--TQSCVLTHVTTSIEAINRG-VPLDLVFQSIAGTEAANAGF
GINLNVLQEGYEAGLSLKRGT---------LGQNLMYFETGQGSALSANAHHG-----VD
QQTCETRAYAVARHFKPFL--------------VNTVVGFIGPEYLYNGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDTLLTLLGVAGINFIMGIPGSDDIMLNYQTTSF
HDALYARQTLGLKPGPEFEAWLARTGIFTQADGRVRFGDNLPPA--FR--QALA------
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----QLA-----------------------------------------------------
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>gi|220921383|ref|YP_002496684.1| Ethanolamine ammonia lyase large subunit
[Methylobacterium nodulans ORS 2060]
------------------------------------------------MAYRHVVGPRSW
VF------------------------------------SDLAELMAKASPIRSGD-----
RLAGIAAGSAEESVAARWCLAEVPLADLVNR-------PLIPYEEDDVTRLILDTHDAGA
FAPIAHVTVGGFREFLLT--A---DTAALAALAPGITPEIAAAVSKIMRNQDLILVARKC
RVVTRFRNTIGLPGTMAVRLQPNHPSDDPAGITAAILDGLSYGCGDAVIGINPASDSVQA
LTRLLHLLDDLIARFAIP--TQGCVLAHVTTTLEAIGRG-VPVDLVFQSIAGTQGANAAF
GVTLPLLRQAQEAALSLRRGT---------LGDNVMYFETGQGSALSAEAHHG-----ID
QQTLEARAYAVARAFRPLL--------------VNTVVGFIGPEYLYDGKEIIRAGLEDH
FCGKLMGVPLGCDVCYTNHAEADQDDMDTLLTLLGAAGVTYIMGVPGADDVMLNYQSTSF
HDQLYLREVLGLKRVPEFAAWLERIGLTD-AAGALIPGGGTPLLAAAP--GLAA------
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>gi|104779889|ref|YP_606387.1| ethanolamine ammonia-lyase, heavy chain [Pseudomonas
entomophila L48]
-----------------------------------------------MASFVHTVGHQIY
RF------------------------------------DSLKEVMAKASPARSGD-----
YLAGVAASNDGERVAAQMALADIPLTHFLNE-------ALIPYEQDEVTRLIIDTHDKQA
FAPVSHLTVGGLRDWLLGEQA---DEHSLRALAPGLTPEMAAAVSKIMRVQDLVLVAQKI
RVVTQFRGTMGLRGRLSTRLQPNHPTDEPAGIAASILDGLLYGNGDAMIGINPATDSIAS
ICALLEMLDAIIQRYQIP--TQACVLTHVTTSIEAINRG-VPLDLVFQSIAGTEAANASF
GINLNVLQEGYEAGLSLKRGT---------VGQNLMYFETGQGSALSANAHHG-----VD
QQTCETRAYAVARHFKPFL--------------VNTVVGFIGPEYLYNGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDTLLTLLGVAGINFIMGIPGSDDIMLNYQTTSF
HDALYARQTLGLKPGPEFEAWLERTGIFTQADGRVRFGDNLPPA--FR--HALA------
----HLA-----------------------------------------------------
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>gi|159898781|ref|YP_001545028.1| ethanolamine ammonia lyase large subunit
[Herpetosiphon aurantiacus ATCC 23779]
-----------------------------------------------MTSYQHSIRQRQY
QF------------------------------------DSLKTLLAKATPERSGD-----
ALAGLIAASAEERVAAQWCLADVPLTTFLNE-------VVIPYETDEVTRLIIDSHDQAA
FAPIRHLTVGGLREWLLDYRT---DSQQLAAVAAGITPEMAAAVSKIMRNQDLIAVAKKC
QVITRFRNTLGLAGRFSSRLQPNHPTDDPQGIAAAIFDGLLYGCGDAVIGINPATDSPQA
MTSLLHLIDELRQRYAMP--VQSCVLAHVTTALQVIELG-APVDLVFQSIAGTEAANRSF
GIDLALLHEANQAARGLQRGT---------IGNNVMYFETGQGSALSANAHHG-----VD
QQTCEARAYAVARAFEPLL--------------LNTVVGFIGPEYLYDGKQITRAALEDH
FCGKLLGLPMGCDACYTNHAEADQNDIDNLLVLLASAGCTYVMGVPGADDIMLNYQSSSY
HDIRFVQTTLGLRPAPEFEAWLQQLGISD-QAGRLI-ANERHRL--LQ--SAAQ------
----LGAL----------------------------------------------------
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>gi|146341484|ref|YP_001206532.1| ethanolamine ammonia-lyase heavy chain
(ethanolamine ammonia-lyase large subunit) [Bradyrhizobium sp. ORS278]
------------------------------------------------MGFSHTLGGTTY
RF------------------------------------DDLRTLLAKATPLRSGD-----
VLAGLAAQDAAERVAARMALADLPLRHFLNE-------AVIPYESDEVTRLIVDQHDGAA
FAAIASLTVGSFREWLLSDAT---DATMLAAVSLGLTPEMVAAVCKIMRLQDLVTVAAKC
EVITRFRCTIGLKGTMSTRLQPNHPLDDPKGVAASILDGLMYGVGDATIGMNPASDDVDT
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MVRLLDMIETLRLASDAP--IQSCVLAHVTTALKAIERR-APVDLVFQSLAGTEEANRGF
GITLALLDEALAAANSLQRCP---------AGGNVMYFETGQGSELSSSGHCG-----VD
QQTLEARCYAVARRYRPLL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGLPMGCDVCYTNHAEADQDDMDALLTLLGIAGCTYIMGVPGADDIMLNYQSTSF
HDALYVRKVLGKRAAPEFEAWLAATGISD-AKGELRFEPERLMPALPL--LGAE------
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>gi|148545832|ref|YP_001265934.1| ethanolamine ammonia lyase large subunit
[Pseudomonas putida F1]
-----------------------------------------------MASFVHTVGHLVY
RF------------------------------------DSLKDVMAKASPARSGD-----
CLAGVAASNDGERVAAQMALANIPLTHFLNE-------ALIPYEADEVTRLIIDTHDAQA
FAPVSHLTVGGLRDWLLSEEA---NEDSLRALAPGLTPEMAAAVSKIMRVQDLVLVAQKI
RVVTRFRGTMGLRGRLSTRLQPNHPTDEPAGIAASILDGLLYGNGDAMIGINPATDSIAS
ICALLEMLDAIIQRYDIP--TQSCVLTHVTTSIEAINRG-VPLDLVFQSIAGTEAANAGF
GINLNVLQEGYEAGLSLKRGT---------LGQNLMYFETGQGSALSANAHHG-----VD
QQTCETRAYAVARHFKPFL--------------VNTVVGFIGPEYLYNGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDTLLTLLGVAGINFIMGIPGSDDIMLNYQTTSF
HDALYARQTLGLKPGPEFEAWLARTGIFTQADGRVRFGDNLPPA--FR--QALA------
----QLA-----------------------------------------------------
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>gi|94314821|ref|YP_588030.1| ethanolamine ammonia-lyase heavy chain [Ralstonia
metallidurans CH34]
------------------------------------------------MAFTHTVGVRRH
VF------------------------------------DDLRTLLAKASPARSGD-----
ALAGIAAASEEERMAARMALADMPLAHCLAE-------PLVPYEADEVTRLIVDSHDAQA
FAALASLTVGEFRDWLLRHDT---DTATLARVAPGVTPEMAAAVSKLMRNQDLVAVARKC
AVVTAFRNTIGLPGRLSVRLQPNHPTDDPRGIAASIIDGLLFGCGDATIGINPASDNLGA
ITTLLKLLDDIRIRYEIP--TQSCVLTHVTNTLRVMELG-APVDLVFQSVAGSQAANAAF
GISLALLEEARQAALSLRRGT---------VGHNVMYFETGQGSALSANAHHG-----VD
QQTMEARAYAVARRFEPLL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGVPMGCDVCYTNHAEADQDDMDNLLTLFGVAGINFIMGVPGADDIMLNYQSTSF
HDALYLREVLGLRPAPEFEAWLRKMGIVD-AGGRLLEPGTRQAL--LT--MADT------
----L-------------------------------------------------------
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>gi|152968880|ref|YP_001333989.1| ethanolamine ammonia-lyase, heavy chain
[Klebsiella pneumoniae subsp. pneumoniae MGH 78578]
-------------------------------------------------MYKTTLSGQVW
RF------------------------------------DSLKTLMAKASPARSGD-----
ALAGIIATSAEERMAAKMALAEVPLTDILDN-------PLIPYEQDEVTRLILDTHDAQG
FAALRHLTVGDFRDWLLDDAT---DTATLQRVARAITPEMAAAVSKLMRNQDLILAASKC
QVVTRFRNTIGLPGHLSVRLQPNHPTDDLKGIAASMLDGLLYGAGDAVIGINPASDSLPV
LAQLNVMLDDIIQRFAIP--TQSCILTHVTNTLQLIERG-APVDLVFQSVAGTEAANSGF
GINLAMLQEAREAALSLRRGT---------LGNNVMYFETGQGSCLSANAHHG-----VD
QQTCEARAYAVARHFEPLL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLMGLPIGCDVCYTNHAEADQDDMDTLLTLLCAAGLTFLIGVPGADDIMLNYQSTSF
HDALYARRLLGLKHAPEFADWLAKMQIID-PHGALRLTDARHPL--LS--VLPQ----GA
SV----------------------------------------------------------
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>gi|77461212|ref|YP_350719.1| ethanolamine ammonia-lyase heavy chain [Pseudomonas
fluorescens PfO-1]
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-----------------------------------------------MAAFAHTVGAQTY
RF------------------------------------DSLKDVMAKASPARSGD-----
FLAGVAALNDGERVAAQMALADIPLTHFLQE-------ALIPYEADEVTRLIIDSHDKQA
FAVVSHLTVGGFRDWLLSEAA---DESSLRALAPGLTPEMVAAVSKIMRVQDLVLVAQKI
RVVTKFRGTLGLRGRLSTRLQPNHPTDEPSGIAASILDGLLYGNGDAMIGINPATDSIAS
ICAMLEMLDAIIQRYDIP--TQACVLTHVTTSIEAINRG-VPLDLVFQSIAGTEAANASF
GINLNILQEGYEAGLSLNRGT---------LGQNLMYFETGQGSALSANAHHG-----VD
QQTCETRAYAVARHFKPFL--------------VNTVVGFIGPEYLYNGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDTLLTLLGVAGINFIMGIPGSDDIMLNYQTTSF
HDALYARQTLGLKPAPEFEQWLAKMGIFTQADGKVRFGNNLPPA--FR--QALA------
----QLG-----------------------------------------------------
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>gi|66043895|ref|YP_233736.1| ethanolamine ammonia lyase large subunit [Pseudomonas
syringae pv. syringae B728a]
-----------------------------------------------MASFSHSVGAQTY
RF------------------------------------DSLKEVMAKASPARSGD-----
YLAEVAAQNDGERVAAQMALANIPLKHFLEE-------ALIPYEQDEVTRLIIDTHDKLA
FAPVSHLTVGGFRDWLLSDKA---DETSLRALAPGLTPEMAAAVSKIMRVQDLVLVAQKI
RVVTRFRNTMGLRGRLSTRLQPNHPTDDPSGIAASVLDGLLYGNGDAMIGINPATDSTSS
IVALLEMLDAIVQRYEIP--TQSCVLTHVTTSIEVINRG-VPVDLVFQSITGTEAANASF
GISLKLLQEGYEAGLSLNRGT---------LGQNLMYFETGQGSALSANAHHG-----VD
QQTCETRAYAVARHFNPFL--------------VNTVVGFIGPEYLYNGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDTLLTLLGVAGINFIMGIPGSDDIMLNYQTTSF
HDALYARQSLGLRPAPEYEAWLEKMGIFTQADGRVRFGDSLPPA--FR--QALA------
----HLA-----------------------------------------------------
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>gi|28867955|ref|NP_790574.1| ethanolamine ammonia-lyase, heavy subunit [Pseudomonas
syringae pv. tomato str. DC3000]
-----------------------------------------------MASFSHSVGAQTY
RF------------------------------------DSLKEVMAKASPARSGD-----
YLAEVAAQNDAERVAAQMALANIPLKHFLEE-------ALIPYEQDEVTRLIIDTHDKLT
FAPVSHLTVGGFRDWLLSDQA---DETSLRALAPGLTPEMAAAVSKIMRVQDLILVAQKI
RVVTRFRNTMGLRGRLSTRLQPNHPTDDPSGIAASVLDGLLYGNGDAMIGINPATDSTSS
IVALLEMLDAIIQRYDIP--TQSCVLTHVTTSIEVINRG-VPVDLVFQSITGTEAANASF
GINLKLLQEGYEAGLSLNRGT---------LGQNLMYFETGQGSALSANAHHG-----VD
QQTCETRAYAVARHFNPFL--------------VNTVVGFIGPEYLYNGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDTLLTLLGVAGINFIMGIPGSDDIMLNYQTTSF
HDALYARQSLGLRPAPEYEAWLEKMGIFTQTDGRVRFGDSLPPA--FR--QALA------
----HLA-----------------------------------------------------
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>gi|53724039|ref|YP_104486.1| ethanolamine ammonia-lyase heavy chain [Burkholderia
mallei ATCC 23344]
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-------------------------------------------MLAKASPLRSGD-----
QLAGVAASTEEERVAAKMALASAPLTAFLNE-------AVIPYEDDEVTRLVVDTHSRDA
FAEISHLTVGDFRNWLLSPAA---DAAALERIAPGLTPEMVAAVSKLMRNQDLIAAARKR
RVVTRFRNTVGLPGRMSVRLQPNHPTDDVKGIAASMLDGLMYGCGDAMIGINPATDSLAA
ITKLLAMIDAFRERYRVP--TQSCVLTHVTNTIAAIDKG-APVDLVFQSIAGTEKANASF
GISLALLAEAREAALALKRGT---------VGNNLMYFETGQGSALSANAHHG-----VD
QQTCEVRAYAVARAFEPFL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAQADQDDMDNLLTLLGAAGINFIMGIPGADDVMLNYQSTSF
HDQLYVREVLGLRRAPEFEEWLETMEITD-AHGALRAASARVPL--LA--GAND------
----WMGRCA--------------------------------------------------
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>gi|218530187|ref|YP_002421003.1| Ethanolamine ammonia lyase large subunit
[Methylobacterium chloromethanicum CM4]
------------------------------------------------MPYRHTVGPRTH
VF------------------------------------ADLATLMAKATPVRSGD-----
CLAGIAAESAEENMAARWCLAEVPLKEILAR-------PLIPYDEDDVTRLILDDHDEAA
FAEIAALTVGDFREFLLT--A---SSETLARIAPGVTPEIAAAVSKIMRNQDLILVAKKC
RVVTRFRNTIGLPGTLAVRLQPNHPTDDPAGVTASILDGLSYGCGDAVIGINPVSDSIQT
MGTLLRLFDGIIGRLEIP--TQACVLTHVTTTLDAMNRG-LPVDLVFQSIAGTQRANASF
GVTLPILQEAHEAALALKRGT---------LGDNVMYFETGQGSALSADAHHG-----ID
QQTLEARAYAVARRYRPLL--------------VNTVVGFIGPEYLYNGKEIIRAGLEDH
FCGKLMGVPLGVDVCYTNHAEADQDDMDTLLTLLGAAGCTYVMGIPGADDVMLNYQSTSF
HDQLYIREVLGLRRAPEFEEWLARIGLTD-ADGTLLPGGAEARL--LT--AAPE------
----LAA-----------------------------------------------------
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>gi|163851379|ref|YP_001639422.1| ethanolamine ammonia lyase large subunit
[Methylobacterium extorquens PA1]
------------------------------------------------MPYRHTVGPRTH
VF------------------------------------ADLATLMAKATPVRSGD-----
CLAGIAAESAEENMAARWCLAEVPLREILAR-------PLIPYDEDDVTRLILDDHDEAA
FAEIAALTVGDFREFLLT--A---SSETLARIAPGVTPEIAAAVSKIMRNQDLILVAKKC
RVVTRFRNTIGLPGTLAVRLQPNHPTDDPAGVTASILDGLSYGCGDAVIGINPVSDSIQT
MGTLLRLFDGIIGRLEIP--TQACVLTHVTTTLDAMNRG-LPVDLVFQSIAGTQRANASF
GVTLPILQEAHEAALALKRGT---------LGDNVMYFETGQGSALSADAHHG-----ID
QQTLEARAYAVARRYRPLL--------------VNTVVGFIGPEYLYNGKEIIRAGLEDH
FCGKLMGVPLGVDVCYTNHAEADQDDMDTLLTLLGAAGCTYVMGIPGADDVMLNYQSTSF
HDQLYIREVLGLRRAPEFEEWLARIGLTD-ADGALLPGGAEARL--LT--AAPE------
----LAA-----------------------------------------------------
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>gi|170739179|ref|YP_001767834.1| ethanolamine ammonia lyase large subunit
[Methylobacterium sp. 4-46]
------------------------------------------------MVYRHVVGPRTW
LF------------------------------------ADLAELMAKASPIRSGD-----
RLAGLAAGSAEESVAARWCLAEVPLADLMNR-------PLIPYEADDVTRLILDSHDAAA
FAAIAHLTVGDFREFLLT--A---DAAALARIAPGITPEIAAAVSKIMRNQDLILVARKC
RVVTRFRNTIGLPGTMAVRLQPNHPGDDPAGITAAILDGLAYGCGDAVIGINPVSDSVQA
ISRLLHLLDDLIARLEIP--TQGCVLTHVTTTLEAIRRG-VPVDLVFQSIAGTQAANASF
GVTLPLLAEAREAALSLKRGT---------LGEDVMYFETGQGSALSADAHHG-----ID
QQTLEARAYAVARAFRPLL--------------VNTVVGFIGPEYLYDGKEIIRAGLEDH
FCGKLMGVPLGCDVCYTNHAEADQDDMDTLLTLLGAAGVSYVMGVPGADDVMLNYQSTSF
HDQLYLREVLGLKRAPEFAAWLARIGLTD-AAGALLPGGA-RPL--LA--AAPG------
----LAA-----------------------------------------------------
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>gi|15599219|ref|NP_252713.1| ethanolamine ammonia-lyase large subunit [Pseudomonas
aeruginosa PAO1]
-----------------------------------------------MARFTHSVGGETY
RF------------------------------------DSLKDVMAKASPARSGD-----
FLAGVAASNDGERVAAQMALADIPLKHFLDE-------ALIPYEDDEVTRLIIDTHQRDA
FAPVSHLTVGGFRDWLLGDAA---DEASLRALAPGLTPEMAAAVSKIMRVQDLVLVAQKI
RVVTRFRNTLGLRGRLSTRLQPNHPTDDPAGIAASILDGLLFGNGDAMLGINPATDSMAS
ICALLEMLDAIIQRYEIP--TQACVLTHVTSSIEAINRG-VPLDLVFQSIAGTEAANASF
GISLKILQEGYEAGLSQKRGT---------LGNNLMYFETGQGSALSANAHHG-----VD
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QQTCETRAYAVARHFKPFL--------------VNTVVGFIGPEYLYNGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDMLLTLLGVAGINFIMGIPGSDDVMLNYQTTSF
HDALYARQTLGLKPAPEFEDWLQRMGIFTQADGRIRFGDELPPA--FR--QALA------
----QLA-----------------------------------------------------
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>gi|71735666|ref|YP_276772.1| ethanolamine ammonia-lyase, heavy subunit [Pseudomonas
syringae pv. phaseolicola 1448A]
-----------------------------------------------MASFSHSVGAQTY
RF------------------------------------DSLKEVMAKASPARSGD-----
YLAEVAAQSDGERVAAQMTLANIPLKHFLEE-------ALIPYEQDEVTRLIIDTHDKLA
FAPVSHLTVGGFRDWLLSEQA---DETSLRALAPGLTPEMAAAVSKIMRVQDLVLVAQKI
RVVTRFRNTMGLRGRLSTRLQPNHPTDDPSGIAASVLDGLLYGNGDAMIGINPATDSTSS
IVALLEMLDAIVQRYEIP--TQSCVLTHVTTSIEVINCG-VPVDLVFQSITGTEAANASF
GISLKLLQEGYEAGLSLNRGT---------LGKNLMYFETGQGSALSANAHHG-----VD
QQTCETRAYAVARHFNPFL--------------VNTVVGFIGPEYLYNGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDTLLTLLGVAGINFIMGIPGSDDIMLNYQTTSF
HDALYARQSLGLRPAPEYEAWLEKMGIFTQTDGRVRFGDSLPPA--FR--QALA------
----HLA-----------------------------------------------------
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>gi|217978558|ref|YP_002362705.1| Ethanolamine ammonia lyase large subunit
[Methylocella silvestris BL2]
------------------------------------------------MTYAKSVGGRTY
RF------------------------------------PDLKTLLAKASPARSGD-----
YLAGVAAEDDSERAAAQMALSDTPLKAFLNE-------VVIPYEDDEVTRLIIDRHDADA
FAPVSGLTVGDFRNWLLGAEA---NEAALTKLSPGVTPEMAAAVSKLMRVQDLILVARKC
RVVTRLRNTIGLAGRLSTRLQPNHPTDDPAGIAASILDGLLYGSGDAVIGINPATDSVPA
VCALLTMLDEVIHKYEIP--TQSCVLTHVTTSIEAINRG-VPVDLVFQSVAGTEAANKSF
GVDLAVLKEGREAALALKRGT---------VGDNVMYFETGQGSALSANAHHG-----VD
QQTCEARAYAVAREFHPLL--------------VNTVVGFIGPEYLYNGKQIIRAGLEDH
FCGKLLGLPMGCDICYTNHAEADQDDMDMLLTLLPAAGCSFIMGIPGSDDIMLNYQTTSF
HDALYVREVLGLRMAPEFESWLIRKGVFE-GADHPRPRKALSSM--FA--PALA------
----RIA-----------------------------------------------------
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>gi|152994514|ref|YP_001339349.1| ethanolamine ammonia lyase large subunit
[Marinomonas sp. MWYL1]
-----------------------------------------MSKPNSTFQFKNIVGERTF
GF------------------------------------VDLADLMAKATPARSGD-----
RLAGVAAQSAEERAIAQMTLADVPLSLFLEQ-------ALVPYEEDEITRLILDDHDKSA
FSAISHLTVGGFRDWLLSDLA---SSEILIQIRAGVTPEMAAAVSKIMRNQDLILVAKKC
HVKTAFRNTIGLPGHLSTRLQPNHPTDDLTGIAASMLDGLLYANGDAVIGINPATDNVQQ
ATRLIKMMDEVIQHYEIP--TQSCVLTHVTNTIECIEQG-APVDLVFQSIGGTQATNDSF
GFNLATLAEAQAAALSLNRGT---------VGNNVMYFETGQGSALSANANHG-----LD
QQTCEARAYAVARKFNPLL--------------VNTVVGFIGPEYLYDGKEITRAGLEDH
FCGKLLGLPMGCDVCYTNHAEADQNDMDNLLTLLGVAGCTFVMGIPGSDDIMLNYQTTSF
HDALYARRVLGLKPAPEFDLWLAKMEIFK-NNEQFTLNHQLPDA--FH--KSLN----RM
IGGKS-------------------------------------------------------
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>gi|152984792|ref|YP_001346468.1| ethanolamine ammonia-lyase large subunit
[Pseudomonas aeruginosa PA7]
-----------------------------------------------MARFTHSVGGETY
RF------------------------------------DSLKDVMAKASPARSGD-----
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FLAGVAASNDGERVAAQMALADIPLKHFLDE-------ALIPYEDDEVTRLIIDTHQRDA
FAPVSHLTVGGFRDWLLGDAA---DEASLRALAPGLTPEMAAAVSKIMRVQDLVLVAQKI
RVVTRFRNTLGLRGRLSTRLQPNHPTDDPAGIAASILDGLLFGNGDAMLGINPATDSMAS
ICALLEMLDAIIQRYEIP--TQACVLTHVTSSIEAINRG-VPLDLVFQSIAGTEAANASF
GISLKILQEGYEAGLSQKRGT---------LGNNLMYFETGQGSALSANAHHG-----VD
QQTCETRAYAVARHFKPFL--------------VNTVVGFIGPEYLYNGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDMLLTLLGVAGINFIMGIPGSDDVMLNYQTTSF
HDALYARQTLGLKPAPEFEDWLQRMGIFTQADGRIRFGEELPPA--FR--QALA------
----QLA-----------------------------------------------------
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>gi|91977449|ref|YP_570108.1| ethanolamine ammonia lyase large subunit
[Rhodopseudomonas palustris BisB5]
------------------------------------------------MRYRTAIDQQLF
AF------------------------------------DSLKQVMAYASPARSGD-----
YLAGIGAATAQERMAARHVLAEVPLKQFLNE-------ALIPYEDDNITRLIIDGHDAKA
FAPVSHMTVGDFRNWLLSEQA---TTQALAALAQGLTPEMVAAVSKIMRNQDLIAVARKV
RVVTRFRNTIGLAGHLAVRLQPNHPTDDLRGVAASTLDGLLMGSGDAVIGLNPASDSLPV
LGDLLRMLDEVIHRFEIP--TQSCVLTHVTNTVQLINDG-APVDLVFQSIGGTEKTNLSF
GVTPEILHEAREAALSLKRGT---------VGDNVMYFETGQGSALSADANFG-----VD
QQTCEARAYALARLYQPLL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGLPLGCDICYTNHAEADQDDMDTLLVLLGAAGISFIMGIPGADDVMLNYQSTSF
HDALFLRDLMNLKRAPEFEMWLQRMQITD-DAGRLRPPSPNPLLGGMG--KLKS------
----LVA-----------------------------------------------------
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>gi|158425188|ref|YP_001526480.1| ethanolamine ammonia-lyase large subunit
[Azorhizobium caulinodans ORS 571]
------------------------------------------------MTYVHQVGSRRF
AF------------------------------------ADLKELMAKATPPRSGD-----
MLAGIAAATAEENVAAKMALADVPLKTFLSE-------ALVPYETDEVTRLIIDGHDAAA
FAPVSAFTVGDFRDWLLSEAA---DSAALARLAPGLTPEMVAAVSKLMRNQDLILIAKKC
RVVTRFRNTIGLPGTLAVRLQPNHPTDDPAGISAAMLDGLLYGCGDAVIGINPASDSLPV
LDRLIKLTAEVIERFDIP--TQSCILTHVTSSIELMNRG-APVDLVFQSIAGTEAANRSF
GIDLAVLKEGTDAARALKRGT---------VGQNAMYFETGQGSALSANAHHG-----VD
QQTLEARAYGVARVFEPLL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGVPLGVDVCYTNHAEADQDDMDTLLTLLAAAGVTYIMGIPGADDVMLNYQSTSF
HDALYVREVFGARRAPEFEGWLERMAITG-PDGRLLPATGSHPL--LG--FATE------
----RAA-----------------------------------------------------
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>gi|188581160|ref|YP_001924605.1| Ethanolamine ammonia lyase large subunit
[Methylobacterium populi BJ001]
------------------------------------------------MPYRHTVGPRTH
VF------------------------------------ADLATLMAKATPVRSGD-----
CLAGIAAESAEENMAARWCLAEVPLKEILAR-------PLIPYEADDVTRLILDDHDEAA
FAEIASLTVGDFREFLLT--A---SSETLARIAPGVTPEIAAAVSKIMRNQDLILVARKC
RVVTRFRNTIGLPGTLAVRLQPNHPTDDPAGVTASILDGLSYGCGDAVIGINPVSDSIQT
MGTLLTLFDSIIERLEIP--TQACVLTHVTTTLDAMNRG-LPVDLVFQSIAGTQRANASF
GVTLPILQEAHEAALALKRGT---------LGDNVMYFETGQGSALSADAHHG-----ID
QQTLEARAYAVARRYRPLL--------------VNTVVGFIGPEYLYDGKEIIRAGLEDH
FCGKLMGVPLGVDVCYTNHAEADQDDMDTLLTLLGAAGCTYVMGIPGADDVMLNYQSTSF
HDQLYIREVLGLRRAPEFEEWLARIGLTD-ASGTLLPGGAESRL--LT--AAPD------
----LAA-----------------------------------------------------
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>gi|116694056|ref|YP_728267.1| ethanolamine ammonia-lyase heavy chain [Ralstonia
eutropha H16]
------------------------------------------------MAYTHTIGTHRH
VF------------------------------------ADLRTLLARASPARSGD-----
ALAGVAAASEQERMAARLALAEVPLKQFLTE-------ALVPYEDDEVTRLILDRHDGAA
FAAIGATTVGDLRNWLLLHET---DSAMLARVAPGITPEMAAAVSKLMRNQDLVAVARKC
QVVTRFRSTVGLPGRLSVRLQPNHPTDDPKGIAASIIDGLLYGCGDATIGVNPASDNLGA
IVSLLRMIDELRSRFDIP--TQSCVLTHVTNTLRAIGQG-APVDLVFQSVAGSERANAAF
GISLALLAEAHDAAQALARGT---------VGDNLMYFETGQGSALSANAHHG-----VD
QQTMEARAYAVARAFAPLL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLMGVPMGCDVCYTNHAEADQDDMDTLLTLFGVAGINFIMGVPGADDIMLNYQSTSF
HDALYLREVLGLRPAPEFEAWLQRMGIAD-ASGRLLEPAARQPL--LQ--MAHS------
----L-------------------------------------------------------
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>gi|148253763|ref|YP_001238348.1| ethanolamine ammonia-lyase heavy chain
[Bradyrhizobium sp. BTAi1]
----------------------------------------------MTGAFRSRHRGETH
VF------------------------------------DDLKTLLACASPRRSGD-----
ELAGVAADSAARRVAARMALADVPLRRFLDE-------PLIPYETDEVTRLILDSHDAAA
FAPVAALTVGQFREWLLSWEA---DADRLATLAPGLTPEMVAAVSKLCGNGDLIAIAAKC
RVVTAFRSTIGLPGRLSSRLQPNDPTDDPQAIAAGTLDGLLFGMGDAVIGINPATDNVEA
CIRLLSMLDDIRCKFEVP--TQSCVLSHVTTSIQAIEQG-APLDLVFQSIAGTEAANAGF
GVTLALLAEAQDAAQSLKRGT---------IGSNVMYFETGQGAALSADAHHG-----LD
QQTVEARAYAVARAFSPLL--------------VNTVVGFIGPEYLYDAKEIIRAGLEDH
FCAKLLGVPMGCDVCYTNHAEADQDDMDDLALLLAAANVNFLIAVPGADDIMLNYQSLSH
HDVMRLRHLLNRRPAPEFEAWLARMGLLD-EHGRVPPLPRSAPA--VT--RLIG------
----RGARA---------------------------------------------------
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>gi|169633292|ref|YP_001707028.1| ethanolamine ammonia-lyase, heavy chain
[Acinetobacter baumannii SDF]
------------------------------------------------MSYRNIVANQQY
HF------------------------------------ADLKTLMAKATPLRSGD-----
ELAGVAARDATEHVAAQMTLADVPLKTFLNE-------VVIDYETDEITRLIIDEHDLAA
FTPISHFTVGDFRNWLLGEDA---TAQSLKALASGLTPEMVAAVSKIMRNQDLIYVASKC
EVVTQFRNTIGLKGHLSTRLQPNHPTDDVLGISASILDGLMYGNGDAVIGINPATDNLHN
LSELLKLLDHVIQEYQIP--TQSCVLTHISSGIQLAEKN-VPIDLMFQSIAGTQLANEGF
GISLDLLQEGYEATLSLKRGI---------IGQNVMYFETGQGSALSSNAHHG-----VD
QQTLETRAYAVARKYNPLL--------------VNTVVGFIGPEYLFNGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHADADQNDMDVLLTLFGAAGINFIMGIPGSDDVMLNYQTTSF
HDALYLRQLLGLKPAPEFSAWLEQQGIFKQQNSQICWANHMPDQ--FS--RLLMN-----
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>gi|73539312|ref|YP_299679.1| ethanolamine ammonia-lyase heavy chain [Ralstonia
eutropha JMP134]
------------------------------------------------MAFTHTVGQHRH
VF------------------------------------ADLRTLLAKASPARSGD-----
YLAGIAAASEEERMAARMALAAVPLTQFLSE-------ALVPYEDDEVTRLIVDSHDAVA
FAEIASLTVGDFRNWLLLHET---DSTTLATVARGITPEMAAAVSKLMRNQDLIAVARKC
HVVTRFRSTVGLPGRLSVRLQPNHPTDDPKGIAASIIDGLMYGCGDATIGVNPVSDSLGA
IVSLLRMIDDLRCRYDIP--TQSCVLTHVTHTLRAMEQG-APVDLVFQSVAGSERANAAF
GISLSLLAEAHDAAQALARGT---------VGDNVMYFETGQGSALSANAHHG-----VD
QQTMEARAYAVARRFSPLL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGVPMGCDVCYTNHAEADQDDMDTLLTLFGVAGINFIMGVPGADDIMLNYQSTSF
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HDALYLREVLGLRPAPEFEAWLQRMGIAD-GSGRLLEPAERQPL--LE--LAHT------
----L-------------------------------------------------------
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>gi|119900118|ref|YP_935331.1| ethanolamine ammonia-lyase large subunit [Azoarcus
sp. BH72]
------------------------------------------------MSYRHTLDHHTW
VF------------------------------------ADLRELMAKASPARSGD-----
QLAGIAAASAVERMAARMCLAELPLARFLDE-------ALIPYESDEVTRLIIDSHDRAA
FAPVAHLTVGDFRDWLLSDHA---DEAALAALRPGLTPEMAAAVSKLMRNQDLVRVAQKC
RVVTRFRNTIGLPGRLSVRLQPNHPTDDARGIAAAIVDGLLYGAGDAVIGVNPASDSIAA
LTKLVHMLDEVIARLDLP--TQSCVLTHVTNTVHMIEGG-APVDLVFQSVAGTEAANAAF
GISLATLREAREAALSLKRGT---------VGDNVMYFETGQGSALSANAHHG-----VD
QQTCEARAYAVAREFKPLL--------------TNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGLPLGCDVCYTNHAEADQDDMDNLLTLLGVAGVSFIMGVPGADDIMLNYQSTSF
HDGLYLRRALGLRRAPEFEDWLQRMQLVD-AAGRALPISPQHPA--LA--ALRR------
----LTP-----------------------------------------------------
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>gi|146307704|ref|YP_001188169.1| ethanolamine ammonia lyase large subunit
[Pseudomonas mendocina ymp]
------------------------------------------------MPYQTTIGNLVY
RF------------------------------------ADLKTLLAKASPARSGD-----
YLAGLAAATYEERMAAKLALAEVPLKRFLDE-------ALIPYEQDEVTRLIIDRHDAAA
FAPISHLTVGDLRDWLLLEKT---DSVRLAAVAAGLTPEMVAAVSKLMRNQDLILVARKC
QVISRFRNTLGLPGHLAVRLQPNHPTDDVRGIAASMLDGLLYGSGDATVGINPASDSLPT
LMRLWQMMDEVRQHFEIP--MQSCVLTHVTTQIQAIEAG-APIDLVFQSIAGTEATNAGF
GVSLAILREAHEAALSLGRGT---------LGDNVMYFETGQGSALSAGGHHG-----VD
QQTCEARAYAVAREFRPLL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCAKLLGLPMGCDVCYTNHAEADQDDMDSLLTLLGAAGINFIMGIPGADDIMLNYQSTSF
HDALYLRSVLGLKRAPEFDAWLARMAITE-PTGRLREIGRGHHL--LK--QLPH------
----ISGAA---------------------------------------------------
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>gi|154247955|ref|YP_001418913.1| ethanolamine ammonia lyase large subunit
[Xanthobacter autotrophicus Py2]
------------------------------------------------MAYVHRIGAKTF
VF------------------------------------ADLKELMAKATPPRSGD-----
MLAGIAAATAEENVAARMCLADVPLKAFLSE-------ALVPYETDEVTRLILDSHDGDA
FAPVSAMTVGDFRDFLLSHEA---TSQVLAGLARGLTPEMAAAVSKIMRNQDLILVAKKC
RVVTRFRNTIGLPGTMAVRLQPNHPTDDAAGVSAAILDGLLYGCGDAVIGINPASDSLPV
IDRLLKLMDEVITRFEIP--TQSCVLTHVTTSIGLMERG-APVDLVFQSIAGTQGANRSF
GIDLKVLAEGADAARALKRGT---------VGQNAMYFETGQGSALSAGEHHG-----VD
QQTLEARAYGVARAFEPLL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGVPLGVDVCYTNHAEADQDDMDTLLTLLGAAGVTYIMGIPGADDVMLNYQSTSF
HDALYIRELLGLKRAPEFEAWLERMDITA-PDGRLLPADARHPL--LG--YVAG------
----RAA-----------------------------------------------------
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>gi|188591931|ref|YP_001796529.1| ethanolamine ammonia-lyase, heavy chain
[Cupriavidus taiwanensis]
------------------------------------------------MAYTHTIGNHRH
VF------------------------------------ADLRTLLARASPARSGD-----
ALAGLAAQSEQERMAARLALADVPLTRFLNE-------ALVPYEEDEVTRLIHDRHDAAA
FAAIDATTVGDLRNWLLRQET---DSAMLARVAPGITPEMAAAVSKLMRNQDLVAVARKC
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QVVTRFRSTVGLPGRLAVRLQPNHPTDDPKGIAASIIDGLLYGCGDATIGVNPASDNLGA
IVSLLRMIDELRSRFDIP--TQSCVLTHVTNTLRAIGQG-APVDLVFQSVAGSERANAAF
GISLSLLAEAHDAAQALARGT---------VGDNLMYFETGQGSALSADAHHG-----VD
QQTMEARAYAVARAFSPLL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLMGVPMGCDVCYTNHAEADQDDMDTLLTLFGVAGINFIMGVPGADDIMLNYQSTSF
HDALYLREVLGLRPAPEFEAWLQRIGIAD-GAGRLLEPAARQPL--LQ--MAHT------
----L-------------------------------------------------------
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>gi|169795572|ref|YP_001713365.1| ethanolamine ammonia-lyase, heavy chain
[Acinetobacter baumannii AYE]
------------------------------------------------MSYRNIVANQQY
HF------------------------------------ADLKTLMAKATPLRSGD-----
ELAGVAARDATEHVAAQMTLADVPLKTFLNE-------VLVDYETDEITRLIIDEHDLAA
FAPISHFTVGDFRNWLLGEDA---TAESLKALASGLTPEMVAAVSKIMRNQDLIYVASKC
EVVTQFRNTIGLKGHLSTRLQPNHPTDDVLGISASILDGLMYGNGDAVIGINPATDNLHN
LSELLKLLDHVIQEYQIP--TQSCVLTHISSGIQLAEKN-VPIDLMFQSIAGTQLANEGF
GISLDLIQEGYDATLSLKRGT---------IGQNVMYFETGQGSALSSNAHHG-----VD
QQTLETRAYAVARKYNPLL--------------VNTVVGFIGPEYLFNGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHADADQNDMDVLLTLFGAAGINFIMGIPGSDDVMLNYQTTSF
HDALYLRQLLGLKPAPEFSAWLEQQGIFKQQNSQICWADHMPDQ--FS--RLLMN-----
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>gi|21243099|ref|NP_642681.1| ethanolamine ammonia-lyase large subunit [Xanthomonas
axonopodis pv. citri str. 306]
-----------------------------------------------MSGFAFTAGGERF
RF------------------------------------ADLKQLLAKATPARSGD-----
QLAGLAADSGLQRVAAQMALADLPLQHFLQE-------AVVPYEADEVTRLIIDQHDAVA
FAAVAHLTVGGFRDWLLSAQA---DEAALTALAPGLTPEMVAAVSKLMRVQDLILVAQKT
RVVTRFRNTLGLRGRLSTRLQPNHPTDDATGIAASVLDGLLYGNGDAVIGINPASDSLAA
TTALLRMLGAVISGYRIP--TQSCVLAHITTTIEAIGRG-VPVDLVFQSIAGTEAANASF
GINLALLQEGYEAGLSLRRGN---------VGDNVMYFETGQGSALSANAHHG-----VD
QQTCEVRAYAVARHYKPLL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDMLLTLLGTAGINFIMGIPGSDDVMLNYQTTSF
HDALYARQALGLRAAPEFEQWLEQHDILQLRDGRFELGSDVPAP--FR--RALA------
----QASGRAAP------------------------------------------------
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>gi|184158620|ref|YP_001846959.1| ethanolamine ammonia-lyase, large subunit
[Acinetobacter baumannii ACICU]
------------------------------------------------MSYRNIVANQQY
HF------------------------------------ADLKTLMAKATPLRSGD-----
ELAGVAARDATEHVAAQMTLADVPLKTFLNE-------VVVDYDTDEITRLIIDEHDLAA
FAPISHFTVGDFRNWLLGEDA---TPESLKALASGLTPEMVAAVSKIMRNQDLIYVASKC
EVVTQFRNTIGLKGHLSTRLQPNHPTDDVLGISASILDGLMYGNGDAVIGINPATDNLHN
LSELLKLLDHVIQEYQIP--TQSCVLTHISSGIQLAEKN-VPIDLMFQSIAGTQLANEGF
GISLDLLQEGYEATLALKRGT---------IGQNVMYFETGQGSALSSNAHHG-----VD
QQTLETRAYAVARKYNPLL--------------VNTVVGFIGPEYLFNGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHADADQNDMDVLLTLFGAAGINFIMGIPGSDDVMLNYQTTSF
HDALYLRQLLCLKPAPEFSAWLEQQGIFKQQNSQICWADHMPDQ--FS--RLLMN-----
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>gi|148255138|ref|YP_001239723.1| ethanolamine ammonia-lyase heavy chain
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[Bradyrhizobium sp. BTAi1]
------------------------------------------------MGFSHSLGGTTY
RF------------------------------------DDLRTLLAKATPPRSGD-----
VLAGLAAQDAAERVAARMALADLPLRHFLDE-------AVIPYESDEVTRLIVDQHDGSA
FAEIASLTVGAFREWLLSDAT---DARRLSAVSPGLTPEMVAAVCKIMRLQDLVTVAAKC
EVVTRFRCTIGLPGRMSTRLQPNHPLDDPKGVAASILDGLMYGVGDATIGINPASDDLDT
MLRLLDMIETLRLASHAP--IQSCVLAHVTTALKAIERR-APVDLVFQSLAGTEEANRGF
GITLAQLDEALDAAEGLARGP---------AGANLMYFETGQGSELSSSGHCG-----VD
QQTLEARCYAVARRYRPLL--------------VNTVVGFIGPEYLYDGKQIMRAGLEDH
FCGKLLGLPMGCDVCYTNHAEADQDDMDALLTLLGVAGCTYIMGVPGADDIMLNYQSTSF
HDALYIRKVLGKRAAPEFEAWLAATGISD-GKGELRFDPARLMP--SL--PLLG----AE
G-----------------------------------------------------------
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>gi|66768176|ref|YP_242938.1| ethanolamine ammonia-lyase large subunit [Xanthomonas
campestris pv. campestris str. 8004]
-----------------------------------------------MSGFAFSAGGERF
RF------------------------------------ADLKDLLAKATPARSGD-----
QLAGLAAHSELQRVAAQMALAELPLRHFLDE-------AVVPYESDEVTRLIVDQHDAAA
FAPVAHLTVGGFRDWLLGAQA---DDAALAALAPGLMPEMVAAVSKLMRVQDLILVAQKT
RVVTRFRNTLGLRGRLSTRLQPNHPTDDATGIAASVLDGLLYGNGDAVIGINPASDSLAA
TTALLRMLDAVITGYGIP--TQACVLAHITTTIDAINRG-VPVDLVFQSIAGTEAANTSF
GINLALLQEGLDAGLSQQRGS---------VGNNVMYFETGQGSALSANAHHG-----VD
QQTCEVRAYAVARQFNPLL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDMLLTLLGTAGINFIMGIPGSDDVMLNYQTTSF
HDALYARQALGLRPAPEFEHWLDTQGILRLRDGRFELGSEMPAP--FR--KALS------
----QLDAEQRG------------------------------------------------
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>gi|145297995|ref|YP_001140836.1| ethanolamine ammonia-lyase, large subunit
[Aeromonas salmonicida subsp. salmonicida A449]
-------------------------------------------------MYRTQLSHHGY
QF------------------------------------PDLRTLMAKATPARSGD-----
YLAGVAAHSAEERMAARMALADLPLKTFLNE-------ALIPYEQDEVTRLIMDNHDHAA
FAPISHLTVGDFRNWLLSETA---NSQTLAHIAPGITPEMAAAVSKLMRNQDLILAAKKC
RVVTAFRNTIGLPGHLSVRLQPNHPTDDPQGIAAAMLDGLLYGAGDAVVGINPASDNLPV
LASLNQMLDEVIQRFAIP--TQSCILTHVTNTLQLIERN-VPVDLVFQSIAGTEAANRGF
GIDLALLQEAYDAALSLGRGT---------LGNNVMYFETGQGSCLSANAHHG-----LD
QQTCEARAYGVARHFKPLL--------------CNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGVPLGCDVCYTNHAEADQDDMDTLLTLLGNAGLTFLIGVPGADDIMLNYQSTSF
HDALYIRELLGLKHAPEFADWLVRMQLTN-PGGQLLDASLRHPL--LT--AFGQ------
--SGKVA-----------------------------------------------------
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>gi|29831087|ref|NP_825721.1| ethanolamine ammonia-lyase large subunit [Streptomyces
avermitilis MA-4680]
-----------------------------------------------MSTYTARLGGRTH
SF------------------------------------PSLAALLAAASPERSGD-----
RLAGLAADSAEARVAARWALAEVPLARFLAE-------PVIPYEDDDVTRLIVDTHDARA
FAPVAGLCVGEFREWLLSDAA---DAGSLAALAPGLTPEMVAAVSKLMGNADLVAVARKA
RVVTAFRSTIGLPGRLATRLQPNHPTDDPAGVAAALLDGLLLGSGDAVIGINPATDSPKA
VRDLLELLDGVIRRYAIP--TQSCVLCHVTTSIDLMERG-APVDLVFQSIAGTQAANASF
GVTLGLLDEAYDAARGLGRGT---------AGQNALYFETGQGSALSANAHHG-----VD
QQTVEARAYAVARRYDPLL--------------VNTVVGFIGPEYLYDGRQILRAALEDH
FCGKLLGLPMGLDICYTNHADADDDDIATMLTMLGVAGASFVICTPGGDDIMLNYQSASY
HDALYLREVLGLRPAPEFEDWLSRIGLLD-DAGAIRDVTGTAHP--LT--AIGR------
----ELAA----------------------------------------------------
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>gi|157371673|ref|YP_001479662.1| ethanolamine ammonia lyase large subunit [Serratia
proteamaculans 568]
-------------------------------------------------MYQATLSRRSY
RF------------------------------------SDLRQLMAKASPARSGD-----
YLAEVAADSAEERMAARIALAEVPLKTFLQQ-------LLVPYEQDEVTRLIIDSHDALA
FAPISHLTVGDFRDWLLSEQA---DSAMLAQVAPGITPEMAAAVSKLMRNQDLILVAKKC
RVITRFRNTIGLPGHLSVRLQPNHPTDSLQGIAASMLDGLLYGSGDAVVGINPASDSLPL
LEKLNHMLDDVIQRFAIP--TQSCVLTHVTNTLRLIERG-APVDLVFQSIAGTEAANSGF
GINLALLAEAQQAALSLNRGT---------LGNNVMYFETGQGSCLSSNAHHG-----VD
QQTCEARAYAVARHFSPLL--------------INTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGLPLGCDVCYTNHAEADQDDMDTLLTLLATAGLTFLIGVPGADDIMLNYQSTSF
HDALYIRELLGLKHAPEFADWLTKMQITD-DLGRLRDTAANHPL--LL--ALQG----EQ
P-----------------------------------------------------------
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>gi|21231698|ref|NP_637615.1| ethanolamine ammonia-lyase large subunit [Xanthomonas
campestris pv. campestris str. ATCC 33913]
-----------------------------------------------MSGFAFSAGGERF
RF------------------------------------ADLKDLLAKATPARSGD-----
QLAGLAAHSELQRVAAQMALAELPLRHFLDE-------AVVPYESDEVTRLIVDQHDAAA
FAPVAHLTVGGFRDWLLGAQA---DDAALAALAPGLMPEMVAAVSKLMRVQDLILVAQKT
RVVTRFRNTLGLRGRLSTRLQPNHPTDDATGIAASVLDGLLYGNGDAVIGINPASDSLAA
TTALLRMLDAVITGYGIP--TQACVLAHITTTIDAINRG-VPVDLVFQSIAGTEAANTSF
GINLALLQGGLDAGLSQQRGS---------VGNNVMYFETGQGSALSANAHHG-----VD
QQTCEVRAYAVARQFNPLL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHAEADQDDMDMLLTLLGTAGINFIMGIPGSDDVMLNYQTTSF
HDALYARQALGLRPAPEFEHWLDTQGILRLRDGRFELGSEMPAP--FR--KALS------
----QLDAEQRG------------------------------------------------
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>gi|220919791|ref|YP_002495094.1| Ethanolamine ammonia lyase large subunit
[Methylobacterium nodulans ORS 2060]
-----------------------------------------------MATYQCTLGGERH
TF------------------------------------ADLKAVLAAASALKSGD-----
ELAGIAAANSKVRMAARFVLADTPLMTFLED-------LVVPYEDDEVTRLIIDSHDRNA
FAPVASLTVGGLRDWLLSEAA---DETALTALAPGLTPEMVAAVSKLMRNQDLISVASKC
RVVTAFRTTLGLRGRLATRLQPNHPTDDARGIAASVLDGLLYGVGDAVIGINPATDSVSN
AIALMEMLDAVRQEYRIP--TQTCVLTHVTNCIEIMNRG-APVDLVFQSVAGTEAANRGF
GVDLNVLHEAYDAARGLNRGS---------VGQNAMYFETGQGSALSSGSHHG-----VD
QQTVETRAYAVARAFAPLL--------------VNTVVGFIGPEYLYDGKQITRAGLEDH
FCGKLLGLPMGCDVCYTNHAEADQDDMDGLMTLLSAAGCTFLIAIPGSDDIMLNYQSLSF
HDVLYLRSLLGVRAAPEFEAWLQEMGVND---GRTAARNQTQLEARFM--GRLIDGRAA-
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>gi|86748840|ref|YP_485336.1| ethanolamine ammonia lyase large subunit
[Rhodopseudomonas palustris HaA2]
------------------------------------------------MLYRHAIGNVAY
VF------------------------------------DNLRDLLARATPPRSGD-----
RLAGVAADSAEQMVAARMALAEVPLRQFLNE-------TVIPYEDDEVTRLIVDSHDAQS
FAPIAALTVGGFRDWLLSDAA---TPATLAAIARGVTPEMAAAVSKLMRNQDLILVAKKC
SVVTRFRNTIGLPGRMSVRLQPNHPFDDVRGITASTLDGLLLGAGDACIGINPASDDPAV
LGQLVRLLDDVITRLAIP--TQSCVLTHVTTSLRLMEEG-VPVDLVFQSIAGTEAANRSF
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GIDLSILKEAHDAGLSLKRGT---------VGENVMYFETGQGSALSADAHHG-----VD
QQTCEARAYAVARAYAPLL--------------VNSVVGFIGPEYLYDGKEIIRAGLEDH
FCGKLLGLPLGVDICYTNHAEADQDDMDTLLTLLATAGVSFIMGVPGADDVMLNYQSTSF
HDALYVRELLGLKRAPEFDDWLVRTGLSQ-ADLRLTAADGRLPD--FA-ARLIA------
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>gi|91792433|ref|YP_562084.1| ethanolamine ammonia lyase large subunit [Shewanella
denitrificans OS217]
-------------------------------------------------MYQHSVAGQNY
RF------------------------------------NDLTQLLAKASPARSGD-----
NLAGIAAASETERMAAKMCLAEQPLKIFLQD-------LLIPYEEDEVSRLIIDNHQMSA
FLTISHLTVGDFRNWLLLDST---CSQTLSAVCAGITPEMAAAVSKIMRNQDLIKVAKKC
FNPTAFRNSLGLTQGLSSRIQPNNPTDDPRGIAASLLDGLLYGCGDAVIGINPASDSLPL
LERLYYLLDEVISHYQIP--TQSCILTHVSNQIQLIEQG-APVDLVFQSIAGTEKANDSF
GINLALLQEAQSAALALARGT---------VGNNLMYFETGQGAALSANSHHG-----ID
QQTCEARAYGVARHFSPLL--------------VNSVVGFIGPEYLYDSKQIIRAGLEDH
FCGKLLGLPMGCDVCYTNHAQADQDDIDSLMILLANAGVTFLMGVPGGDDIMLSYQSTSY
HDILYLRQVCGLSAAPEFELWLQKMQLMD-PQGKMLTVTAKHPL--FK--ELPQ------
----RLAQTRPL------------------------------------------------
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>gi|116254098|ref|YP_769936.1| putative ethanolamine ammonia-lyase heavy chain
[Rhizobium leguminosarum bv. viciae 3841]
-----------------------------------------------MTTYSIVLGRERH
VF------------------------------------QDLKSVLACASPLKSGD-----
VLAGIAASSNERRVAARYLLADMPLKTFLED-------LVIPYEIDEVSRLIVDRHDWMA
FASVSHMTVGEFRDWLLSYDA---TSEKLLAIPAGLTPEMVAAVSKIMRNHDLITVAGKC
RVVTAFRSTIGLPGRLSSRLQPNHPTDDPEGVAGSTLDGLLYGIGDAVIGINPATDNLEA
CTRLMVLFDRLRERFEIP--TQSCVLTHVTTSIKAIEAG-APLDLVFQSIAGSEAANKGF
GVDLAVLREGQQAALSMKRGT---------VGNNVMYLETGQGSALSADAHHG-----VD
EQTIETRAYAVARELNPLL--------------VNTVVGFIGPEYLFDAKQIIRAGLEDH
FCGKVLGVPMGVDVCYTNHAEADQDDMDNLMVLLTVAGVSFLIAVPGADDVMLNYQSLSY
HDIVGLRHQFNRPPAPEFEAWLHRMGMLD-HTGRLAPASASGAF--SR--NLLS------
----YRASA---------------------------------------------------
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>gi|222107180|ref|YP_002547971.1| ethanolamine ammonia-lyase large subunit
[Agrobacterium vitis S4]
-----------------------------------------------MAAYSIILGRERH
VF------------------------------------DDLKSLMACASPPKSGD-----
QLAGIAASSNERRVAARYVLADLPLKTFLQD-------MLIPYEIDEVTRLIIDSHDVAA
FASVSHMTVGQFRDWLLSYEA---TSEVLAALAPGLTPEMVAAVSKLMRNHDLITVAAKC
SVITAFRSTIGLSGRLSSRLQPNHPTDDPEGVAGSTLDGLLYGVGDAVIGINPASDNLEA
CTRLMHLFDKLRDRFEIP--TQSCVLTHVTTSIQAIEAG-APLDLVFQSVAGTQAANKGF
GVDLAVLREGREAALSLKRGT---------VGDNVMYLETGQGSALSADAHHG-----VD
EQTLEVRAYAVAREVKPLL--------------VNTVVGFIGPEYLYDAKQIIRAGLEDH
FCGKLLGVPMGVDVCYTNHAEADQDDMDNLMVLLTVAGVNFLIAVPGADDVMLNYQSLSY
HDIVGLRHQFNRPPAPEFEAWLKRMGMID-RSGRLAPLPQSNAF--SR--NLLS------
----YKASA---------------------------------------------------
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>gi|39936810|ref|NP_949086.1| ethanolamine ammonia lyase large subunit
[Rhodopseudomonas palustris CGA009]
------------------------------------------------MIYRHSIGNVSF
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VF------------------------------------DDLRDLLAKASPPRSGD-----
RLAGIAADSAEQMVAARMALANLPLRQFLSE-------MVIPYEADEVTRLIADRHDAAA
FAPVASLTVGGFRDWLLSDAA---TPVALAALAPGLTPEMVAAVSKLMRNQDLILVAKKC
SVVTRFRNTIGLPGRMSVRLQPNHPFDDARGITASILDGLLLGAGDACIGINPASDDPAV
LGQLVRLLDDIIAHLAIP--TQGCVLTHVTTTLRLIEQG-APVDLTFQSIAGTEAANRSF
GIDLALLAEAHQATLAQKRGT---------VGDNVMYFETGQGSALSANAHHG-----VD
QQTCEARAYAVARAFSPLL--------------VNSVVGFIGPEYLYDGKQIVRAGLEDH
FCGKLLGLPLGVDICYTNHAEADQDDMDTLLTLLAAAGVNFIMGVPGADDVMLNYQSTSF
HDALYVRDLFGLKRAPEFDDWLIRAGFSGPDHRPLTDGALLPEI--AA--RLIA------
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>gi|90423219|ref|YP_531589.1| ethanolamine ammonia lyase large subunit
[Rhodopseudomonas palustris BisB18]
------------------------------------------------MIYRHTIDHHSF
VF------------------------------------ADLRDLLAKATPARSGD-----
RLAGLAADSAEQMIAARMALAELPLRQFLNE-------AVVPYETDEVTRLILDSHDAAA
FAPIATLTVGGFRDWLLSDAA---TPAVLAGIARGVTPEMAAAVSKLMRNQDLILVAKKC
AVVTRFRNTIGLNGRMSVRLQPNHPFDDERAITASVVDGLTLGSGDACIGINPASDDPAV
LGRLVQLLDDIITRFQIP--TQSCVLTHVTTTLSLIEQG-LPVDLVFQSIAGTEAANRSF
GVDLALLKQAHQAGLSLARGS---------VGNNVMYFETGQGSALSANAHHG-----VD
QQTCEARAYAVARAFDPLL--------------VNSVVGFIGPEYLADGKQIIRAGLEDH
FCGKLLGLPLGVDICYTNHAEADQDDMDTLLTCLAAAGVTFIMGIPGADDVMLNYQSTSF
HDALYVRELFGLKRAPEFDDWLLRAGLAD-ADFRLSERELLLPE--FA-ARLIA------
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>gi|114328555|ref|YP_745712.1| ethanolamine ammonia-lyase heavy chain [Granulibacter
bethesdensis CGDNIH1]
-----------------------------------------------MASHTATAGGERH
RF------------------------------------DDLKSVLAAATPRRSGD-----
ELAGLAASSDAQRVAARFVLADLPLRSFLNE-------AVVPYEVDEVTRLIIDTHDAAA
FAPIAHLTVGGFREWLLSHEA---DAAALAAVAPGITPEMAAAVCKLMRNQDLIAVARKC
RVIAGFRNTLGLEGRLATRLQPNHPTDDLRGIAAATLDGLLYGTGDAVIGINPASDNVPN
CIALLEMLDELRQRYSIP--TQSCVLTHVTNALEIMKRG-APVDLVFQSIAGTEAANRGF
GIDLAILRESHEAALSLKRGT---------VGQNVMYFETGQGAALSADAHHG-----LD
QQTVETRAYAVARAFNPLL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGLPMGCDVCYTNHAEADQDDMDTLMTLLTVAGVTFLIAVPGADDVMLNYQSLSF
HDALYLRSVLGVKAAPEFETWLEQMDLKD-RSGRIRALPPQDER--VV--RLIA------
----EATSHG--------------------------------------------------
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>gi|83592368|ref|YP_426120.1| ethanolamine ammonia-lyase heavy chain [Rhodospirillum
rubrum ATCC 11170]
-----------------------------------------------MGLYRATVGGTRY
DF------------------------------------ADLRTVMACASPRRSGD-----
ELAGLAAESDAQRMAARLVLADLPLRAFLDT-------PLVPYESDEVTRLIIDTHDGAA
FAPVASLTVGGFRDWLLSYAA---DSAALAALAPGLTPEMVAAVSKLMRNADLIAVAAKC
QVITGFRTTLGLPGRLASRLQPNHPTDDPAGIAASTLDGLLFGMGDAVIGINPATDNVGA
CVTLLEMLDAVRQRFDIP--SQSCVLTHVTNSIEAINRG-APLDLVFQSVAGTEAANAGF
GISLSLLGEAREAALSLRRGT---------VGDNVMYFETGQGAALSADAHHG-----VD
QQTVEVRAYAVCRAFKPLI--------------VNTVVGFIGPEYLYDSKQIIRAGLEDH
CCGKLLGLPMGVDVCYTNHAEADQDDMDTLMTLLGVAGVTFLIGVPGADDVMLNYQSLSY
HDILGLRHLLDRRPAPEFADWLARMGMSD-AGGRLPPLDASAPA--LR--RLLA------
-------SGG--------------------------------------------------
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>gi|209544507|ref|YP_002276736.1| Ethanolamine ammonia lyase large subunit
[Gluconacetobacter diazotrophicus PAl 5]
------------------------------------------------MPYRIILDSERY
NF------------------------------------AHLRHVLACASPARSGD-----
ELAGLAAADPVERMAARHVLADIPLRDFLND-------VPVPYEDDEVTRLIVDTHDAAS
FAPVAHMTVGQFRDWLLSYTA---DGDAITALGPGLTPEIVSAVSKLMRNQDLIAAARKI
RVVTAFRNTQGLPGRLGTRLQPNHPTDDARGIAASLLDGLLLGVGDAVLGINPATDSIAN
GIVLLDMLEQVRTRYAIP--AQTCVLTHITNAIAMMARG-APVDLVFQSVAGTQAANAGF
GVSLSVLAEAHDAARSLNRGT---------VGHNVMYFETGQGSALSAGAHHG-----MD
QQTAEVRAYAVARAFSPLL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLMGLPMGCDACYTNHAEADQDDMDNLMMLLTVAGVNFLIAVPGGDDVMLSYQSLSH
HDMLTLRSSFGVRAAPEFEAWLHEMNLLD-PDGRLRVNAPQSLG--RI--LGPG------
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>gi|27378105|ref|NP_769634.1| ethanolamine ammonia-lyase heavy chain [Bradyrhizobium
japonicum USDA 110]
MQNEDGRGVNAPLSLVERKVSYFSVLIRRYSFRIVLESAFGRRTPEGTLVYRHTIDATTY
AF------------------------------------PDLRDLLAKATPPRSGD-----
RLAGIAAASAEQMIAARMALADVPLGQFLQE-------ALIPYETDEVTRLVIDSHDARA
FAPVASLTVGAFRDWLLSDAA---TPEILRKLAPGITPEMAAAVSKLMRNQDLILAARKC
EVTTAFRNTIGLKGRMSTRLQPNHPFDDARGITASILDGILLGAGDACIGINPASDDPTV
IAQLLRLLDEIIARLKLP--TQGCVLTHVTTTLSLIGQG-VPVDLVFQSVAGTEAANRSF
GVDLDLLREAQEAGRSQRRGT---------VGQNVMYFETGQGSALSANAHHG-----VD
QQTCEARAYAVARAYAPLL--------------VNSVVGFIGPEYLYDGKEIIRAGLEDH
FCGKLLGLPLGVDICYTNHAEADQDDMDNLLTLLAAAGVTFIMGVPGADDVMLNYQSTSF
HDALYVRDVFGLRRAPEFDDWLAQSGIVG-ADFRLAGDAGLLPD--FA-SRLIA------
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>gi|115523822|ref|YP_780733.1| ethanolamine ammonia lyase large subunit
[Rhodopseudomonas palustris BisA53]
------------------------------------------------MIYRHAIGQHVF
LF------------------------------------NDLRDLLAKASPIRSGD-----
QLAGIAAQSAEQMIAARMALAELPLRQFLAE-------AVIPYESDEVTRLIVDGHDAAA
FAPVAALTVGEFRDWLLSDQA---TPAVLARLAPGLTPEMAAAVSKLMRNQDLILAANKI
AVTTRFRNTIGLPGRFSTRLQPNHPFDDERAITASILDGLMLGSGDACIGINPASDDPAV
IGRLVALLDELITRWRIP--TQGCVLTHLTTTLGLIEQR-LPVDLVFQSIAGTEAANRSF
GVDLALLREGHDAGLSMKRGS---------VGDNVMYFETGQGSALSANAHHG-----VD
QQTCEARAYAVARAFDPLL--------------VNSVVGFIGPEYLADGKQIIRAGLEDH
FCGKLLGLPIGVDICYTNHADADQDDMDTLLTCLAAAGVTFIMGVPGADDVMLNYQSTSF
HDALYVREVFGRKRAPEFDAWLVQVGLAD-EDAQLAERDALLPE--FA--SRLI----AA
P-----------------------------------------------------------
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>gi|162146138|ref|YP_001600597.1| putative ethanolamine ammonia-lyase heavy chain
[Gluconacetobacter diazotrophicus PAl 5]
-----------MPLSARDKLLSGNQSHSLQISERASLFGRQKRRIIPTVPYRIILDSERY
NF------------------------------------AHLRHVLACASPARSGD-----
ELAGLAAADPVERMAARHVLADIPLRDFLND-------VPVPYEDDEVTRLIVDTHDAAS
FAPVAHMTVGQFRDWLLSYTA---DGDAITALGPGLTPEIVSAVSKLMRNQDLIAAARKI
RVVTAFRNTQGLPGRLGTRLQPNHPTDDARGIAASLLDGLLLGVGDAVLGINPATDSIAN
GIVLLDMLEQVRTRYAIP--AQTCVLTHITNAIAMMARG-APVDLVFQSVAGTQAANAGF
GVSLSVLAEAHDAARSLNRGT---------VGHNVMYFETGQGSALSAGAHHG-----MD
QQTAEVRAYAVARAFSPLL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
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FCGKLMGLPMGCDACYTNHAEADQDDMDNLMMLLTVAGVNFLIAVPGGDDVMLSYQSLSH
HDMLTLRSSFGVRAAPEFEAWLHEMNLLD-PDGRLRVNAPQSLG--RI--LGPG------
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>gi|111224925|ref|YP_715719.1| ethanolamine ammonia-lyase, large subunit [Frankia
alni ACN14a]
----------------------MHRRATCVRGRSASASGSRLGREVAAVAYRMTVRGERH
VF------------------------------------ADLAELFAKANEEKSGD-----
QLAGIAAGSARQRVAAKLALADVTLGEIVAA----------PLIDDAVTDLILRGQDAAL
FAPLASLTVGEFRELVLSPSF--PARWRDDGLARAITPEIAAATAKIMSDKDLICAAKPL
RTVTRCRNTIGEAGVLGVRVQPNHPADDLEGILLSVLDGLLHGCGDAVLGVNPARESVEQ
VGTILRGLGALVDALALP--TQTCVLAHLTTQLAALAAG-APVDLLFQSVAGTEAANTSF
GITLDLLAEGREAVLAHHRRD----RSGDFVGEQVMYFETGQGSALSADAHHG-----VD
QLTCEARAHGVARAFDPFL--------------VNSVVGFIGPEYLADARQITRAGLEDH
FVGKLLGLPMGCDVCYTNHVDADQNTNDDLLVLLVAAGCTFVMGVPSADDVMLGYQSTSY
HDAAGMRELFNLHAAPEFTAWLTDRGLL--VDGHLADPTGPVAA--LL--TAGL----DD
ALAALPTRPALPSGPTR-------------------------------------------
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>gi|222080799|ref|YP_002542527.1| ethanolamine ammonia-lyase large subunit
[Agrobacterium radiobacter K84]
------------------------------------------------MPYTTTIENTVF
RF------------------------------------GDLKDLLAKATPERSGD-----
QLAGIAASGPVERLAAQMALADLPLKAFLSE-------EVISSDDDEVSALIAARHDAAA
FAPISSLTVGEFREWLLKPET---GQRALEAVTYGVTPEMVAAVSKIMRLQDLISVAAKR
EVVTRFRNTIGLRGRLSTRNQPNHPTDDSRGIAASAIDGLLMGSGDAVIGVNPATDSVAD
YIRIVSLLDELRERLAIP--TQTCCLGHVTTAIRAIEAG-APVDLVFQSVAGSQKANAGF
GIDLSLLKEAYEAGRSLKRGM---------PGANVMYFETGQGAALSADAHFG-----VD
QQTMEVRAYAVAREFDPML--------------VNTVVGFIGPEYLFNGKQIIRAGLEDH
FCGKLLGLPMGVDVCYTNHADADQEDMDTLLTLLCAANVNFVITVPGADDIMLNYQSLAH
HDAIYCRETLNRAPAPEFERWLCEIGLTD-RAGALVGAPAMLTD--YF--SSST------
----LVGA----------------------------------------------------
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>gi|169629874|ref|YP_001703523.1| ethanolamine ammonia-lyase, heavy subunit
[Mycobacterium abscessus]
------------------------------------------------MKYRQQVAGVNY
AF------------------------------------DGLVDVMAKATPLRSGD-----
ELAGCAAGSDAERAAAAWVLADLPLDTFLNE-------AVVPYESDEVTRLIIDSHDRGA
YSAVSHLTVGGFRDWLLESASRDDGARRIAEVSAGITPEMAAAVSKIMRNQDLIAVGAAM
HVSAAFRTTIGGKGTLATRLQPNHPTDDPRGVAAAVLDGLLLGCGDAVIGINPATDSPEA
TGDLLKLLDSIRSRYDIP--TQSCVLSHITTTIGLIERG-APVDLTFQSIAGTEGANSAF
GVDIALLREGRDATRALRRGT---------VGDNVMYLETGQGSALSSRAHLGAGGKPVD
QQTLEARAYAVARDLEPFL--------------VNTVVGFIGPEYLYDGKQIVRAGLEDH
FCGKLLGLPMGVDVCYTNHAEADQNDMDTLLILLAAAGVAFVITVPGADDVMLGYQSLSF
HDVLQARRTLGLRPAPEFEQWLHAIGMVD-DDGRLTPFDVTSSP--LR--ALTI------
----SGAR----------------------------------------------------
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>gi|118470052|ref|YP_885934.1| ethanolamine ammonia-lyase, large subunit
[Mycobacterium smegmatis str. MC2 155]
------------------------------------------------MRYRQQVSGVTY
TF------------------------------------DGLVEVMAKATPLRSGD-----
QLAGCAAEHDGERAAAAWVLADLPLDVFLNE-------ELVPYDTDEVTRLIMDTHDRQA
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FSSVSHLTVGGFRDWLLDVAAEDDSAARLAAVAPGLTPEMVAAVSKIMRNQDLIAVSAAA
RVTAALRTTVGIPGTMATRLQPNHPTDDPRGIAAAVLDGLLLGCGDAVIGINPATDSPQA
TADLLYLLDGIRTRYDIP--AQSCVLSHITTTIGLIEAG-APVDLVFQSIAGTEGANTAF
GVNLQLLREGNEAARSLNRGT---------VGNNVMYLETGQGSALSSGAHLGVGGKPVD
QQTLEARAYAVARDLSPLL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGLPMGVDVCYTNHAEADQNDMDTLLMLLAAAGVAFVITVPGADDVMLGYQSLSF
HDVLVARRTLGLRPAPEFETWLRKVGMVD-DAGRLTPFDVSRSP--LR--ELTV------
----AEAS----------------------------------------------------
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>gi|183980689|ref|YP_001848980.1| ethanolamine ammonia-lyase large subunit, EutB
[Mycobacterium marinum M]
------------------------------------------------MSYRQTISGTTY
AF------------------------------------DGLVDVLAKATPLRSGD-----
QLAGCAAEHDAERAAAAWVLADMPLTTFLSD-------VVVPYETDEVTRLIIDSHDRQA
FAPISHLTVGGLRDWLLDTAARDDSAARIAAIAPGLTPEMVAAVCKIMRNQDLILVAAAT
TATAAFRTTIGLPGRLATRLQPNHPTDDPRGIAAGMLDGLLMGCGDAVVGINPATDSPQA
TADLLHLLDDIRQRFEIP--MQSCVLCHVTTTTELIDKG-VPVDLVFQSIAGTEGANSSF
GVNIPMLLEANEAARSLGRGT---------VGDNVMYLETGQGSALSAGAHLGTGGKPVD
QQTLEARAYAVARTLQPLL--------------INTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGLPMGVDVCYTNHAEADQDDMDTLLTLLGVAGAAFVIAVPGADDIMLGYQSLSF
HDPLYVRQVLRLRPAPEFEAWLTGLGMAD-ANGRILPIDLATSP--LR--ALAT------
----GA------------------------------------------------------
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>gi|169630908|ref|YP_001704557.1| ethanolamine ammonia-lyase, large subunit
[Mycobacterium abscessus]
-----------------------------------------------MSTFRHIAGPVTY
QF------------------------------------GSLAEVLAKASPPRSGD-----
ELAGCAAHSDAERAAARWVLAEVPLAAFLTE-------EIVPYDTDEVTRLILDSHDAAA
FAVISHLTVGDFRDWLLETITKPHGAQILKEVSPGLTPEMVAAVSKLMRNQDLIAVGAAV
RNHSAFRTTIGLPGTLATRLQPNHPTDDARGIAAATLDGLLLGCGDAVIGINPATDSPHA
AGDLLRLIDDIRLRFDIP--TQSCVLAHVTTTIELIERN-LPVDLVFQSIAGTEGANESF
GVNLALLREANEAGRSLSRGT---------VGNNVMYLETGQGSALSAGAHLGVGGVAVD
QQTLEARAYAVAREVEPLL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGLPMGVDVCYTNHAEADSDDMDVLLTVLTAAGVAFVIAVPGADDVMLGYQSLSF
HDALFARRTFGLRPAPEFNDWLERMGMLE-RDGGLREIAVSDSP--LR--ALI-------
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>gi|111023047|ref|YP_706019.1| ethanolamine ammonia-lyase heavy chain [Rhodococcus
jostii RHA1]
-----------------------------------------------MTTYSHGVAGTGY
TF------------------------------------DGLVDLMAKATPLRSGD-----
ELAGCAASSDAERAAAQWALADVPLGTFLNE-------LVVPYEDDEVTRLIIDSHDRVA
FGEISHLTVGGLRDWLLDVAARDGAAETFRRVAPGLTPEMVAAVSKIMRNQDLIAVARAV
TVTAGFRTTLGVPGHLGTRLQPNHPTDDPRGIAAATLDGLLLGCGDAVIGINPATDSPHA
TAELLHLLDDIRQRFDIP--AQSCVLSHVTTTMGLIEEG-VPVDLVFQSIAGTQGANSSF
GVDISLLREANAAGRSLKRGT---------VGDNVMYLETGQGSALSAGAHLGTGGRPVD
QQTLETRAYAVARDLEPLL--------------INTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGLPMGVDVCYTNHAEADQDDMDTLLTLLGVAGAAFVIAVPGADDVMLGYQSLSF
HDVLYARQVLGLRPAPEFEDWMRRLGMVD-DAGRVLPVDAAASP--LR--ALTV------
----AR------------------------------------------------------
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>gi|54024156|ref|YP_118398.1| putative ethanolamine ammonia-lyase large subunit
[Nocardia farcinica IFM 10152]
------------------------------------------------MTYHQSVSGRNY
SF------------------------------------GSLVEVLAKATPLRSGD-----
QLAGCAAESDAERAAACWVLADLPLTTFLDE-------QVVPYETDAVTRLIVDGHDRAA
FAPIAHLTVGGFRDWLLATAAGPDAAATLSGVAAGLTPEMVAAVSKLMRNQDLIAVAKAA
TVTSAFRTTIGLPGRIATRLQPNHPTDDPRGIAAATLDGLLMGCGDAVIGINPATDSPRA
TADLLHLLDDIRTRFDIP--MQSCVLSHVTTTMALIERN-VPVDLVFQSIAGTEGANASF
GITLPMLAEANEAARSLGRGT---------VGDNVMYLETGQGSALSAGAHLGTGGLPVD
QQTLEARAYAVARALDPLL--------------VNTVVGFIGPEYLYDGKQIIRAGLEDH
FCGKLLGLPMGVDVCYTNHAEADQDDMDTLLTLLGVAGAAFVIAVPGADDVMLGYQSLSF
HDALYVRQVLGLRAAPEFETWLHGLGMAD-EAGRIRPVDAAASP--LL--ALTT------
----R-------------------------------------------------------
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>gi|126642149|ref|YP_001085133.1| ethanolamine ammonia-lyase heavy chain
[Acinetobacter baumannii ATCC 17978]
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-----------------MTLADVPLKTFLNE-------VVIDYETDEITRLIIDEHDLAA
FAPISHFTVGDFRNWLLGEDA---TPESLKALASGLTPEMVAAVSKIMRNQDLIYVASKC
EVVTQFRNTIGLKGHLSTRLQPNHPTDDVLGISASILDGLMYGNGDAVIGINPATDNLHN
LSELLKLLDHVIQEYQIP--TQSCVLTHISSGIQLAEKN-VPIDLMFQSIAGTQLANEGF
GISLDLLQEGYEATLSLKRGT---------IGQNVMYFETGQGSALSSNAHHG-----VD
QQTLETRAYAVARKYNPLL--------------VNTVVGFIGPEYLFNGKQIIRAGLEDH
FCGKLLGVPMGCDICYTNHADADQNDMDVLLTLFGAAGINFIMGIPGSDDVMLNYQTTSF
HDALYLRQLLGLKPAPEFSAWLEQQGIFKQQNSQICWADHMPDQ--FS--RLLM-N----
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>gi|170749715|ref|YP_001755975.1| ethanolamine ammonia lyase large subunit
[Methylobacterium radiotolerans JCM 2831]
------------------------------------------------MAYATTIEGTRF
TF------------------------------------PDLRSLLAKATPERSGD-----
QLAGLCAEGPVERLAAQIALADLPLKTFLAE-------ELIPSDEDEVSDLIARRHDAAA
FAPVSSLTVGAFREWLLAPAA---DARALAALSPGLTPEMVAAVSKICRLQDLVAVAAKR
PVVTRFRSTIGLPGRLATRNQPNHPTDSSEGILISALDGLLMGSGDAVIGVNPATDSLPD
YIRIVELLETLRLRLDVP--TQHCCLGHVTVAIEAMARG-APVDLVFQSVAGSQKANAGF
GVDLAVLREASQAARALGRCP---------EGGQFMYFETGQGSALSADAHWG-----VD
QQTMEARAYAVAREFDPLL--------------VNTVVGFIGPEYLYNGKQIIRAGLEDH
FCGKLLGLPMGVDVCYTNHADADGEDMDALLTLLCAAGVNFVITVPGADDVMLNYQSLSH
HDAVFARETLGRPPAPEFEAWLRAVRITD-AQGQLASAAGVLPQ--AL--AEAS------
----RLLPGRAA------------------------------------------------
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>gi|89055068|ref|YP_510519.1| ethanolamine ammonia-lyase heavy chain [Jannaschia sp.
CCS1]
------------------------------------------------MGYRTDISGTRY
TF------------------------------------ASLKRLLAKASPERSGD-----
HLAGLAADSPLERLAAQMCLADAPLRDFLDD--------VLEVDGDAVSRLIADQHDAQA
FESISALTVGGFRDWLLDPGV---TGVELAQIAWGLTPEMVAAVSKIMRAQDLIAVAAKI
EVVTRFRSTIGLRGRLSTRNQPNHPTDDSRGIALSALDGLLMGAGDAVIGVNPATDSVED
FTRVCEVLEAIRTQLDIP--TQHCCLGHVTTALAAMERG-APVDLVFQSVAGSQAANDGF
GVTLEMLDEAHAAARALGRAP---------DGANLMYFETGQGAALSANAHHG-----MD
QQTMETRAYAVARRYKPLL--------------VNTVVGFIGPEYLADGKQIIRAGLEDH
FCGKLLGLPMGVDVCYTNHSYADQEDMDILLTTLAAAGVSFVITVPGADDIMLNYQSLSF
HDAHFIRDTLGRPPAPEFAAWMEANGIGS-ADVRLPPLETALAQ--LR--LPGS------
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>gi|118579639|ref|YP_900889.1| ethanolamine ammonia lyase large subunit [Pelobacter
propionicus DSM 2379]
------------MKRLFLIAAMLVVGILTLSTNSHAIAIKSVKPGEDVFKYIQRVKG-SF
DQ------------------------------------VLYQQVIGASNAFKEGD-----
KTIGVAADTNTSRENARKLLANTKIKDITNH----------PLHNDDLYKFIAKSVDPAQ
YAKIKDWTMGRMKAFLLDK-----SEAEIKSVMYGMNSEVVGCLPKLMSNKELIAVNRKI
FNPLP-GTKIGAKGYLSARIQPNSPTDDPEEIMMQVLSAFSYGVGDLVLGTNPVDGTKEQ
TARVEASLKDVVDTFKLNGTIPWCVLAHIDVQREIFNEKPELIDCMFQSLAGTDTANKTF
DISVEKMVDHAKSRAGQRYGL---------------YFETGQGSDFTNGGAEG-----VD
MVVLESRKYGMARGLQQVL---AQVQPQGAYLHVNDVAGFIGPEVFRTKEQLVRCCLEDI
LMGKLQGITIGLDICSTLHMSVSLDDLEWCQDQIMPANPAYLMALPTRNDPMLSYLTTSY
QDHVRIRSKFGYKVNDTMWDFFKRIQVID-KNGKPTKHFGDPIWVYYQYCKAKGDTRSQQ
EIMAEGKQKFDAIHNTWLKTGNKVPLASGYGKNIWDLNPQLDKKIRELYADAKKAIWAEF
TPEFLKSVPDSVQLGTLSKDRENYIVHPETGEQLNKQSVATLQKLRDSWQGQTPDVQIVV
SDGLNAKSIMAPEHTLPYITALRKELQAAGLTADKKNIVISSGRVRAGYMVGDVLFNNAD
PGKARAVVHIIGERPGTGQDAFSVYIAAPKGKVWAEKKVDHNIVKVQSGISKQATKPADA
AKQTVKLIKELMAS---
>gi|116878401|ref|YP_355897.2| ethanolamine ammonia-lyase, large subunit [Pelobacter
carbinolicus DSM 2380]
----------MLQKGKFVAGITGALVMTFLASMAGAVTIGGVKPGEDVMQYVNRTKGK-F
DQ------------------------------------TTYQQVIGAANAFKEGD-----
EGLGVAADTEADRVNARKLLANTKIKDIFEN----------PLFVDGQEELIRKTTDKAK
YNKIKNMTMGELKNFLLTK-----SEADIKAIMGGLHSDVIGSVVKLMSNDELIRVGSKI
FNPLP-GSKIGAKGYIGARIQPNSPTDNKEDIQMQVFDGFSYGVGDIIIGTNPVDSQLEA
TLRVENALKEIVTAFGLEKTIPWCVLSHIDGQAAAEKEEPGSTAIWFQSLAGTESANKTF
DLTIQKM-------IDYAKMR---------TGPYSLYFETGQGADYTNGHGHG-----FD
MVVHESRKYGFSRALKQVTAKAKGVTEDQVWLHVNDVAGFIGPEVFKTREQLVRCCLEDI
VMGKLHGLVLGLDICSTLHMPVTLDDLAWCQDQIAPANPAYLMALPTRNDPMLSYLTTGF
QDHVRIREKFGFKVNDAMWDFYKKIEVID-ANGKPTKHFGDPAWVYYK--FRQA----KG
DKRSFKEIYAEGQKKIANVRGRGVDLAVGYGENIWDLEPVTNKRIHDLYDDAKISLWAEF
TPEFIDSIPNAVSIKSKAHDRENYISAPGTGEELSASAVATLDKLAASWGNKAPDVQVVI
SDGLNAKAIMDDGHLMPYLKELKKQCKKAGLTLSDKNIVVTGGRVRAGYKAGETLFSKV-
GSKAKAVVHIIGERPGSGHHAFSAYLVKVKPSTWAKTGSVDHDSSKVLSGISDTGLVPAE
AARQTVKLLMEM-----
>gi|108762129|ref|YP_631356.1| ethanolamine ammonia-lyase, large subunit/small
subunit [Myxococcus xanthus DK 1622]
-----------------------------------------MKSGEDVFGYVQRLRG-AF
DD------------------------------------TLYKQVLGAANTFKEGD-----
ALVGVAAADENSRANARRLLGHTRLEDVRRH----------PLHQDALHALSLEAEDSQA
ATLTADWTLGRLRKFLLES-----DEAAIHAIGPGLGSDTIGCVVKLMSDAELIALGSKV
FNPLP-GSKVGARGYMGARIQPNSPTDNVDDIRWQVFDGFSYAVGDVVLGCNPVSSTPES
VAAIESALLEVLVTFGLTDVLPHCVLSHIDVQAEVERRQPGTTGVWFQSIAGSDSANATF
DISVEKM-------LAYADGR---------TGPYGLYFETGQGADFTNGHGHG-----YD
MVLHESRKYGFARALSQRV--ARARQGAAPWVHLNDVAGFIGPEVFRTREQLVRCCLEDI
AMGKLHGLTIGLDICSTLHMDVSLDDLDWCIERIMPANPAYLMSLPTKNDPMLGYLTTGF
QDHVRIREQFGYKVDDRMWAFFQRLGVID-AEGKPTRHFGDPVWVYLQ--YLRA----KG
DSRPEADIRADAEQQLSAIRARGVPMARGHGTHPWDLEPALDAELRRVYVDSKKSLWTEL
TPAFITAVPEGVRLVSKSQDRTEYILHPETGEQLDASSLEAVRAMRARHAGRYDVQLMVS
DGLNALAIMDEGQLAPYLETLRAALIAAGYQPAPEHLVLTSGRVRAGYRVGEALYAGMED
AARHRGLIHVIGERPGTGHHTFSAYITAPSGAVWSQPGKVDHNITRVVSGVALTAYAPSL
AAPETVRLLQQLAPRGG
>gi|77918106|ref|YP_355921.1| ethanolamine ammonia-lyase, large/small subunit fusion
[Pelobacter carbinolicus DSM 2380]
----------MRLRSKFLYGITFGLALTFVASLAGAVAIRDVKPGEDVFAYVTRVKGQ-F
DQ------------------------------------PLYQQVLGAANSFKEGD-----
EAIGVAADDDASRENARKLLANTKIKDLMAK----------PLFVDAQYDLITNTTDMAQ
YNKVKDWTLGELKDFLLTK-----SESQIKGIMYGLHSDIIGNVVKMMSNDELTRIGQTV
FNPLP-GSNIGAKGYLSARIQPNSPTDNADDIVWQVFDAYAYAVGDLVVGTNPVDSEAAN
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IENIELALRDVMQTFDVDKYNPWCVLSHIDVQAEVEKNNPGSTAIWFQSLAGVVDANKTF
DLTLQKM-------MDYARMR---------TGKYGLYHETGQGADFTNGHGKG-----FD
MVVHESRKYGFARALKQQV-AAAQTDGQGAWCHVNDVAGFIGPEIFKTREQLVRCCLEDI
AMGKLHGLIIGLDICSTLHMPVTLDDLDWCQDQIAPANPGYLMALPTKNDPMLSYLTTAY
QDHVRMREKFGYKINDDMWNFFKKIEIID-ANGKPTEHFGDPIWVYYK--YQLA----KG
DTRSMKEIYAEGQKKVDEIQARGVPLAIGYGENIWDLEPKTNKAIHDLYDDAKISLWAEF
TPEFIASIPNAVTVQTKSADREDYVAHPSTGEEFSDAAVATLEKLRAAWGGKAPDVQIVL
SDGLNAKALMDEDHLMPFMDELKSEMAKAGWTVAKENIVVTSGRVRAGYQAGDILFKDP-
ASTPKAIIHIIGERPGSGHHAYSVYMTRVAPATWA-AGTVDHDVTKVISGISNTGLDPRK
AARQTVRLLQSM-----
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%%  EutC [targeting tail implicated]

>gi++|16765777|ref|NP_461392.1| ethanolamine ammonia-lyase small subunit [Salmonella
typhimurium LT2]
--MDQKQIEEIVRSVMASMGQ------------------------------------DVP
QPAAPSTQEGAKPQCAAPTVTESCALDLGSAEAKAWIGVENPHRADVLTELRRSTAARVC
TGRAGPRPRTQALLRFLADHSRSKDTVLKEVPEEWVKAQGL----------------LEV
RSEISDKNLYLTRPDMGRRLSPEAIDALKS-------QCVMNP----------DVQVVVS
DGLSTDAITANYEEILPPLLAGLKQA---G-LNVGTPFFVRYGRVKIEDQIGEILGAKVV
ILLVGERPGLGQSESLSCYAVYSPRVATTVEADRTCISNIH-QGGTPPVEAAAVIVDLAK
RMLEQKASGINMTR---------------------------------------------
>gi++|161612797|ref|YP_001586762.1| ethanolamine ammonia-lyase small subunit
[Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7]
--MDQKQIEEIVRSVMASMGQ------------------------------------DVP
QPVAPSTQEGAKPQCAAPTVTESCALDLGSAEAKAWIGVENPHRADVLTELRRSTAARVC
TGRAGPRPRTQALLRFLADHSRSKDTVLKEVPEEWVKAQGL----------------LEV
RSEISDKNLYLTRPDMGRRLSPEAIDALKS-------QCVMNP----------DVQVVVS
DGLSTDAITANYEEILPPLLAGLKQA---G-LNVGTPFFVRYGRVKIEDQIGEILGAKVV
ILLVGERPGLGQSESLSCYAVYSPRVATTVEADRTCISNIH-QGGTPPVEAAAVIVDLAK
RMLEQKASGINMTR---------------------------------------------
>gi++|197251424|ref|YP_002147411.1| ethanolamine ammonia-lyase, light chain
[Salmonella enterica subsp. enterica serovar Agona str. SL483]
--MDQKQIEEIVRSVMASMGQ------------------------------------DVP
QPVAPSTQAGAKPQCAAPTVTESCALDLGSAEAKAWIGVENPHRADVLTELRRSTAARVC
TGRAGPRPRTQALLRFLADHSRSKDTVLKEVPEEWVKAQGL----------------LEV
RSEISDKNLYLTRPDMGRRLSPEAIDALKS-------QCVMNP----------DVQVVVS
DGLSTDAITANYEEILPPLLAGLKQA---G-LNVGTPFFVRYGRVKIEDQIGEILGAKVV
ILLVGERPGLGQSESLSCYAVYSPRVATTVEADRTCISNIH-QGGTPPVEAAAVIVDLAK
RMLEQKASGINMTR---------------------------------------------
>gi++|16761375|ref|NP_456992.1| ethanolamine ammonia-lyase small subunit [Salmonella
enterica subsp. enterica serovar Typhi str. CT18]
--MDQKQIEEIVRSVMASMGQ------------------------------------DVP
QPVAPSTQEGAKPQCAAPTVTESCALDLGSAEAKAWIGVENPHRADVLTELRRSTAARVC
TGRAGPRPRTQALLRFLADHSRSKDTVLKEVPEEWGKAQGL----------------LEV
RSEISDKNLYLTRPDMGRRLSPEAIDALKS-------QCVMNP----------DVQVVVS
DGLSTDAITANYEEILPPLLAGLKQA---G-LNVGTPFFVRYGRVKIEDQIGEILGAKVV
ILLVGERPGLGQSESLSCYAVYSPRVATTVEADRTCISNIH-QGGTPPVEAAAVIVDLAK
RMLEQKASGINMTR---------------------------------------------
>gi++|56412659|ref|YP_149734.1| ethanolamine ammonia-lyase small subunit [Salmonella
enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]
--MDQKQIEEIVRSVMASMGQ------------------------------------DVP
QPVAPSKQEGAKPQCASPTVTESCALDLGSAEAKAWIGVENPHRADVLTELRRSTAARVC
TGRAGPRPRTQALLRFLADHSRSKDTVLKEVPEEWVKAQGL----------------LEV
RSEISDKNLYLTRPDMGRRLSPEAIDALKS-------QCVMNP----------DVQVVVS
DGLSTDAITANYEEILPPLLAGLKQA---G-LNVGTPFFVRYGRVKIEDQIGEILGAKVV
ILLVGERPGLGQSESLSCYAVYSPRVATTVEADRTCISNIH-QGGTPPVEAAAVIVDLAK
RMLEQKASGINMTR---------------------------------------------
>gi++|161502393|ref|YP_001569505.1| ethanolamine ammonia-lyase small subunit
[Salmonella enterica subsp. arizonae serovar 62:z4,z23:--]
--MDQKQIEEIVRSVMASMGQ------------------------------------DVP
QPVAPSTQEGAKPQRAAPTATESCALDLGSAEAKAWIGVENPHRADVLTELRRSTAARVC
```

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TGRAGPRPRTQALLRFLADHSRSKDTVLKEVPEEWVKAQGL----------------LEV
RSEISDKNRYLTRPDMGRRLSQEAIDALKS-------QCVMNP----------DVQVVIS
DGLSTDAITANYEEILPPLLAGLKQA---G-LKVGTPFFVRYGRVKIEDQIGELLGAKVV
ILLVGERPGLGQSESLSCYAVYSPRVTTTVEADRTCISNIH-QGGTPPVEAAAVIVDLAK
RMLEQKASGINMTR---------------------------------------------
>gi++|26248816|ref|NP_754856.1| ethanolamine ammonia-lyase small subunit
[Escherichia coli CFT073]
--MDQKQIEEIVRSVMASMGQ---------------------------------------
TAPAPSEAKCATTNCAAPVTSESCALDLGSAEAKAWIGVENPHRADVLTELRRSTVARVC
TGRAGPRPRTQALLRFLADHSRSKDTVLKEVPEEWVKAQGL----------------LEV
RSEISDKNLYLTRPDMGRRLCAEAVEALKA-------QCVANP----------DVQVVIS
DGLSTDAITVNYEEILPPLMAGLKQA---G-LKVGTPFFVRYGRVKIEDQIGEILGAKVV
ILLVGERPGLGQSESLSCYAVYSPRMATTVEADRTCISNIH-QGGTPPVEAAAVIVDLAK
RMLEQKASGINMTR---------------------------------------------
>gi++|16130365|ref|NP_416935.1| ethanolamine ammonia-lyase, small subunit (light
chain) [Escherichia coli str. K-12 substr. MG1655]
--MDQKQIEEIVRSVMASMGQ---------------------------------------
AAPAPSEAKCATTNCAAPVTSESCALDLGSAEAKAWIGVENPHRADVLTELRRSTVARVC
TGRAGPRPRTQALLRFLADHSRSKDTVLKEVPEEWVKAQGL----------------LEV
RSEISDKNLYLTRPDMGRRLCAEAVEALKA-------QCVANP----------DVQVVIS
DGLSTDAITVNYEEILPPLMAGLKQA---G-LKVGTPFFVRYGRVKIEDQIGEILGAKVV
ILLVGERPGLGQSESLSCYAVYSPRMATTVEADRTCISNIH-QGGTPPVEAAAVIVDLAK
RMLEQKASGINMTR---------------------------------------------
>gi++|218700906|ref|YP_002408535.1| ethanolamine ammonia-lyase, small subunit (light
chain) [Escherichia coli IAI39]
--MDQKQIEEIVRSVMASMGQ---------------------------------------
AAPAPSEAKCATTTCAAPVTSESCALDLGSAEAKAWIGVENPHRADVLTELRRSTVARVC
TGRAGPRPRTQALLRFLADHSRSKDTVLKEVPEEWVKAQGL----------------LEV
RSEISDKNLYLTRPDMGRRLCAEAVEALKA-------QCVANP----------DVQVVIS
DGLSTDAITVNYEEILPPLMAGLKQA---G-LKVGTPFFVRYGRVKIEDQIGEILGAKVV
ILLVGERPGLGQSESLSCYAVYSPRMATTVEADRTCISNIH-QGGTPPVEAAAVIVDLAK
RMLEQKASGINMTR---------------------------------------------
>gi++|152971314|ref|YP_001336423.1| ethanolamine ammonia-lyase small subunit
[Klebsiella pneumoniae subsp. pneumoniae MGH 78578]
--MDQKQIEDIVRSVMASMGQ-----------------------------------PQSQ
PQAPAASTPACHAACASEAVVESCALDLGSAEAKAWIGVQHPHRAEVLTELKRSTAARVC
TGRAGPRPRTQALLRFLADHSRSKDTVLKEVPEAWVKAQGL----------------LEV
RSEISDKNLYLTRPDMGRRLSPEAIDALKA-------QCVMDP----------DVQVVVS
DGLSTDAITANYEEILPPLLAGLKQA---G-LKVGTPFFVRYGRVKIEDQIGEILGAKVV
ILLVGERPGLGQSESLSCYAVYSPRVATTVEADRTCISNIH-QGGTPPVEAAAVIVDLAK
RMLEQKASGINMSR---------------------------------------------
>gi++|218690575|ref|YP_002398787.1| ethanolamine ammonia-lyase, small subunit (light
chain) [Escherichia coli ED1a]
--MDQKQIEEIVRSVMASMGQ---------------------------------------
TAPAPSEAKCTTTNCAAPVTSESCALDLGSAEAKAWIGVENPHRADVLTELRRSTVARVC
TGRAGPRPRTQALLRFLADHSRSKDTVLKEVPEEWVKAQGL----------------LEV
RSEISDKNLYLTRPDMGRRLCAEAVEALKA-------QCVANP----------DVQVVIS
DGLSTDAITVNYEEILPPLMAGLKQA---G-LKVGTPFFVRYGRVKIEDQIGEILGAKVV
ILLVGERPGLGQSESLSCYAVYSPRMATTVEADRTCISNIH-QGGTPPVEAAAVIVDLAK
RMLEQKASGINMTR---------------------------------------------
>gi++|74312975|ref|YP_311394.1| ethanolamine ammonia-lyase small subunit [Shigella
sonnei Ss046]
--MDQKQIEEIVRSVMASMGQ---------------------------------------
AAPAPSEAKCATTNCAAPVTSESCALDLGSAEAKAWIGVENPHRADVLTELRRSTVARVC
TGRTGPRPRTQALLRFLADHSRSKDTVLKEVPEEWVKAQGL----------------LEV
RSEISDKNLYLTRPDMGRRLCAEAVEALKA-------QCVANP----------DVQVVIS
DGLSTDAITVNYEEILPPLMAGLKQA---G-LKVGTPFFVRYGRVKIEDQIGEILGAKVV
ILLVGERPGLGQSESLSCYAVYSPRMATTVEADRTCISNIH-QGGTPPVEAAAVIVDLAK
RMLEQKASGINMTR---------------------------------------------
>gi++|157158237|ref|YP_001463769.1| ethanolamine ammonia-lyase small subunit
[Escherichia coli E24377A]
--MDQKQIEEIVRSVMASMGQ---------------------------------------
TAPAPSEAKCTTTTCAAPVTSESCALDLGSAEAKAWIGVENPHRADVLTELRRSTVARVC
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TGRAGPRPRTQALLRFLADHSRSKDTVLKEVPEEWVKAQGL----------------LEV
RSEISDKNLYLTRPDMGRRLCAEAVEALKA-------QCVANP----------DVQVVIS
DGLSTDAITVNYEEILPPLMAGLKQA---G-LKVGTPFFVRYGRVKIEDQIGEILGAKVV
ILLVGERPGLGQSESLSCYAVYSPRMATTVEADRTCISNIH-QGGTPPVEAAAVIVDLAK
RMLEQKASGINMTR---------------------------------------------
>gi++|209919921|ref|YP_002294005.1| ethanolamine ammonia-lyase light chain
[Escherichia coli SE11]
--MDQKQIEEIVRSVMASMGQ---------------------------------------
AAPAPSEAKCAATTCAAPVTSESCALDLGSAEAKAWIGVENPHRADVLTELRRSTVARVC
TGRAGPRPRTQALLRFLADHSRSKDTVLKEVPEEWVKAQGL----------------LEV
RSEISNKNLYLTRPDMGRRLCAEAVEALKA-------QCVANP----------DVQVVIS
DGLSTDAITVNYEEILPPLMAGLKQA---G-LKVGTPFFVRYGRVKIEDQIGEILGAKVV
ILLVGERPGLGQSESLSCYAVYSPRMATTVEADRTCISNIH-QGGTPPVEAAAVIVDLAK
RMLEQKASGINMTR---------------------------------------------
>gi++|170683185|ref|YP_001744631.1| ethanolamine ammonia-lyase, light chain
[Escherichia coli SMS-3-5]
--MDQKQIEEIVRSVMASMGQ---------------------------------------
AAPAPSEAKCATTTCTTPVTSESCALDLGSAEAKAWIGVENPHRADVLTELRRSTVARVC
TGRAGPRPRTQALLRFLADHSRSKDTVLKEVPEEWVKAQGL----------------LEV
RSEISDKNLYLTRPDMGRRLCAEAVEALKA-------QCVANP----------DVQVVIS
DGLSTDAITVNYEEILPPLMAGLKQA---G-LKVGTPFFVRYGRVKIEDQIGEILGAKVV
ILLVGERPGLGQSESLSCYAVYSPRIATTVEADRTCISNIH-QGGTPPVEAAAVIVDLAK
RMLEQKASGINMTR---------------------------------------------
>gi++|218548118|ref|YP_002381909.1| ethanolamine ammonia-lyase, small subunit (light
chain) [Escherichia fergusonii ATCC 35469]
--MDQKQIEEIVRSVMASMGQ---------------------------------------
AAPAPSEAKCATTTCAAPVTSESCALDLGSAEAKAWIGVENPHRADVLTELRRSTVARVC
TGRAGPRPRTQALLRFLADHSRSKDTVLKEVPEEWVKAQGL----------------LEV
RSEISDKNLYLTRPDMGRRLCAEAVEALKA-------QCVANP----------DVQVVIS
DGLSTDAITVNYEEILPPLMAGLKQA---G-LKVGTPFFVRYGRVKIEDQIGELLGAKVV
ILLVGERPGLGQSESLSCYAVYSPCMATTVEADRTCISNIH-QGGTPPVEAAAVIVDLAK
RMLEQKASGINMTR---------------------------------------------
>gi++|82777834|ref|YP_404183.1| ethanolamine ammonia-lyase small subunit [Shigella
dysenteriae Sd197]
--MDQKQIEEIVRSVMASMGQ---------------------------------------
TAPAPSEAKCTTTTCAAPVTSESCALDLGSAEAKAWIGVENPHRADVLTELRRSTVARVC
TGRAGPRPRTQALLRFLADHSRSKDTVLKEVPEEWGKAQGL----------------LEV
RSEISDKNLYLTRPDMGRRLCAEAVEALKA-------QCVANP----------DVQVVIS
DGLSTDAITVNYEEILPPLMAGLKQA---G-LKVGTPFFVRYGRVKIEDQIGEILGAKVV
ILLVGERPGLGQSESLSCYAVYSPRMATTVEADRTCISNIH-QGGTPPVEAAAVIVDLAK
RMLEQKASGINMTR---------------------------------------------
>gi++|15802971|ref|NP_289001.1| ethanolamine ammonia-lyase small subunit
[Escherichia coli O157:H7 EDL933]
--MDQKQIEEIVRSVMASMGQ---------------------------------------
TAPAPSEAKCATTTCAAPVTSESCALDLGSAEAKVWIGVENPHRADVLTELRRSTVARVC
TGRAGPRPRTLALLRFLADHSRSKDTVLKEVPEEWVKAQGL----------------LEV
RSEISDKNLYLTRPDMGRRLCAEAVEALKA-------QCVANP----------DVQVVIS
DGLSTDAITVNYEEILPPLMAGLKQA---G-LKVGTPFFVRYGRVKIEDQIGEILGAKVV
ILLVGERPGLGQSESLSCYAVYSPRMATTVEADRTCISNIH-QGGTPPVEAAAVIVDLAK
RMLEQKASGINMTR---------------------------------------------
>gi++|15832565|ref|NP_311338.1| ethanolamine ammonia-lyase small subunit
[Escherichia coli O157:H7 str. Sakai]
--MDQKQIEEIVRSVMASMGQ---------------------------------------
TAPAPSEAKCATTTCAAPVTSESCALDLGSAEAKVWIGVENPHRADVLTELRRSTVARVC
TGHAGPRPRTLALLRFLADHSRSKDTVLKEVPEEWVKAQGL----------------LEV
RSEISDKNLYLTRPDMGRRLCAEAVEALKA-------QCVANP----------DVQVVIS
DGLSTDAITVNYEEILPPLMAGLKQA---G-LKVGTPFFVRYGRVKIEDQIGEILGAKVV
ILLVGERPGLGQSESLSCYAVYSPRMATTVEADRTCISNIH-QGGTPPVEAAAVIVDLAK
RMLEQKASGINMTR---------------------------------------------
>gi++|206576189|ref|YP_002237214.1| ethanolamine ammonia-lyase, light chain
[Klebsiella pneumoniae 342]
--MDQKQIEDIVRSVMASMGQ----------------------------------PQTQP
EAPVATTPACHAAACATDATVESCALDLGSAEAKAWIGVQHSHRAEVLTELKRSTAARVC
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TGRAGPRPRTLALLRFLADHSRSKDTVLKEVPEAWVKAQGL----------------LEV
RSEISDKNRYLTRPDLGRRLSPEAIDALKA-------QCVMDP----------DVQVVVS
DGLSTDAITANYEEILPPLLAGLKQA---G-LKVGTPFFVRYGRVKIEDQIGEILGAKVV
ILLVGERPGLGQSESLSCYAVYSPRVATTVEADRTCISNIH-QGGTPPVEAAAVIVDLAK
RMLEQKASGINMSR---------------------------------------------
>gi++|82544899|ref|YP_408846.1| ethanolamine ammonia-lyase small subunit [Shigella
boydii Sb227]
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------------------MTSESCALDLGSAEAKAWIGVENPHRADVLTELRRSTVARVC
TGRAGPRPRTQALLRFLADHSRSKDTVLKEVPEEWVKAQGL----------------LEV
RSEISDKNLYLTRPDMGRRLCAEAVEALKA-------QCVANP----------DVQVVIS
DGLSTDAITVNYEEILPPLMAGLKQA---G-LKVGTPFFVRYGRVKIEDQIGEILGAKVV
ILLVGERPGLGQSESLSCYAVYSPRMATTVEADRTCISNIH-QGGTPPVEAAAVIVDLAK
RMLEQKASGINMTR---------------------------------------------
>gi++|120554167|ref|YP_958518.1| ethanolamine ammonia-lyase small subunit
[Marinobacter aquaeolei VT8]
--MDEQTIQSIVNSVLRELGE-----------------KDLPAGQVTRVQPEGKSTQRND
PPAYKPSETAGRQGQTESADTGDGLEDLSLEKFVHWNGIENAHNASVNSDMVKQTAARVC
QGRAGPRPRTRSLLRFLADHSRSKDTVVKEVSPEWLEKKNL----------------WEV
QTCISDKSEYLRRPDLGRKLSDDAKKTIGE-------RCKKSP----------QVQVVIS
DGLSTDAVTNNLDEIIPPLMKGLESA---G-FTVGTPFFLRYGRVKAQDEIGNLLQADAN
LLLIGERPGLGQSESLSCYCVYKPTEK-TVESDRMVISNIH-KGGTPPIEAAAVIVDLTR
KMLEQKASGLNLKR---------------------------------------------
>gi++|18309881|ref|NP_561815.1| ethanolamine ammonia-lyase small subunit
[Clostridium perfringens str. 13]
--MNEKDLKLMVEQLVSQMVG-------------------------------------QV
DMQSVEKVVKEVSKNQSQVESDEFIPDITEIDIKKQLLVDNPADREAYLEMKAKTPARLG
SGRAGARYKTITALRMRADHAAAQDSVFSDVSEEFIKKNNF----------------IPV
KTMCTDKDEYVTRPDLGRRFSPETTEIIKE-------KCDKNP----------KVQIMVG
DGLSSAAIEANVEDILPSIEQGLKMY---G-LNVGPILFVKYCRVPAMDAVGEATGADVV
CLLVGERPGLVTAESMSAYIAYKPKVG-MPEAKRTVISNIH-KGGTTAVEAGAHIAELIK
TMLDKKASGIDLK----------------------------------------------
>gi++|187733752|ref|YP_001881238.1| ethanolamine ammonia-lyase, light chain
[Shigella boydii CDC 3083-94]
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---------MNYEEILPPLMAGLKQA---G-LKVGTPFFVRYGRVKIEDQIGEILGAKVV
ILLVGERPGLGQSESLSCYAVYSPRMATTVEADRTCISNIH-QGGTPPVEAAAVIVDLAK
RMLEQKASGINMTR---------------------------------------------
>gi++|89897707|ref|YP_521194.1| ethanolamine ammonia-lyase small subunit
[Desulfitobacterium hafniense Y51]
MHTAEKELERILQGILDELLK--------------------------------EGSSFSA
KNLPGEKETLISKGLKDTPAHELGQEDMVTLMSADEVLVSKPANLEAIKAMKATTPARIG
IGRAGARMKTASLLKFLADHAVAQDAVFADVSPEFLSRMNL----------------FAV
QSSARNKEEFLTHPELGRRLSEESLQIITQ-------KCEKNI----------QVQIIVV
DGLSSSAIEANIPDLLPALTQGLAVS---G-IKTGDPFFVRYGRVWVEDQVASLVNADVV
VSLIGERPGLGTAESLSAYMIYRPDET-TVEADRTVISNIH-KGGIPPAEAGAHLADVIK
QILKARASGVRLNRQIV-----VS-----------------------------------
>gi++|150388099|ref|YP_001318148.1| ethanolamine ammonia-lyase small subunit
[Alkaliphilus metalliredigens QYMF]
-MISEQAVKEMVQQIVEQMTI-----------------------------------GQKQ
TTEDKYTQETDGKEQPEICIEDKNLKDLTEIKMQDYFAVPNPENKEVYLGLKEQTPARVG
IWRTGSRNSTETLLRFRADHAVAMDAVFTYVSEELLEEVGL----------------FSV
NTLCRNKDEYMTRPDLGRKFSQETIEMIKE-------KCVKSP----------QVQIYVS
DGLSSTAIEANIKDILPSIMQGLENE---G-LKVGTPFFVKHGRVPAMDVISETLDAGAT
VVLIGERPGLATGESMSCYMTYGGTVG-MPESRRTVISNIH-RGGTPATEAGAHIAQIVK
EMINQKASGLDLKL---------------------------------------------
>gi++|19703432|ref|NP_602994.1| ethanolamine ammonia-lyase small subunit
[Fusobacterium nucleatum subsp. nucleatum ATCC 25586]
-MVSELELKEIIGKVLKEMAV---------------------------------------
EGKTEGQAVTETKKTSESHIEDGIIDDITKEDLREIVELKNATNKEEFLKYKRKTPARLG
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ISRAGSRYTTHTMLRLRADHAAAQDAVLSSVNEDFLKANNL----------------FIV
KSRCEDKDQYITRPDLGRRLDEESVKTLKE-------KCVQNP----------TVQVFVA
DGLSSTAIEANIEDCLPALLNGLKSY---G-ISVGTPFFAKLARVGLADDVSEVLGAEVT
CVLIGERPGLATAESMSAYITYKGYVG-IPEAKRTVVSNIH-VKGTPAAEAGAHIAHIIK
KVLDAKASGQDLKL---------------------------------------------
>gi++|158319838|ref|YP_001512345.1| ethanolamine ammonia-lyase small subunit
[Alkaliphilus oremlandii OhILAs]
--MDELNLKEMIKSILNEMVG-------------------------------EAPPAVIN
SNSTAERSVGTMQTTKPQGVEERFIPDITAVDIRKQFLVPNAADKEGYLKMKSYTPARLG
LWRAGPRYMTEPSLRFRADHAAAQDAVFSYYVDEDLVKELGF---------------VEV
VTECKDKDEYLTRPDLGRKFSNEAINTIKK-------VVKPNQ----------KVQVIVG
DGLSSAAIEANIKDVLPSLRQGLKMF---G-LDFGEVVFIKHCRVPAMDPIGEATGAEVV
CLLIGERPGLVTAESMSAYIAYKPTIG-MPEARRTVVSNIH-RQGTPAVEAGAYIAEIIK
RMLDNKASGLDLKEK--------------------------------------------
>gi++|125717384|ref|YP_001034517.1| ethanolamine ammonia-lyase small subunit
[Streptococcus sanguinis SK36]
--MDELQLKEMIRSLLNEMGG--------------------------DSAVKETAATDQN
KAEKPAVSLQEEVKQDTSVIEDGIIPDITEVDIQEQFLVPNAINEEAYRKIKKFTPARLG
LWRAGDRYKTQSVLRFRADHAAAQDAVFSYYVSDDFIKEMGF---------------IPV
QTKATTKDEYLTRPDFGRVFPEDQQAIIKE-------KCKPNA----------KVQIVVG
DGLSSSAIEANVKDFLPALKQGLKMF---G-LDFGEVLFIKHARVAAMDQIAELTGAEVI
CMLVGERPGLVTAESMSAYLAYKPTVG-MPEAKRTVVSNIH-KGGTPAVEAGAYVAEIIK
KILDNKKSGIDLK----------------------------------------------
>gi++|16800209|ref|NP_470477.1| ethanolamine ammonia-lyase small subunit [Listeria
innocua Clip11262]
--MNEQELKQMIEGILTEMSG---------------------------------------
GKTTDTVAAAPTKSVVETVVTEGSIPDITEVDIKKQLLVPEPADREGYLKMKQMTPARLG
LWRAGPRYKTETILRFRADHAVAQDSVFSYYVSEDLVKEMNF---------------IPV
NTKCHDKDEYLTRPDLGREFDDEMVEVIRA-------NTTKNA----------KLQIVVG
DGLSSAAIEANIKDILPSIKQGLKMY---N-LDFDNIIFVKHCRVPSMDQIGEITGADVV
CLLVGERPGLVTAESMSAYIAYKPTVG-MPEARRTVISNIH-SGGTPPVEAGAYIAELIH
NMLEKKCSGIDLK----------------------------------------------
>gi++|217964755|ref|YP_002350433.1| ethanolamine ammonia-lyase, light chain
[Listeria monocytogenes HCC23]
--MNEQELKQMIEGILTEMSG---------------------------------------
GKTTDTVAAAPTKSVVETVVTEGSIPDITEVDIKKQLLVPEPADREGYLKMKQMTPARLG
LWRAGPRYKTETILRFRADHAVAQDSVFSYYVSEDLVKEMNF---------------IPV
NTKCQDKDEYLTRPDLGREFDNEMVEVIRA-------NTTKNA----------KLQIVVG
DGLSSAAIEANIKDILPSIKQGLKMY---N-LDFDNIIFVKHCRVPSMDQIGEITGADVV
CLLVGERPGLVTAESMSAYIAYKPTIG-MPEARRTVISNIH-SGGTPPVEAGAYIAELIH
NMLEKKCSGIDLK----------------------------------------------
>gi++|46907396|ref|YP_013785.1| ethanolamine ammonia-lyase small subunit [Listeria
monocytogenes str. 4b F2365]
--MNEQELKQMIEGILTEMSG---------------------------------------
GKTTDTVAAAPTKSVVETVITEGSIPDITEVDIKKQLLVPEPADREGYLKMKQMTPARLG
LWRAGPRYKTETILRFRADHAVAQDSVFSYYVSEDLVKEMNF---------------IPV
NTKCQDKDEYLTRPDLGREFDNEMVEVIRA-------NTTKNA----------KLQIVVG
DGLSSAAIEANIKDILPSIKQGLKMY---N-LDFDNIIFVKHCRVPSMDQIGEITGADVV
CLLVGERPGLVTAESMSAYIAYKPTIG-MPEARRTVISNIH-SGGTPPVEAGAYIAELIH
NMLEKKCSGIDLK----------------------------------------------
>gi++|16803216|ref|NP_464701.1| ethanolamine ammonia-lyase small subunit [Listeria
monocytogenes EGD-e]
--MNEQELKQMIEGILTEMSG---------------------------------------
GKTTDTVAAVPTKSVVETVVTEGSIPDITEVDIKKQLLVPEPADREGYLKMKQMTPARLG
LWRAGPRYKTETILRFRADHAVAQDSVFSYYVSEDLVKEMNF---------------IPV
NTKCQDKDEYLTRPDLGREFDDEMVEVIRA-------NTTKNA----------KLQIVVG
DGLSSAAIEANIKDILPSIKQGLKMY---N-LDFDNIIFVKHCRVPSMDKIGEITGADVV
CLLVGERPGLVTAESMSAYIAYKPTVG-MPEARRTVISNIH-SGGTPPVEAGAYIAELIH
NMLEKKCSGIDLK----------------------------------------------
>gi++|116872550|ref|YP_849331.1| ethanolamine ammonia-lyase small subunit [Listeria
welshimeri serovar 6b str. SLCC5334]
--MNEQELKQMIEGILTEMSG---------------------------------------
GKTTETVEATPAKAITETVVTEGSIPDITEVDIKKQLLVPEPADREGYLKMKQMTPARLG
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LWRAGPRYKTETILRFRADHAVAQDSVFSYVSEDLVKEMNF----------------TPV
NTKCQDKDEYLTRPDLGREFDDEMVEVIRA-------NTTKNA----------KLQIVVG
DGLSSAAIEANIKDILPSIKQGLKMY---N-LDFDNIIFVKHCRVPSMDQIGEITGADVV
CLLVGERPGLVTAESMSAYIAYKPTIG-MPEARRTVISNIH-SGGTPPVEAGAYIAELIH
NMLEKKCSGIDLK-----------------------------------------------
>gi++|126699524|ref|YP_001088421.1| ethanolamine ammonia-lyase small subunit
[Clostridium difficile 630]
--MNEKDLKALVEQLVGQMVG---------------------------------------
ELDTNVVSETVKKATEVVVDNNACIDDITEVDIRKQLLVKNPKDAEAYLDMKAKTPARLG
IGRAGTRYKTETVLRFRADHAAAQDAVFSYVDEEFIKENNM----------------FAV
ETLCKDKDEYLTRPDLGRKFSPETINNIKS-------KFGTNQ----------KVLILVG
DGLSSAAIEANLKDCVPAIKQGLKMY---G-IDSSEILFVKHCRVGAMDHLGEELGCEVI
CMLVGERPGLVTAESMSAYIAYKPYIG-MAEAKRTVISNIH-KGGTTAVEAGAHIAELIK
TMLDKKASGIDLK-----------------------------------------------
>gi++|119718252|ref|YP_925217.1| ethanolamine ammonia-lyase light chain
[Nocardioides sp. JS614]
--MSTDELRSIVAEVLAELAEPGDAFARLTTPATTAGPSGPTSTPAPEESDAPSSAATEP
AAVPASSATEITRPTLSGAPVSIEVSDPTVPEARHRIGVENPANPSGLANLAASTAARIA
VGRAGPRPRTESVLLFGADHAVTQDAIFGDVPTALLDQFGL----------------FAV
QTKVTTQDEFLLRPDLGRELDDAAKLVVAE-------KCVKGP----------QVQIVVG
DGLSAAAVTNNLPQIYPVLEAGLRDA---G-LTLGTPFFVRYCRVGVINDINDIVGADVV
VLLIGERPGLGVADALSVYSGWRPTAG-KTDAHRDVICMITQNGGTNPLEAGAFAVEHVK
NVMKHQASGVELRLQES------------------GTR----------------------
>gi++|160880777|ref|YP_001559745.1| ethanolamine ammonia-lyase small subunit
[Clostridium phytofermentans ISDg]
--MDEQSLRKMVEQMVEQMVG-------------------------------------GG
TNVKSTTSTSSVGQGSATAISSECLPDITKIDIKSWFLLDHAKNKEEYLHMKSKTPARLG
VGRAGARYKTMTMLRVRADHAAAQDAVFSDVSEEFIKKNKF----------------VFV
KTLCKDKDEYLTRPDLGRRFGKEELEVIKK-------TCGQSP----------KVLIIVG
DGLSSSAIEANVEDMIPAIKQGLSMF---Q-INVPPILFIKYARVGAMDDIGQATDADVI
CMLVGERPGLVTAESMSAYICYKAKHG-VPESKRTVISNIH-RGGTTPVEAGAHAAELIK
KMLDKKASGIELKG----------------------------------------------
>gi++|28211784|ref|NP_782728.1| ethanolamine ammonia-lyase small subunit
[Clostridium tetani E88]
-MFSESDLKRLVEEVLVEMTT---------------------------------------
KEGANIKDTPVSQPTPTVVDEDGIIPDITEVDIRTNLLVDNPENAEEYLKMKKHTPARIG
VGKAGTRYKTETILRFRADHAAAQDAVFTDVDEKILEEMNL----------------ETI
QTMCSSKDEFITRPDLGRKISKEELSKLS--------SYKKNA----------QVQIYVS
DGLSSKAVEANVKNILPALIQGLEGY---G-ISVGKPFFVKLGRVGAMDVISEEFGADVT
CVLIGERPGLVTAESMSAYIAYKGTVG-MPESRRTVVSNIH-KGGTPAVEAGAYIADIIK
LMLEKKASGLDLKL----------------------------------------------
>gi++|169827648|ref|YP_001697806.1| ethanolamine ammonia-lyase light chain
[Lysinibacillus sphaericus C3-41]
-MITQLVMEKMEKTTEGQASE-------VTTTPTEPLIKFYDTTATSGATEIAEPMSTST
KSEPLIQLYQHGTPQQAHIAPVAVEQPLNVAVPIKPFQFEADTLTESIQAAKKHTPARIG
VGRAGTRPKTKTWLKFRLDHAAAVDAVYGEVTEDLLQKLDV----------------FQV
TTKVTDKEEYITRPDLGRRLSDEAKSLIQQ-------KCKQQP----------KVQVIIS
NGLSASAIEENVQDVYLALQQSLSNL---N-IDLGTTFYIDKGRVALMDEIGELLQAEVI
VYLIGERPGLVSAESMSAYLCYKPRIG-TVEAERMVISNIH-KGGIPPLEAGAYLGTIVQ
KILHYQASGVELVAKEG-------------------------------------------
>gi++|29376186|ref|NP_815340.1| ethanolamine ammonia-lyase small subunit
[Enterococcus faecalis V583]
--MNEKELKEMIAGILTEMVA--------------------------------DNQAVST
ATVTAEEKPVTTHVTETTEIEEGLIPDITEVDLRKQLLLKNAVDPEALLKMKAFSPARLG
VGRAGTRYMTSSTLRFRADHAAAQDAVFSDVSEDLVKEMNF----------------IST
KTICNSKDEYLTRPDYGRQFDEENSEIIRK-------NTTPKA----------KIQMVVG
DGLSSAAIEANIKEVLPAIKQGLNMY---N-LDFDNVVFVKYCRVPAMDKIGEITDADVV
CLLVGERPGLVTAESMSAYIAYKPTVG-MPEARRTVISNIH-KGGTPAVEAGAYIAEIIK
KMLDKKKSGIDLKEAE--------------------------------------------
>gi|37526861|ref|NP_930205.1| ethanolamine ammonia-lyase small subunit [Photorhabdus
luminescens subsp. laumondii TTO1]
----------------------------------------------------MNQKTIEK
NVSERVSNLKPHASPEITNEIESCMPDLGSLEAKQWIGVQNPNRIEVLQELRRSTVARVG
```

```
TGRSGPRPRTQALLRFQADHSRSKDTVLKEVPTEWIEKQGL----------------LEV
QSQVSDKNLYLTRPDLGRKLSANAVETLLT-------QCKTAP----------DVQVVIS
DGLSTDAITTNYEDLVPPLLKGLEQA---G-MCIGTPFFVRYGRVKIEDQIGELLKAKVV
VLLIGERPGLGQSESLSCYAVYQPTVEKTVEADRTCISNIH-RGGTPPIEAAAIIVDLAK
NMLEQQASGIALSR---------------------------------------------
>gi|15895974|ref|NP_349323.1| ethanolamine ammonia-lyase small subunit [Clostridium
acetobutylicum ATCC 824]
------------------------------------------------------------
---------------------------------MENLLKIYDIKEEELSELKALTPARIC
VGRAGTRLKTNTFLKFRADHAVAMDAVWSSVDEKLIDTLNF----------------LKV
QTLAKDKEEYITRPDLGRKFSEETLDYIKN-------NCINEP----------DVQIIAG
DGLSATAINANLRKIYFVIVEKLKSR---G-YKVGTPIFVKYARVATMDKISEELNAKVT
IILIGERPGLATGESMSSYMAYESSTK-KPESQRTVVSNIH-NKGIPSVDAGKEIVRIID
IMMKEKKSGVELRI---------------------------------------------
>gi|111224926|ref|YP_715720.1| ethanolamine ammonia-lyase light chain (ethanolamine
ammonia-lyase small subunit) [Frankia alni ACN14a]
--------MTPDSDPTAASPE---------------------------------------
-----------------------------RTSPDRGPAAVPVDLAALAERVRAVTPARVF
VGRTGTSYRTANLLALRADHAAARDAVDAELDLAGPALAAT----T-ER-FGL----FVV
QSAAADRAEYLRRPDLGRRLSDAGRAQVAA-------RCPPGA----------DLQIVIG
DGLSAAAVDAQVPALLPALLTAAAEA---G-WSTGQPFAVRQCRVGVMNDIGDLLHPTVI
VLLIGERPGLATAESLSAYLAHRPRSG-HTDADRNLLSNIH-RRGVTPTQAVDRITGLAQ
TVRAAGTSGVSIKEPPT---------------APQIHT---------------------
>gi|146341485|ref|YP_001206533.1| ethanolamine ammonia-lyase light chain
(ethanolamine ammonia-lyase small subunit) [Bradyrhizobium sp. ORS278]
------------------------------------------------------------
------------------------------MMNGVENKAPATSSADDWTWLSRYTEARIA
LGRCGPGVPTSAHLGFQAAHAEARDAVLKPFDAEQLAADAT----A-RG-WPA----LAV
HSRAADRATYLQRPDEGRLLSPASEALLS--------EPRAPA----------DIVLVVA
DGLSSRAVQVNALPVLDTLMPLLAAT---G-RRLSPIIIASQGRVALADHVGELFGASAS
IILIGERPGLSAADSLGLYLTWMPRRG-RVDSERNCISNVR-HGGLAPDDAAKQSAELIA
RMFQHQAAGVSLARLPQ----------LPALEDGSS-----------------------
>gi|86748842|ref|YP_485338.1| ethanolamine ammonia-lyase small subunit
[Rhodopseudomonas palustris HaA2]
------------------------------------------------------------
-------------------------------------MTSSPTAPPALSDLRRLTPARVA
LGRAGVSLTTDALLDFTLAHARARDAVHAAFDAAAVAAELG----A-LG-LTP----LQV
SSRAQSRRDYLARPDLGRQLDPASRAMLE--------AHPSTA----------DLALVIG
DGLSPVAVAAQAGEVVRRLLPRLAAS---G-IGVGPAAVVTGARVALGDEIGALLGARIV
LVLIGERPGLSAPASLGAYVTLGPRPG-RTDADRNCVSNIH-AAGISPDEAAFKIAWLVR
ESMARGASGVALKDESG--------------EGGSTPA------ELPGPG---------
>gi|115523824|ref|YP_780735.1| ethanolamine ammonia-lyase small subunit
[Rhodopseudomonas palustris BisA53]
------------------------------------------------------------
-------------------------------------MTKPTPTIHSLRDLRRLTPARVG
LGRSGASVPTKALLDFTLDHARARDAVHASFDGAALTGELS------ALGLAV----HEV
RSRVRGRHDYLVRPDLGRQLDPESRDRLAG-------IGGPGG----------DLVLVIG
DGLSPGAVHARAAAVVGRLLKRLTEA---G-IAVGPAVVANGARVALGDEIGALLGARMV
AVLIGERPGLSSPASLGAYLTYAPRPG-LTDAERNCVSNIH-PAGLSEDEAAFKIGWLIR
EALARRLSGVALKDDSM-------------LEAATAAR------ELSAPG---------
>gi|148255137|ref|YP_001239722.1| ethanolamine ammonia-lyase light chain
[Bradyrhizobium sp. BTAi1]
------------------------------------------------------------
-------------------------------MSETDDQAPATSSSDDWSWLSRYTAARIA
LGRCGPGLPTSAHLGFQAAHAEARDAVLKPFDAAGCAADVT----A-RG-WPA----IVV
RSRAADRATYLQRPDAGRLLAPDSEALLS--------EPRAPA----------DIALVVA
DGLSSRAVQVNALPVLDTLMPLLAAT---G-RRLSPIIVAAQGRVALADHVGELFDASAS
IILIGERPGLSAADSLGLYLTWMPRRG-RVDSERNCISNVR-HGGLAPEDAAKQAAELIA
RMFKHRAAGVSLARLPQ-------------LPAPDGS----------------------
>gi|90423221|ref|YP_531591.1| ethanolamine ammonia-lyase small subunit
[Rhodopseudomonas palustris BisB18]
------------------------------------------------------------
-------------------------------------MNPRPPLLQSPRDLRRLTPARVG
```

```
LGRTGASLPTQALLDFTLDHARARDAVHSTFDSARLAAELA----A-LG-LAS----CEV
SSRARGRRDYLVRPDLGRQLDPASHDALARR------GVGAPC----------DLALMVG
DGLSPTAVNARAVDVVRGLLPRLAAA---D-LTIGVAAVATGARVALGDEIGVLLGARMV
LVLIGERPGLSAPASMGAYLTFAPRPG-ITDAERNCVSNIH-AAGISNDEAAYKIGWLLR
ESFARQISGVALKDDSA-------------LQARDLAP------RRVEQT---------
>gi|39936808|ref|NP_949084.1| ethanolamine ammonia-lyase small subunit
[Rhodopseudomonas palustris CGA009]
------------------------------------------------------------
-------------------------------------MNSPATPPRSLAELRRLTPARVA
LGRAGASLPTEALLDFTLAHARARDAVHAGFDATAIAAELQ----A-LG-LPT----LPV
SSRAADRRDYLARPDLGRQLDPASRAVLD--------GAGKAV----------DVALVIG
DGLSPVAVAAQATAVVRHLLPRLAAV---R-IGVGAAVVATGARVALGDEIGAALGARMV
VVLIGERPGLSAPASLGAYLTFGPRPG-LTDADRNCVSNIH-ASGISADEAAHKIAWLVG
EGLVRKATGVTLKDESG------------SLMPELPKS---------------------
>gi|170749714|ref|YP_001755974.1| ethanolamine ammonia-lyase [Methylobacterium
radiotolerans JCM 2831]
------------------------------------------------------------
---------------------------------MSDPAEPARPGPPTLRDLRGLTQARIA
LGAHGAGLPTGAALAFGLDHARAREAVWTPLDAAAIREALR----V-EG-LDS----VEV
RSAVADRTEYLRRPDKGRSLDPGAASALDG-------HG-PGF----------DVAVVIA
DGLSATAVALNAVPAAAALAARVRRA---G-WSLAPVVVALQGRVAIGDPIGARLGARCV
VVLIGERPGLSASDSLGCYVTFGPEPG-LPDARRNCISNIR-EGGLAVEAAAGQMEALLR
AMLAQGTSGVALRRGDP--------ADPPALPDARD-----------------------
>gi|71733540|ref|YP_276773.1| ethanolamine ammonia-lyase small subunit [Pseudomonas
syringae pv. phaseolicola 1448A]
------------------------------------------------------------
----------------------------------MNEIQDNAAPANPWLELRRLTSARIA
LGRTGTSLPTSAQLDFQAAHAQARDAVHLAFDHAAISAQLT------EKGRET----ILL
HSAAADRDSYLQRPDLGRRLNEESAQALREYAA----AHPGGL----------DLAVVVA
DGLSALAVHRHAVPFLTRLEEQANVE---G-WSLSPVIMVEQGRVAVADEVGELLGAKMV
VILIGERPGLSSPDSLGLYFTYAPKVG-LNDAHRNCISNVR-LEGLSYGMAAHRLLYLMR
EACRRQISGVNLKDEAQ----------LQTLDSDGSAEHSGKPIGNFLLDGPAAPH---
>gi|222080798|ref|YP_002542526.1| Ethanolamine ammonia-lyase [Agrobacterium
radiobacter K84]
------------------------------------------------------------
-----------------------------------MANSVINARAIGIADLKDMTDARVA
LGRFGAGAPTKAAQAFLLDHARAREAVWSSVDQEGLQRQLL------DLQLDA----VVV
ESLAGDRSQYVRRPDLGRKLSATSLAQLDAIR-----HGDDGF----------DVVIIVA
DGLSASAVDINAAAVVGALADRLRRH---G-FSLAPVVIASQARVALSDPIGEALAAKTA
IMLIGERPGLSAADSLGAYVTYSPRSD-TPDSRRNCVSNIR-EGGLPIAAAADQIIELVI
AMRMTGISGVGLKDAVA------------KLEVTA------------------------
>gi|21243100|ref|NP_642682.1| ethanolamine ammonia-lyase small subunit [Xanthomonas
axonopodis pv. citri str. 306]
------------------------------------------------------------
------------------------------------MSVPSTPPRDAWAQLRQLTPARIA
LGRVGTSLPTDAHLEFQLAHAQARDAVHLAFDPAPLQAALE------QRGRSN----ILL
QSAAADRHQYLQRPDLGRRLAEEAAAQLRGLTA----VHGGRH----------DVAVVVA
DGLSALAVHRHAARMLDQIDALASQE---G-WSLAPVVLVRQGRVAIGDEVGELLDARTV
IVLIGERPGLSSPDSLGLYLTYTPRVG-LTDAARNCISNIR-AEGLSYAEATHKLGYLLR
EAFRRKLSGVQLKDEAE----------QPALLSGPADVAPRTFLLPD------------
>gi|217978557|ref|YP_002362704.1| Ethanolamine ammonia-lyase [Methylocella
silvestris BL2]
------------------------------------------------------------
--------------------------------------MNDLVVVNPWEGLRRLTQARIA
LGRAGVSIPTKPLLDFQFAHARARDAVHLPMDREGLCARME------AAQFPV----IEL
HSAAPDRTTYLQRPDLGRKLGADSREKLAALAA----KGAHGF----------DIAFVVA
DGLSAFAVNEHALSMLEAIRPKLTEA---G-WRMAPVALVEQGRVAIGDEIGAIFGAEIV
VILIGERPGLSAPDSLGLYMTYAPRVG-LTDEARNCISNVR-PEGQSFGAAAHRLDYLLK
EAKRRKLSGVDLKDESE----------MKVLPTEGKQDQTNFLISEGAVPPV-------
>gi|66043894|ref|YP_233735.1| ethanolamine ammonia-lyase small subunit [Pseudomonas
syringae pv. syringae B728a]
------------------------------------------------------------
----------------------------------MNELQDSAAPANPWLELRRLTPARIA
```

```
LGRTGTSLPTSAQLDFQAAHAQARDAVHLAFDHAAISAQLT------EKGRET----LLL
HSAAADRDSYLQRPDLGRRLNDESAQTLRDYAA----AHPGGL----------DLAIVVA
DGLSALAVHRHAVPFLIRLEEQASAE---G-WSLSPVIMVEQGRVAVADEVGELLGAKMV
VILIGERPGLSSPDSLGLYFTYAPKVG-LNDAHRNCISNVR-LEGLSYGMAAHRLLYLMR
EACRRQISGVNLKDEAE----------LQTLESDGAGDHSDKPIGNFLLDGPAAPH---
>gi|28867954|ref|NP_790573.1| ethanolamine ammonia-lyase small subunit [Pseudomonas
syringae pv. tomato str. DC3000]
------------------------------------------------------------
-----------------------------MSDQPMNEVQDNAAPANPWLELRRLTPARIA
LGRTGTSLPTCAQLDFQAAHAQARDAVHLAFDHAAISAQLA------EKGRET----ILL
HSAAADRDSYLQRPDLGRRLNDESAQTLRDYAA----AHPGGL----------DLAVVVA
DGLSALAVHRHAVPFLTRLEEQASAE---G-WTLSPVLMVEQGRVAVADEIGELLGAKMV
VILIGERPGLSSPDSLGLYFTYAPKVG-LNDAHRNCISNVR-LEGLSYAMAAHRLLYLMR
EACKRQISGVSLKDEAQ----------LNTLESDDSAENSDRKIGNFLLDGPAVPH---
>gi|21231699|ref|NP_637616.1| ethanolamine ammonia-lyase small subunit [Xanthomonas
campestris pv. campestris str. ATCC 33913]
------------------------------------------------------------
------------------------------------MSTPTTPPRDAWARLRALTPARIA
LGRAGTSLPTASHLEFQLAHAQARDAVHLAFDPAPLQAVLQ------QRGRRS----VLL
HSAASDRHLYLQRPDLGRRLSDEAAEQLRGTTA----VHGGGA----------DLAVVVA
DGLSALAVHRHAGAMLEQIDALAAHE---G-WSLAPVTLIAQGRVAIGDEVGELLQARAV
IVLIGERPGLSSPDSLGLYLTYAPRVG-HTDAARNCISNIR-GEGLSYAEAGHKLGYLLR
EAFRRKLSGVQLKDEAD----------RPLLGTDTASQAAPRNFLLPE-----------
>gi|66768175|ref|YP_242937.1| ethanolamine ammonia-lyase small subunit [Xanthomonas
campestris pv. campestris str. 8004]
------------------------------------------------------------
------------------------------------MSTPTTPPRDAWARLRALTPARIA
LGRAGTSLPTASHLEFQLAHAQARDAVHLAFDPAPLQAVLQ------QRGRRS----VLL
HSAASDRHLYLQRPDLGRRLSDEAAEQLRGTTA----VHGGGA----------DLAVVVA
DGLSALAVHRHAGAMLEHIDALAAHE---G-WSLAPVTLIAQGRVAIGDEVGELLQAQAV
IVLIGERPGLSSPDSLGLYLTYAPRVG-HTDAARNCISNIR-GEGLSYAEAGHKLGYLLR
EAFRRKLSGVQLKDEAD----------RPLLGTDTASQAAP---RNFLLPE--------
>gi|27378107|ref|NP_769636.1| ethanolamine ammonia-lyase small subunit
[Bradyrhizobium japonicum USDA 110]
------------------------------------------------------------
-------------------------------------MSDPAVPRRPTLDLRSFTPARVA
LGRSGASVPTRALLDFTLDHARARDAVHAVFDVPRLLADLG------ALGLAV----TEA
RSRAADRRDYLRRPDLGRQLDAGSIEALAR-------IASRPC----------QLAIVIG
DGLSAAAVHAHAVALVTRLLPLLAAD---DAVALGHVVVASGARVALGDQIGAILGARMV
VTLIGERPGLSAPDSLGAYLTFAPTPG-RTDAERNCVSNIH-HAGLSNDEAAFKIAWLLR
EGLAREVTGVALKDESA--------DRAPRRIGTSLPE---------------------
>gi|17547845|ref|NP_521247.1| ethanolamine ammonia-lyase small subunit [Ralstonia
solanacearum GMI1000]
------------------------------------------------------------
-------------------------------MTDERDDTPATVTQNPWQALRRLTPARIA
LGRAGVSLPTRPQLAFQAAHAQARDAVHLPFDPAALQAQLH------AQGHAT----LLL
HSAARDRDQYLQRPDLGRQLDAPSAQLLGDHAA----AHPGGV----------DIALVVA
DGLSALAVHRHAAPLIAGVAEGVRAQ---G-WSMAPIALVEQGRVAVADEVGERLGARMV
VILIGERPGLSSPDSLGLYFTYAPRVG-LTDAARNCISNVR-PEGLGYAAAAHKLLYLMR
EAWRRQGSGVLLKEAAE----------VPLLEAGRRNFLLD------------------
>gi|167647492|ref|YP_001685155.1| ethanolamine ammonia-lyase [Caulobacter sp. K31]
------------------------------------------------------------
---------------------------------MSGPILPKGVTPDPWTALRRHTPARIA
LGRTGSSLPTSEVLGFALAHAQARDAVHAPFEAQATAAAIQ----A-LG-LET----LIV
DSAAPDRASYLRRPDLGRTLSQAGRAALS--------PGRGSH----------DLAIVIA
DGLSSTAVHAHAAPLVEALLPAVREA---G-WSLAPVVIARQARVALGDAVGELLGARLV
ILLVGERPGLSSPDSLGAYITFGPRVG-RTDAERNCVSNIR-AEGLGYGAAAFKLAWHAR
EALRLGLTGVALKDESD-----------TALLDVTTPR------IAPAGSRSPTG----
>gi|183221859|ref|YP_001839855.1| ethanolamine ammonia-lyase, light chain
(ethanolamine ammonia-lyase small subunit) [Leptospira biflexa serovar Patoc strain
'Patoc 1 (Paris)']
------------------------------------------------------------
-----------------------------------------MSDLDQW---KQFTQARIG
```

```
LNRVGGSIATKEMLKFRLDHANAKDAVNQEPNWELIQKQSN----ELCQIYGI--QNIFI
KSQVSSKQEYLLRPDLGRRISEESKLSLF--------PYNLGY----------DLSIVCI
DGLSAKAIDDNLISFLELFFAKIQNT---N-LSIAPLVLSRWGRVALGDEIAEILKAKIC
IVIIGERPGLSAADSLGIYLTYEPKLG-FTDESRNCISNVR-PLGLPFSLAVEKTIYLIK
ECLLQKKSGVLLKDQMP--------GEIKPLNEKKIIP------IQPTVD---------
>gi|170719780|ref|YP_001747468.1| ethanolamine ammonia-lyase small subunit
[Pseudomonas putida W619]
------------------------------------------------------------
------------------------------------MDRQIPTPENPWLALRNLTPARIA
LGRSGISLPTSAQLDFQFAHAQARDAVHLAFDHTALSEQLK------ERGRDS----LVL
HSAASDRNQYLQRPDLGRRLNERSVEQLRQHAK----TNPGGC----------DLAIVVA
DGLSALAVHRHTLPFLARFEEQAAAD---G-WTSAPVVLVEQGRVAVADEVGQLLGARMT
VMLIGERPGLSSPDSLGLYFTYAPKVG-LTDAYRNCISNVR-LEGLSYGMAAHRLLYLMR
EACRRQLSGVNLKDEAE----------VHTIDSENTSNQK----GNFLLGEG-------
>gi|34496639|ref|NP_900854.1| ethanolamine ammonia-lyase small subunit
[Chromobacterium violaceum ATCC 12472]
------------------------------------------------------------
-----------------------------------MKEKQNPVTEDGWGELSRLTAARIA
LGRAGSSLPCRETLRFALAHAQARDAVHTPLDAAALAGELA------ANGHRV----IDI
RSAASSRAEYLQRPDLGRRLDDASRARLLA-------ETDKGC----------DLLILIA
DGLSSRAPAQHAVPLLRELLPRVREM---G-LRVGPLLIAREARVALGDEAGEIMGARMT
AMLIGERPGLSSPDSLGLYLTAAPRAG-RSDAERNCISNVR-PDGLPYPLAAFKLAWLID
AAL-RQPTGVALKDGSA------ADPRWAALAARQASLVRN------------------
>gi|77461213|ref|YP_350720.1| ethanolamine ammonia-lyase small subunit [Pseudomonas
fluorescens Pf0-1]
------------------------------------------------------------
------------------------------------MEKPPVDPQNPWLELRRLTPARIA
LGRTGTSLPTRAQLDFQYAHAQARDAVHLPFDHAALSAQLN------ERQRES----LLL
HSAAVDRNSYLQRPDLGRKLSDQSAQTLREYAQ----AHPGGV----------DLVIVVA
DGLSALAVHRHTLPFLTRLEEQMSAD---E-WSTAPVVLVEQGRVAIGDEIGQLLGAKMV
VMLIGERPGLSSPDSLGLYFTYNPKVG-LTDAYRNCISNVR-LEGLSYGMAAHRLLYLMR
EACRRQLSGVNLKDEAQ----------VQTLESEAGTDMKSNFLLDPPPA---------
>gi|26987280|ref|NP_742705.1| ethanolamine ammonia-lyase small subunit [Pseudomonas
putida KT2440]
------------------------------------------------------------
------------------------------------MDHRTPTPDNPWLALRNLTPARIA
LGRTGTSLPTGAQLDFQFAHAQARDAVHLAFDHAGLASQLS------DRGRES----LVL
HSAASDRHQYLQRPDLGRRLNEDSIATLRQHAQ----ANPGGV----------DLAIVVA
DGLSALAVHRHTLPFLTRFDEQAAAD---G-WTCAPVVLVQQGRVAVADEVGELLGARMT
VMLIGERPGLSSPDSLGLYFTYAPKVG-LTDAYRNCISNIR-LEGLSYGMAAHRLLYLMR
EACRRQLSGVNLKDEAE----------VHSLENEDSANQK----GNFLLGKG-------
>gi|148545831|ref|YP_001265933.1| ethanolamine ammonia-lyase small subunit
[Pseudomonas putida F1]
------------------------------------------------------------
------------------------------------MDHRTPTPDNPWLALRNLTPARIA
LGRTGTSLPTGAQLDFQFAHAQARDAVHLAFDHAGLASQLS------DRGRES----LVL
HSAASDRHQYLQRPDLGRRLNEDSITTLRQHAQ----ANPGGV----------DLAIVVA
DGLSALAVHRHTLPFLTRFDEQAAAD---G-WTSAPVVLVQQGRVAVADEVGELLGARMT
VMLIGERPGLSSPDSLGLYFTYAPKVG-LTDAYRNCISNIR-LEGLSYGMAAHRLLYLMR
EACRRQLSGVNLKDEAE----------VHSLENEDSASQK----GNFLLGKE-------
>gi|167031603|ref|YP_001666834.1| ethanolamine ammonia-lyase small subunit
[Pseudomonas putida GB-1]
------------------------------------------------------------
------------------------------------MDHRTPTPDNPWLALRNLTPARIA
LGRTGTSLPTGAQLDFQFAHAQARDAVHLAFDHAGLASQLS------DRGRDS----LVL
HSAASDRHQYLQRPDLGRRLNEDSIATLRQHTQ----ANPGGV----------DLAIVVA
DGLSALAVHRHTLPFLNRFEEQAAAD---G-WTSAPVVLVQQGRVAVADEVGELLGARMT
VMLIGERPGLSSPDSLGLYFTYAPKVG-LTDAYRNCISNIR-LEGLSYGMAAHRLLYLMR
EACRRQLSGVNLKDEAE----------VHSLESEGSASQK----GNFLLGKG-------
>gi|186474780|ref|YP_001856250.1| ethanolamine ammonia-lyase [Burkholderia phymatum
STM815]
------------------------------------------------------------
--------------------------------------MSDSIEKNAWQALRAFTNARIA
```

```
LGRAGNSLPTAPLLAFNLSHAQARDAVHHPLDVDVLHEQLR------TLGFST----LDV
HSAAPDRAHYLRRPDMGRRLSDESREALTHA------AASEAP----------DVVFVIA
DGLSAFAASKQSVPFLQAVTKRLA-----G-WKIGPVVVARQSRVALGDEIGELLRSKLV
VMLIGERPGLSSPDSLGVYLTYAPKVG-CSDAQRNCISNVR-PEGLDYEAAAHKLHYLLT
HARRLGLTGVGLKDDSD-----------ALLQAPETKP----TIADDSKTR--------
>gi|187922056|ref|YP_001893698.1| ethanolamine ammonia-lyase small subunit 
[Burkholderia phytofirmans PsJN]
------------------------------------------------------------
--------------------------------------MSDFLEKNPWNALRQFTNARIA
LGRAGNSLPTAPLLAFNLSHAQARDAVHHPLDTEVLHEQLR------AQNFKT----LDV
HSAAPDREHYLRRPDLGRRLSEESRVTLAA-------VPNDSP----------EVVFVIG
DGLSAFAASKQSIPLLQAVVPRLAD------WKIGPVVVARQARVALGDEIGELLNAKLV
VMLIGERPGLSSPDSLGIYLTYAPKVG-CSDAQRNCISNVR-PEGLDYPLAAHKLHYLLT
HARRLGLTGVGLKDDSD-----------ALLAETPAAP----AVSDDSNSSAP------
>gi|124267604|ref|YP_001021608.1| ethanolamine ammonia-lyase light chain 
[Methylibium petroleiphilum PM1]
------------------------------------------------------------
-------------------------------------MSGGPVIANPWSVLRRHTPARIG
LGRSGISQPTAPQLDFQLAHAQARDAVHRPLDHEAVDAAVR----A-LG-LPT----LAL
HSAAADRHIYLQRPDLGRRLDEASIARLAAC------TANEQA----------DLALVVA
DGLSALAIERHAAPFIAELRRVLARD-----WRWAPVAIVRQARVAIGDPIGEALGARLA
VVLVGERPGLSSPDSMGVYVTWSPRAG-RVDAERNCISNVR-PEGLPLPQAAARLAWLLG
EARSRQLTGVALKDDSG-----------PALETGGDSG----SFLLAPP----------
>gi|182677068|ref|YP_001831214.1| ethanolamine ammonia-lyase [Beijerinckia indica 
subsp. indica ATCC 9039]
------------------------------------------------------------
---------------------------------------MSDPYADPWVFLREKTPARIA
LGRCGDGLPTARLLEFQRDHARARDAVHAALDSEKLCSELD----P----LKP----IIV
QSQARDRALYLQRPDLGRRLDEASREKLRE----------GFY----------DISLVLA
DGLSALAVQSQAARLGALIEKRLP-------LRFAPPVIALQARVALGDEIASALGARLV
IVLIGERPGLSAADSLGAYITFAPVPGKTTDAQRNCISNIR-PGGLSLEEAARRIGAIAS
YALHLQGTGTMLKEDAA----------LNALAPPEAMKER-------------------
>gi|104779888|ref|YP_606386.1| ethanolamine ammonia-lyase small subunit [Pseudomonas 
entomophila L48]
------------------------------------------------------------
------------------------------------MDRHTPTPDNPWLALRNLTPARIA
LGRTGISLPTGAQLDFQYAHAQARDAVHLPFDHAGLRQQLS------DRGRDS----LLL
HSAASDRHQYLQRPDLGRRLHEDSAQRLREHAQ----ANPGGV----------DLAIVVA
DGLSALAVHRHTLPFLSRFEEQAAAE---G-WTSAPVVLVEQGRVAVADEVGELLGARMT
VMLIGERPGLSSPDSLGLYFTYAPKVG-LTDAYRNCISNVR-LEGLSYGMAAHRLLYLMR
EACRRQLSGVNLKDEAE----------VHSIDSNNTGTKS----GNFLLGEG-------
>gi|114328556|ref|YP_745713.1| ethanolamine ammonia-lyase light chain [Granulibacter 
bethesdensis CGDNIH1]
------------------------------------------------------------
---------------------------MVEKSAGNPPDHTTTPTIDPWAKLRAATSARIG
LGRAGDAMRTRDVLDFQLAHACARDAVHTPLDTAALQAALA----P----RET----ILV
QADVDSRGTYLRRPDLGRRLSPDCTNVLQK----------GDW----------DVVFVIA
DGLSSTAVQVHAAPFLQQVITLLP-----G-WRIAPVVIATQARVALGDDIGERIGAKLC
ALLVGERPGLTAADSLGVYLTYDPKRG-RRDSERNCISNIH-GGGLSYATAADKLTWLMS
EARSRKLTGVALKDDPL-----LPGAAVPTPLSADPPG---------------------
>gi|121605521|ref|YP_982850.1| ethanolamine ammonia-lyase small subunit [Polaromonas 
naphthalenivorans CJ2]
------------------------------------------------------------
-----------------------------------MNTKVSPVTANPWETLRQFTDARIA
LGRAGVSLPTAAHLAFQLAHAQARDAVLVALDVPGLSQSLN----AVSGKQTC----LSL
HSAAADRTVYLQRPDLGRRLDDASRETLEGLKPAGPEPSVRLY----------DLAFVVV
DGLSALAIEQNAAPFLSVLQRRIAAE---N-WSVAPLCIVSQGRVAIGDEVGELLGAKAV
VVLIGERPGLSSPDSMGLYLTWMPRVG-LLDDSRNCISNVR-PAGLRYEEAAYKLHYLLS
QARQRQLTGVDLKDEALADPERLRVSEKNFLLDHSRTP----GASGSQA----------
>gi|157371672|ref|YP_001479661.1| ethanolamine ammonia-lyase [Serratia 
proteamaculans 568]
------------------------------------------------------------
--------------------------------------MSKPVHVNRWDALRAFTDARIA
```

```
LGRTGSSLPTEELLKFGLAHAQARDAVHQPFDSDTLGGALQ------DQGWPT----LTV
HSQAADRTAYLSRPDLGRRLAADSRSLLLD-------LPDKPV----------DLLLVVA
DGLSSKAVHRQALPLLQALRPYLELL---G-LSVAPVVLAHQSRVALGDDIGECLGARAV
AMLIGERPGLSSPDSLGIYLTWGPNTQ-RRESERNCISNVR-PEGLNYPQAAFKLAWLLE
QAFQRRLTGIDLKDESD-----------NPALYGRVSP----LHSQLGG----------
>gi|158425189|ref|YP_001526481.1| ethanolamine ammonia-lyase small subunit
[Azorhizobium caulinodans ORS 571]
------------------------------------------------------------
----------------------------------------MSTKRDPWLGLARHTPARIA
LGRTGASLPTAEVLKFALAHAQARDAVHTPFDAAATAEGVR----A-LG-FET----LDV
TSAAPARDIYLRRPDLGRRLSDESRTRLAA-------RTDAPI----------DLALVVA
DGLSSAAVHAQAVPFLAALKPWIASE---G-WRTGPVVVAREARVALGDEVGQLLKARAV
AVLIGERPGLSSPDSLGLYLTLNPQVG-CNDAQRNCISNVR-AEGLSHEAAAFKLAWLLK
EAFRRSLTGVDLKDESD-----------DFLVDGRPPL------RLA------------
>gi|159898780|ref|YP_001545027.1| ethanolamine ammonia-lyase [Herpetosiphon
aurantiacus ATCC 23779]
------------------------------------------------------------
--------------------------------------MAEQSENELWQRLRQFTNARIG
IGRVGDALPTKANLAFQQDHALARDAVHAQVDFAAIASALQ------PEFPQI----LRL
KSAALDRATYLKRPDLGRSLHVESRLQLEA-------LQTDPC----------IVALVVA
DGLSAVAIERHAVPLLNIIKPQLESL---G-WSLAPLVLVEQGRVAIGDEIGELLKAELV
VILIGERPGLSVADSLGIYLTYAPQRG-RNDAERNCISNIH-PQGLSYVAASDLLMYLLG
QARQRRLTGVALKDERQ------------QLGATNNPTLE-------------------
>gi|91781404|ref|YP_556610.1| ethanolamine ammonia-lyase small subunit [Burkholderia
xenovorans LB400]
------------------------------------------------------------
--------------------------------------MSEFLEKNPWNALRQFTNARIA
LGRAGNSLPTAPLLAFNLSHAQARDAVHHPLDTDVLHEQLR------TQHFTT----LDV
HSAAPDREHYLRRPDLGRRLSEESRVALAA-------VPDGSP----------EVVFVIG
DGLSAFAASKQSLPLLRAVIPRLAD------WKIGPVVVARQARVALGDEIGELLNARLV
VMLIGERPGLSSPDSLGIYLTYGPKVG-CSDAQRNCISNVR-PEGLDYPLAAHKLHYLLT
HARRLGLTGVGLKDDSD-----------ALLADTPAAP----AISGESNPGAA------
>gi|89899398|ref|YP_521869.1| ethanolamine ammonia-lyase small subunit [Rhodoferax
ferrireducens T118]
------------------------------------------------------------
-----------------------------------MDDPTSPVIANPWAALRQFTDARIA
LGRAGVSLPTAAHLDFQLAHAKARDAVHLALDAPQLAQSLN------AARGDQQAPCLLL
HSAAADRPTYLQRPDLGRRLDAASSAAVDALEPAQA-PSPRPY----------DLAFVVV
DGLSALAIEQNAAPFLRILQARIAPE---H-WSVAPICIVKQGRVAIGDEVAERLGAKAV
VVLIGERPGLSAADSMGLYLTWMPRVG-LLDASRNCISNVR-PAGLGFDEAAYKLHYLLS
QARQRQLSGVELKDETGGGPDRVTANQTNFLLDHAHTP----NEAAPPS----------
>gi|188591932|ref|YP_001796530.1| ethanolamine ammonia-lyase, light chain
[Cupriavidus taiwanensis]
------------------------------------------------------------
----------------------------MTAKRQAPVRPDPAAEADPWQRLRRFTRARIA
LGRTGHSQPTDAVLAFGLAHAQARDAVHLALDVDAVATALD------AAGLPH----VAV
HSAAPDREHYLRRPDLGRRLDQASRARLDAT------RPQQAP----------DVVFVIA
DGLSALATQCHALPLLQAARQRLPQD-----WQLGPVVVAEQSRVALGDEIGERLGARQV
VMLIGERPGLSSPDSLGIYLTHAPRVG-RTDAERNCISNVR-PEGLSYAQAADRLVFLLR
GAAALGRSGVDLKDDSA-----------PALPTGSAGP----RPELR------------
>gi|83719369|ref|YP_443773.1| ethanolamine ammonia-lyase small subunit [Burkholderia
thailandensis E264]
------------------------------------------------------------
--------------------------------------MSDAVEKNPWGQLKSFTNARIA
LGRAGNSLPTAPLLAFNLSHAQARDAVHQPLDADALRRDIE------AAGLPT----LGV
QSAAPDRQHYLRRPDLGRRLSDDSRALLAAYGA----GLDEAP----------DVVFVVG
DGLSAFAAAKQALPLLNAMRAKLD-----G-WRVGPVVVARQARVALGDEIGELLGARLV
AMLIGERPGLSSPDSLGVYLTYAPKVG-CHDAQRNCISNVR-PEGLPHDAAAHKLHYLLT
HARRLGMTGVGLKDDSD-----------ALLPASQAEA------ERLAQE---------
>gi|120555852|ref|YP_960203.1| ethanolamine ammonia-lyase small subunit
[Marinobacter aquaeolei VT8]
------------------------------------------------------------
----------------------------------MTNSKFPTVVHNPWRGLRQYTPARIG
```

```
LGRAGVSLPTAELLEFQLAHARARDAVHHPLDIEQLIIEFQ-QIPEMSALGPP----IQL
QSQAPDRACYLQRPDLGRVLSESSSSSLQSSKT----GSAEPP----------DLAIVIA
DGLSARAVQQNAPAFMRSFLRKLAHDGPE--WRVAPPLLVEQGRVAIGDHIGQVLQTQQV
VVLIGERPGLSSPDSLGVYLTHHPEPG-LPDARRNCVSNIR-PAGLGVEQASEKVIYLLK
EARQLGTSGVALKDRSE-------EVELTVSKRGNFLV---------------------
>gi|184158621|ref|YP_001846960.1| ethanolamine ammonia-lyase, small subunit
[Acinetobacter baumannii ACICU]
------------------------------------------------------------
------------------------------MKLNRDIQYPSSTHQDQWEKLKQFTDARIA
LGRAGCSIPTRALLEFQLSHAQAKDAVYQEMDVSYLSEQLA------QQQLQS----FHI
QSNAPNKEIYLKRPDLGRQLSNPSKDTLIKKYA----ENPQQY----------DVCIVVG
DGLSARAIEANAIAFIAALSEHIQQE---N-WSLAPIVLATGSRVALGDEVAEIFKASML
VMLIGERPGLSSPDSMGIYYTWNAYSG-CLDSKRNCISNVR-SAGLSIPVAVQRLMALMR
KSKQLGFSGVNLKDEHQ----------LSNIDHNENAK------LLF------------
>gi|169795571|ref|YP_001713364.1| ethanolamine ammonia-lyase light chain
(ethanolamine ammonia-lyase small subunit) [Acinetobacter baumannii AYE]
------------------------------------------------------------
------------------------------MKLNRDIQYPSSTHQDQWEKLKQFTDARIA
LGRAGCSIPTRALLEFQLSHAQAKDAVYQEMDVSYLSEQLA----Q-QQ-LQS----FHI
QSNAPNKEIYLKRPDLGRQLSNPSKDTLIKKYAE----NPQQY----------DVCIVVG
DGLSARAIEANAIVFIAALSEQIQQE---N-WSLAPIVLATGSRVALGDEVAEIFKASML
VMLIGERPGLSSPDSMGIYYTWNAYSG-CLDSKRNCISNVR-SAGLSIPVAVQRLMALMR
KSKQLGFSGVNLKDEHQ----------LSNIDHNENTK------LLF------------
>gi|154247954|ref|YP_001418912.1| ethanolamine ammonia-lyase [Xanthobacter
autotrophicus Py2]
------------------------------------------------------------
-----------------------------------------MIARDPWAAFSRHTPARIA
LGRTGASLPTEEVLRFALAHAQARDAVHTPFDADGVTADVE----S-LG-FAT----LRV
SSAAPARDIYLRRPDLGRRLSDDSRAMLEA-------AAGDPV----------DLALVVA
DGLSSAAIHAQTKPFLAAFKPFIAQQ---G-WSLAPVLIASGARVALGDEVGALLKARAC
VLLVGERPGLSSPDSLGLYLTFDPQVG-RTDAERNCISNVR-PEGLSFEAAAFKLAWHIR
EALRRQVTGVELKDESD-----------LLLENGRAPA------LLSAS----------
>gi|206577048|ref|YP_002240183.1| putative ethanolamine ammonia-lyase, light chain
[Klebsiella pneumoniae 342]
------------------------------------------------------------
-----------------------------------------MNRPDAWNPLREFTDARIA
LGRSGASLPTREVLNFGLAHARARDAIHQPFASQQLVAPLA----A-LG-LDA----LTV
HSAAPDRHTYLRRPDLGRQLADESRADLAA-------SGVRPA----------DLLLVIG
DGLSSWAVERQAVPLIRALLPYLQTL---G-IGLAPVVLAHQSRVALGDDIGETLKARAV
AILIGERPGLSSPDSLGVYLTWQPHRQ-RLESERNCISNIR-PEGLSHDAAAFKLAWLLE
QAFLRRVTGVQLKDESD-----------NPALHGKIKP------LPPLKE---------
>gi|152968879|ref|YP_001333988.1| ethanolamine ammonia-lyase small subunit
[Klebsiella pneumoniae subsp. pneumoniae MGH 78578]
------------------------------------------------------------
-----------------------------------------MNRPDAWNPLREFTDARIA
LGRSGASLPTREVLNFGLAHARARDAIHQPFASQQLVAPLA----A-LG-LEA----LTV
HSAAPDRHTYLRRPDLGRQLADESRADLAA-------SGVRPA----------DLLLVIG
DGLSSWAVERQAVPLIRALLPYLRTL---G-IGLAPVVLAHQSRVALGDDIGETLKARAV
AILIGERPGLSSPDSLGVYLTWQPHRQ-RLESERNCISNIR-PEGLSHDAAAFKLAWLLE
QAFLRRLTGVGLKDESD-----------NPALHGKIKP----LPPLK------------
>gi|119900119|ref|YP_935332.1| putative ethanolamine ammonia-lyase small subunit
[Azoarcus sp. BH72]
------------------------------------------------------------
---------------------------------MSQPHIPPHLDADPWADLRAYTAARLA
LGRAGASLPTAEVLRFGLAHAQARDAVHIALDTAVLQAELA------ADGFDT----LLA
HSAAPDRGSYLARPDLGRRLADDSAARLRNH------ATTSGC----------DLLLVIG
DGLSSLAVARNARPLVAEIRRGLPAG-----WTLGPVVIATQARVALADEIGQALGARLV
AMLIGERPGLSSPDSLGAYLTWAPQPG-RSDAQRNCISNIR-PEGLGYAEATRRLWWLCA
EARRLGLTGVALKDNSD-----------SALPGADTPP------ALPAADGQAQDHQ--
>gi|83592367|ref|YP_426119.1| ethanolamine ammonia-lyase small subunit
[Rhodospirillum rubrum ATCC 11170]
------------------------------------------------------------
--------------------------------------MTLPPVVDPFARFRAATRARVG
```

```
LGRSGDALPTTALLEFQIAHARARDAVHGAIDAEALARAFA----P----LPT----ATV
HSAASDRAVYLRRPDLGRRLDDESAARLDALG-----EGGQGW----------DVVFVIA
DGLSAAAVAAHAQATVRAALETLGGR-----LSVGPLVIASQSRVALGDDIGARLKARMV
AVLIGERPGLSVADSLGAYITFDPRPG-RRDSERNCISNIH-ADGLHADQAARTLCWLVE
EGLRRRITGIGLKEEAQ--------PRLGAGEGGNLPP------VLDPSDRLGELSS--
>gi|89055067|ref|YP_510518.1| ethanolamine ammonia-lyase small subunit [Jannaschia
sp. CCS1]
------------------------------------------------------------
------------------------------------------MSDHLPGHLSAITQARLT
LGPRRRTQDTRTALAFALDHARAREAVLSELDVDGLATTLA------VADLSH----DVV
TSAAGSRDTYIRRPDLGRRLSPEDRARL---------TPQEPC----------DVALVLG
DGLSAIAVALNGAAFMVALANKLGAC---G-LGTSDVILARQARVALGDDIAQALGAQTV
VMALGERPGLSAADSLGVYITKNPTAT-TPDSARNCLSNIR-EAGLPVADAAHQATTLIK
AMRAFGGSGVALNTALQ--------KNRRLDGDDSASPHRL------------------
>gi|73539313|ref|YP_299680.1| ethanolamine ammonia-lyase small subunit [Ralstonia
eutropha JMP134]
------------------------------------------------------------
----------------------------------MTKPPATVTQQNPWQQLRQFTRARIA
LGRAGHSQTTDTVLAFGLAHAQARDAVHLPLDRAAVESALS------NAGFAT----LSV
RSAAPDRAHYLRRPDLGRRLDDASRDRLSAA------RADSPP----------DVVFVIA
DGLSALAAQRHGVPVLRAVRDRLPHD-----WTVAPVVIAEQSRVALGDEAGELLGARQV
VMLIGERPGLSSPDSLGLYLTYAPRIG-RTDAERNCISNIR-PEGLAYERAANRLVFLLR
GAAALGCSGVALKDDSA-----------HVLPDEAAGP------GNAIET---------
>gi|116622921|ref|YP_825077.1| ethanolamine ammonia-lyase light chain [Solibacter
usitatus Ellin6076]
------------------------------------------------------------
----------------------------------------------MAIDLRAFTPARVG
LARSGNSLATEELLRFQLDHARARDAVYFELDPAAIT-------------LPH----LLV
RSAAHDRATFLRRPDLGRTLDEESRALLAR----------GDY----------DAAIVIA
DGLSAPAVHHHAAALLEVLLPKLT-----G-WRLAPLTVAVQARVALGDEIGEALGARMA
VVLIGERPGLTSPDSLGIYLTWDPRRG-RNDAQRNCISNVR-TEGIGYELAAHKLHSLME
ASRVRQLSGVALKEDAK------------SLPG--------------------------
>gi|126441336|ref|YP_001060931.1| ethanolamine ammonia-lyase small subunit
[Burkholderia pseudomallei 668]
------------------------------------------------------------
--------------------------------------MSDGVEKNPWGQLKSFTNARIA
LGRAGNSLPTAPLLAFNLSHAQARDAVHQPLDADALRRDIE------AAGLPT----LGV
QSAAPDRQHYLRRPDLGRRLADDSRALLAAHGA----ALGEAP----------DLVFVVG
DGLSAFAAAKQALPLLNAMRPKLD-----G-WRVGPVVVARQARVALGDEIGELLGARLV
AMLIGERPGLSSPDSLGVYLTYAPKVG-CHDAQRNCISNVR-PEGLPHDAAAHKLHYLLT
HARRLGITGVGLKDDSD-----------ALLPAAQAQT----RRPVPGLAQE-------
>gi|53720980|ref|YP_109966.1| ethanolamine ammonia-lyase small subunit [Burkholderia
pseudomallei K96243]
------------------------------------------------------------
--------------------------------------MSDGVEKNPWGQLKSFTNARIA
LGRAGNSLPTAPLLAFNLSHAQARDAVHQPLDADALRRDIE------AAGLPT----LGV
QSAAPDRQHYLRRPDLGRRLADDSRALLAAHGA----ALGEAP----------DLVFVVG
DGLSAFAAAKQALPLLNAMRPKLD-----G-WRVGPVVVARQARVALGDEIGELLGARLV
AMLIGERPGLSSPDSLGVYLTYAPKVG-CHDAQRNCISNVR-PEGLPHDAAAHKLHYLLT
HARRLGITGVGLKDDSD-----------ALLPAAQAQT----RRLAPGPAQE-------
>gi|110639426|ref|YP_679635.1| ethanolamine ammonia-lyase small subunit [Cytophaga
hutchinsonii ATCC 33406]
------------------------------------------------------------
------------------------------------------MEEDYWKELRKFTHARIA
IGRAGNALPTSEVLKFRMAHAIARDAVQSEVNMELLQEKLF----D-LG-LNV----QQV
KSHAADRLDYIRHPHKGRLLHEQSRQQLEA-------LHIEKT----------DLCIIFA
DGLSADAVNLHAIPFLTILLKNLSF------WNIAPVVLAEQGRVGLSDPVGEALNARIS
LILLGERPGLSAPTSLGAYITYMPQSG-NTDEKRNCVSNIQ-PAGLSYEQAVEKISYLLH
EMRRQQVSGIMLKDNQQ----------NNFLY---------------------------
>gi|15599220|ref|NP_252714.1| ethanolamine ammonia-lyase small subunit [Pseudomonas
aeruginosa PAO1]
------------------------------------------------------------
---------------------------------MNDKHLPDASAENPWLPLRQLTPARIA
```

```
LGRTGTSLPTRPQLDFQYAHAQARDAVHLPFDHAAISDGLR------QRGRDS----LLL
HSAAADRHVYLQRPDLGRRLDEASVQRLREHAA----GYDGQI----------DLAIVVA
DGLSALAVQRHTLPFLERLEEQALAE---G-WSLSPVVLVEQGRVAVADEIGELLRAKMS
VILIGERPGLSSPDSLGLYFTWAPRVG-LTDAYRNCISNVR-LEGLSYGMAAHRLLYLMR
EACRRQLSGVNLKDEAE----------VQALDGEAPRT------GNFLLARD-------
>gi|115350176|ref|YP_772015.1| ethanolamine ammonia-lyase small subunit
[Burkholderia ambifaria AMMD]
------------------------------------------------------------
--------------------------------------MSDAVEKNPWAQLRSFTNARIA
LGRAGNSLPTAPLLAFNLSHAQARDAVHQPLDADALRREIE-----AAGLLPT----LGV
QSAAPDRDHYLRRPDLGRKLSDDSRGLLAGYGA----ALDDAP----------DVVFVVG
DGLSAFAAAKQALPLLQAVRPRLDAD---G-WRIGPVVVATQARVALGDEIGELLRAKVV
AMLIGERPGLSSPDSLGVYLTWAPKVG-CHDALRNCISNVR-PEGLPHAAAAHKLHYLMT
HARRLGLTGVGLKDDSD-----------ALLPQADAERIGAE-----------------
>gi|53724040|ref|YP_104487.1| ethanolamine ammonia-lyase small subunit [Burkholderia
mallei ATCC 23344]
------------------------------------------------------------
--------------------------------------MSDGVEKNPWGQLKSFTNARIA
LGRAGNSLPTAPLLAFNLSHAQARDAVHQPLDADALRRDIE------AAGLPT----LGV
QSAAPDRQHYLRRPDLGRRLADDSRALLAAHGA----ALGEAP----------DLVFVVG
DGLSAFAAAKQALPLLNAMRPKLD-----G-WRVGPVVVARQARVALGDEIGELLGARLV
AVLIGERPGLSSPDSLGVYLTYAPKVG-CHDAQRNCISNVR-PEGLPHDAAAHKLHYLLT
HARRLGITGVGLKDDSD-----------ALLPAAQAQT----RRLAPGPAQE-------
>gi|107024467|ref|YP_622794.1| ethanolamine ammonia-lyase small subunit
[Burkholderia cenocepacia AU 1054]
------------------------------------------------------------
--------------------------------------MSDAVEKNPWAQLKSFTNARIA
LGRAGNSLPTAPLLAFNLSHAQARDAVHQPLDADALRREIE----A-AGLLPT----LRV
QSAAPDRDHYLRRPDLGRKLSDDSRGLLAGYGA----ALDDAP----------DVVFVVG
DGLSAFAAAKQALPLLQAVRPRLDAD---G-WRIGPVVVATQARVALGDEIGELLRAKVV
AMLIGERPGLSSPDSLGVYLTWAPKVG-CHDALRNCISNVR-PEGLPHAAAAHKLHYLMT
HARRLQLTGVGLKDDSD-----------ALLPAAEAERIGATT----------------
>gi|134294259|ref|YP_001117994.1| ethanolamine ammonia-lyase small subunit
[Burkholderia vietnamiensis G4]
------------------------------------------------------------
--------------------------------------MSDAVEKNPWAQLKAFTNARIA
LGRAGSSLPTAPLLAFNLSHAQARDAVHQPLDSEALRRELD------TAGFAT----LGV
QSAAVDRQHYLRRPDLGRKLSDDGRALLAGYGA----MLDDAP----------DVVFVVG
DGLSAFAAAKQALPLLQAVCPRLHAD---G-WRLGPVVVATQARVALGDEIGELLRARAV
AMLIGERPGLSSPDSLGVYLTWAPKVG-CHDAQRNCISNVR-PEGLPHAAAAHKLHYLMT
EARRLRLTGVGLKDDSD-----------ALLPPQQAERIGAA-----------------
>gi|152994513|ref|YP_001339348.1| ethanolamine ammonia-lyase small subunit
[Marinomonas sp. MWYL1]
------------------------------------------------------------
--------------------------MSQEDKSFPTHPHAEPVTENAWSKLNAFTDARVG
LGRSGVSVPTKHLLAFQLAHAQAIDAVHTQLDTDALSKAMM--EQDWAKDWTKHCAPLLL
HSRATDRSTYLQRPDYGRRLDDESANKLDEHRV----STSQDY----------DLAIVVV
DGLSSLAVEQNTLPFLQALSSHIN-----G-WNLAPVCFVKQGRVAIGDDVCERLNAKCV
LVLIGERPGLSSPDSLGLYLTWGGKVG-LTDAYRNCISNVR-PAGLVYQEAARKAFYLLK
EARTLKLSGVKLKDRSD----------DDLIVDTSKES------KNFLIS---------
>gi|206558464|ref|YP_002229224.1| ethanolamine ammonia-lyase small subunit
[Burkholderia cenocepacia J2315]
------------------------------------------------------------
--------------------------------------MSDAVEKNPWAQLKSFTNARIA
LGRAGNSLPTAPLLAFNLSHAQARDAVHQPLDADALRREIE----A-AGMLPT----LRV
QSAAPDRDHYLRRPDLGRKLSDDSRGLLAGYGA----ALDEAP----------DVAFVVG
DGLSAFAAAKQALPLLQAVRPRLDAD---G-WRIGPVVVATQARVALGDEIGELLRAKVV
AMLIGERPGLSSPDSLGVYLTWAPKVG-CHDALRNCISNVR-PEGLPHAAAAHKLHYLMT
HARRLGLTGVGLKDDSD-----------ALLPAAEAER----IGVTT------------
>gi|116694057|ref|YP_728268.1| ethanolamine ammonia-lyase small subunit [Ralstonia
eutropha H16]
------------------------------------------------------------
-----------------------------MTARRPPPADPANTDADPWQRLRQFTRARVA
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LGRTGHSQTTDAVLAFGLAHAQARDAVHLPLDVGAVTAALD------AAGVPN----LAV
HSAAPDRAHYLRRPDLGRRLDDASRARLAAA------RPGEAP----------DVVFVVA
DGLSALATQTHALPLLDATRPRLPLT-----WRIGPVVVAEQSRVALGDEIGELLGARQV
VMLIGERPGLSSPDSLGIYLTHAPRTG-RTDAERNCISNVR-PEGLPYAQAADRLAFLLR
GAAALGRSGVDLKDDSV-----------PALPEG--------------------------
>gi|29831088|ref|NP_825722.1| ethanolamine ammonia-lyase small subunit [Streptomyces avermitilis MA-4680]
------------------------------------------------------------
------------------------------MTNRPPAAYEGESDRAMWAALRRHTQARIG
LGRAGSALPTRHRLELQAAHAAARDAVHTPFAPDVVAAALT-------G-FPT----IRV
RSAAPDRLGYLQRPDLGRRLDAADRAHLP----------RDDW----------DVVFVVA
DGLSSRAVHEHAAAMVHATTALLPAD-----LRVAPVVLAEQARVALGDDIAHAMGARMT
VVLVGERPGMSAADSLGAYLTYAPRPGTTTDADRNCLSNIRPPLGLAYATAAARLTALMK
RAHELGRTGVDLKDEST-----------ESAEAPALTPTT--------------------
>gi|220919792|ref|YP_002495095.1| Ethanolamine ammonia-lyase light chain [Methylobacterium nodulans ORS 2060]
------------------------------------------------------------
---------MN------------------KPVKEPAPPSSGRSIADPWAALRGVTPARIG
LGRSGNAIPTRGVLDFQYAHALARDAVHEPLDVAALTRALQ----P----LRT----IAV
ASNVPDRGTYLRRPDLGRVLSPESLTAFE---------GLKPA----------DIVFVVA
DGLSATGIQAHAAPLVHACATELA-----D-WDIGPIVLAVQGRVALGDDIAARLGARLC
VMIIGERPGLTVSDSIGIYLTFGPRPG-RQDSERNCISNIHPNGGLSSTQAACKLGWLAR
EALRRQYSGVALKDDMP-----------SILESGAGAP------KLSSS-----------
>gi|94314822|ref|YP_588031.1| ethanolamine ammonia-lyase small subunit [Ralstonia metallidurans CH34]
------------------------------------------------------------
-------------------------------------MSTPANPEDPWARLRQFTRARIA
IGRTGHAQKTASILAFGLAHAQARDAVHLALDVAALETALR---DAGLDALHV----LHA
HGAAADRDQYLRRPDLGRSLDAESRARLV--------PSAQPY----------DVVFVIA
DGLSALAAQRHAVPLLQAVLARLHD------WRVGPVVVARQSRVALGDEIGERLGARQV
VMLIGERPGLSSPDSLGIYLTFDPRVG-RTDAQRNCISNVR-PEGLSYAQAADRLVFLMQ
GAVALGRSGVDLKDDSA------------AVSAALSPP----------------------
>gi|146283994|ref|YP_001174147.1| ethanolamine ammonia-lyase small subunit [Pseudomonas stutzeri A1501]
------------------------------------------------------------
----------------------------------------MNHIPNPWQHLRQLTPARIA
LGRAGTSLPTVAQLDFQFAHAQARDAVHLPLDCAALTAELD------KHGLAC----LPL
HSAASDRQTYLQRPDLGRRLDETSAATLDA-------EAGDGC----------DLALVIA
DGLSALAVQRHAAPMALKIAEQCQAE---G-WSLGPVALVEQGRVAVADEIGQRLKARMV
VILLGERPGLSSPDSLGLYFTWAPQVG-RHDAQRNCISNIR-PEGLSYNLAAHRLLYLMR
EASRRQLSGVQLKDEAD-----------VPALDGQPRA------GNFLLD----------
>gi|152987704|ref|YP_001346467.1| ethanolamine ammonia-lyase small subunit [Pseudomonas aeruginosa PA7]
------------------------------------------------------------
---------------------------------MNDKHLPDASAENPWLPLRQLTPARIA
LGRTGTSLPTRPQLDFQYAHAQARDAVHLPFDHASIGDGLR------QRGRDS----LLL
HSAAADRHVYLQRPDLGRRLDEASVRRLREHAA----GYDGQI----------DLAIVVA
DGLSALAVQRHTLPFLERLEEQALAE---G-WSLSPVVLVEQGRVAVADEIGELLRARMS
VILIGERPGLSSPDSLGLYFTWAPRVG-LTDAYRNCISNVR-LEGLSYGMAAHRLLYLMR
EACRRQLSGVNLKDEAE----------VQSLEGDAPRT------GNFLLARD--------
>gi|162146134|ref|YP_001600593.1| putative ethanolamine ammonia-lyase light chain [Gluconacetobacter diazotrophicus PAl 5]
------------------------------------------------------------
----------------------------------MTAHDLTDPASDPWGPLRRLTSARIG
QARTGDTVAGAEVRAFQLAHARARQAVLAPLRTEALGLDEA----F-----------VPV
RSQAADRGEFVRRPDLGRRLSPDSAAGLVP----------GSY----------DIAFVIA
DGLSALAAERQGPPVLAACRALLP-----G-WRIAPVVVAHNARVALGDDIAQRLGARCV
VMMIGERPGLSVAESLSLYMTWDPYPG-RMDSERNCISNIHPHGGLTPRQAAATLARLLN
EARRIGASGIVLKDEAG-----------ARIA----------------------------
>gi|145297994|ref|YP_001140835.1| ethanolamine ammonia-lyase, light chain [Aeromonas salmonicida subsp. salmonicida A449]
------------------------------------------------------------
-----------------------------------MSDI---VHLNPWLELKRYTSARIA
```

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LGRTGVSLPTEALLAFGLAHAQARDTVHQPLEVAALTKALH----A-TG-HKV----LTV
QSAATSREEYLHRPDLGRRLNDASRLLLSQLPQT---EADLAPLEYQTRQAEADLVIMLG
DGLSSTALHQNALPFIEALQPHLRRL---G-LACAPLVIASQARVALGDEVGELLSARAV
LVMIGERPGLSSPDSLGLYLTWQPRVG-CMDSQRNCISNVR-PAGLDFPQAAHKLAWLLE
QAFNRRLTGVALKDESG--------ELASLIEHDAPRP------PCRPA----------
>gi|146307705|ref|YP_001188170.1| ethanolamine ammonia-lyase light chain
[Pseudomonas mendocina ymp]
------------------------------------------------------------
-------------------------------------MANDLIQHNPWDELRAHTSARIA
LGRVGCSLPTREVLKFGLAHAQARDAVHRPLDFAELKHQLH------AAGFRA----LKV
RSNAEDRQTYLLRPDHGRHLHGDCRLQLQ--------HELPAP----------ELAIVLA
DGLSAVAVQRHALPLLQAFRERFATD-----WANTPVVLAEQGRVAIGDGIGEALRARLV
IVMIGERPGLTSPDSLGLYLTYAPRVG-CPDSARNCISNVR-PEGLPYELAAHKLDYLTR
QALRLQLSGVQLKDDSS-------------LQQVAAQP----D----------------
>gi|188581161|ref|YP_001924606.1| Ethanolamine ammonia-lyase [Methylobacterium
populi BJ001]
------------------------------------------------------------
---------------------------------------MSTQTDALWRRLARLTPARIG
LGRAGAGLPTREVLKFGLAHAQARDAVHTPMDAAAIAGAVE----A-LG-LPT----VTV
TSGAEDRATYLRRPDYGRRLSPEGLKALSD-------TAAEPV----------DLALVVA
DGLSARAVHEGAAALLAAFKPHAERA---G-WRLAPVVVATQARVALGDAAGAALRARAV
VVVIGERPGLSSPDSLGLYVTFDPKPG-RSDAERNCISNVR-PAGLSFDLAAFKLNWLLT
QAFARGLTGVNLKDESD-----------RLIEAGTPDP------AIGRG----------
>gi|91792432|ref|YP_562083.1| ethanolamine ammonia-lyase small subunit [Shewanella
denitrificans OS217]
------------------------------------------------------------
------------------------------------MRPSELVQADPWPELMAFTQARIS
LGRVGTSLPTAQVQALALAHAMARDAVHLPLDVPLLAQGLK----D-LG-FDT----LTV
TSQANNRSQYLLRPDLGRRLHERHFAELEQ-------YQRERP----------SLLLVIA
DGLSSLAVARHSLPLIKEMSTRLPKD-----WTLAPVVIATQGRVALGDEIAQRLNATMV
AILIGERPGLTTPDSLGVYFTYAPRVG-CSDAMRNCISNIH-PQGLDYASAATKLIWLAK
EALKRRVSGVMLKDTAP-------------VNHSLT-----------------------
>gi|218886349|ref|YP_002435670.1| Ethanolamine ammonia-lyase [Desulfovibrio vulgaris
str. 'Miyazaki F']
-------------------MD---------------------------------------
-----------------------------RAPHDDPAAGPAPVTDDTWSDLRRHTEARIA
LGRCGVSLPHDRWLDFRMAHAKARDAVLTPFDMAGVRAALE----R-GG-VQC----LEL
HSAAADTAEFLARPDKGRQLSDASRGILREAAAGQAKGASGAK--------GADICVVVS
SGLSARAVHENAAPFALRFLEQARAA---G-YTATPVALVDHGRVAVADEVAHMLGARLV
VMLIGERPGLSSPNSLGVYLTHAPVPG-CTDEARNCISNVR-PGGLAIEEGVRKLCYLVQ
GAFAVGLTGVNLKDDMP-------GDYLPFAPAHALAD---------------------
>gi|222107181|ref|YP_002547972.1| ethanolamine ammonia-lyase small subunit
[Agrobacterium vitis S4]
------------------------------------------------------------
--------------------------------------MSNSVDFDPFARFRSATRARIG
LGRAGDAMPTQAVLEFQLAHARARDAVHGEVDFEKLATALA----P----IET----VLV
HSLAKDRATYLTRPDLGRMPDSHDLP-----------APGKTY----------EIAFIIA
DGLSAAAVERHAVSVYEATVRRLG-----G-FSVAPVILGKQARVAFGDEAAAAFGAQVA
IVLIGERPGLSVPDSLGAYITFEPRKG-RRDSERNCISNIH-DDGLSYESAAEKISWLVK
EALRLKLSGVDLKENAV---------DGISLPHGAKSLT--------------------
>gi|172059196|ref|YP_001806848.1| ethanolamine ammonia-lyase small subunit
[Burkholderia ambifaria MC40-6]
------------------------------------------------------------
--------------------------------------MSDAVEKNPWAQLRSFTNARIA
LGRAGNSLPTAPLLAFNLSHAQARDAVHQPLDADALRRDIETCGLPTAGLLPT----LGV
QSAAPDRDHYLRRPDLGRKLSDDSRGLLAGYGA----ALDDAP----------DVVFVVG
DGLSAFAAAKQALPLLQAVRPRLDGD---G-WRIGPVVVATQARVALGDEIGELLRAKVV
AMLIGERPGLSSPDSLGVYLTWAPKVG-CHDALRNCISNVR-PEGLPHAAAAHKLHYLMT
QARRLGLTGVGLKDDSD-----------ALLPQADAERIGAE-----------------
>gi|109897750|ref|YP_661005.1| ethanolamine ammonia-lyase small subunit
[Pseudoalteromonas atlantica T6c]
-----------------------------------------------------------M
KKYNDESSHVS------------------NMVNSHASMTSSEVVNNPWRTLRRYTNARIG
```

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LGRAGISLPTSEMLGFQLSHAKARDAVKLRLDTEELQHKLT----E-FSSVLP-CPPMML
HSQAFDRTTFLQRPDLGRKLNDVSRNLLLKFMTQQAGTTQPDY----------DLAIVVA
DGLSSIAVQYNVQPLLRQLITLLKHE--SESWRLAPLTVVEQGRVAVGDEVGEYLNAKAV
LMLIGERPGLSSPDSLGLYFTWAPEIG-LTDARRNCISNIR-PAGLGYDDAAHRALYLLK
EARRLNLSGVALKDRSD-------SPALNALKTNAVPK------RSFLTKPS--------
>gi|161523308|ref|YP_001578320.1| ethanolamine ammonia-lyase small subunit
[Burkholderia multivorans ATCC 17616]
------------------------------------------------------------
--------------------------------------MSDAVEKNPWSELKSFTNARIA
LGRAGSSLPTAPLLAFNLSHAQARDAVHQPLDADALRRELD------AAGFAT----LGV
QSAAPDRQHYLRRPDLGRKLSDDGRALLAGYGA----ALDDAP----------DIVFVVG
DGLSAFAAAKQAVPLLRAVRPRLEAD---G-WQIGPVIVATQARVALGDEIGELLRAKLV
AVLIGERPGLSSPDSLGVYLTWAPKVG-CHDAQRNCISNVR-PEGLSYDAAAHKLHYLVT
HARRLGLTGVGLKDDSD-----------ALLPAAQPERIGAACDRAT-------------
>gi|111023048|ref|YP_706020.1| ethanolamine ammonia-lyase small subunit [Rhodococcus
jostii RHA1]
------------------------------------------------------------
--------------------------------------MSDPVVQDFWAELRATTQARIG
LGRTGDALPTQRVLEFRSAHAAARDAVHQPLDAEALAEQVE----A-VGLGRP----VVV
TSQASDRSEYLRRPDLGRTPADLSA------------VPAVTA----------EVGFVLA
DGLSPRALTDHGVSLLSALVDEFGGT-----YSLAPPVIATQARVALGDHIAQALGVQTL
VLLIGERPGLSVADSVGVYLTHLPRPG-RTDADRNCVSNIHPPEGLGYELAARVVAGLVS
GARKLGRSGVELKDTSR--------ADALAAPSEILEL----------------------
>gi|78064787|ref|YP_367556.1| ethanolamine ammonia-lyase small subunit [Burkholderia
sp. 383]
------------------------------------------------------------
--------------------------------------MSDAVEKNPWAQLKSFTNARIA
LGRAGNSLPTAPLLAFNLSHAQARDAVHQPLDSDALRRELD------AAGFAT----LGV
QSAAPDRQHYLRRPDLGRKLSDEGRALLAAHGDA---ASGDGP----------DVVFVVG
DGLSAFAAAKQALPLLQAVRPRLDAD---D-WRIGPVVVATQARVALGDEIGELLRAKVV
AMLIGERPGLSSPDSLGVYLTWAPKVG-CHDALRNCISNVR-PEGLPYAGAAHKLHYLMT
HARRLGLTGVGLKDDSD-----------ALLPQAEAERIGAD------------------
>gi|220921384|ref|YP_002496685.1| Ethanolamine ammonia-lyase light chain
[Methylobacterium nodulans ORS 2060]
------------------------------------------------------------
-----------------------------------------MSPEEAWRRLSALTPARIG
LGRAGSGLPTRAVLGFALAHAQARDAVHTPLDVAALRAGIE----A-LG-LRN----VAV
ASAAPDRATYLRRPDLGRRLEGLSAERLAA-------AAAAPV----------DLAIVVA
DGLSARAIHEGAVPLLSVLAPAIAGS---G-WSLAPVVVAEQARVALGDAVGAALKARAV
AVLIGERPGLSSPDSLGIYLTFDPRPG-RTDAERNCLSNVR-AAGLKPELAAFKLHWLIG
QAFQRGLTGVALKDESD-----------RLLGAEAATPLPG-------------------
>gi|170739180|ref|YP_001767835.1| ethanolamine ammonia-lyase [Methylobacterium sp.
4-46]
------------------------------------------------------------
-----------MSADETVRPAQAKPPEEALTAEEALTAEEALTPEEAWGRLKALTPARIG
LGRAGSGLPTREVLAFALAHAQARDAVHAPLDAAALRAGIE----G-LG-LPV----LAI
ASRAPDRATYLRRPDLGRQPDPEGLARLAA-------AAGDPV----------DLAIVVA
DGLSARAVHEGAVPLLAALAPAIAGS---G-WSLAPIVLAEQARVALGDAVGAALRARAV
AVLIGERPGLSSPDSLGIYLTLDPRPG-RTDAERNCLSNVR-AAGLRPDLAAFKLHWLLG
EAFRRGLTGVALKDESD-----------RLLGSDAAAP------LTAPP-----------
>gi|163851380|ref|YP_001639423.1| ethanolamine ammonia-lyase [Methylobacterium
extorquens PA1]
------------------------------------------------------------
---------------------------------------MSTQTDTLWQRLARLTPARIG
LGRAGAGLPTREVLKFGLAHAQARDAVHTPMDAAAIAGAIE------VLGLPT----VTV
TSGAEDRATYLRRPDYGRRLSPESLKALSDSAAD---SAAEPV----------DLAIVVA
DGLSARAVHEGAAALLAAFKPHAEAA---G-WRLAPVTIATQARVALGDAAGAALRARAV
VVVIGERPGLSSPDSLGLYVTFDPKPG-RSDAERNCISNVR-PAGLSFELAAFKLNWLLT
QAFSRGLTGVNLKDESD-----------RLLEAAAPDP------AIGGF-----------
>gi|116254099|ref|YP_769937.1| ethanolamine ammonia-lyase small subunit [Rhizobium
leguminosarum bv. viciae 3841]
------------------------------------------------------------
---------------------------------------MSPFERDPFARFRNATRARIG
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LGRAGDALPTSAILDFQLAHARARDAVHGQVDFVALAKQLA----P----VPT----VRI
RSRAKDRTIYLARPDLGRQTNTADLP-----------SSGDRY----------DIAFIIA
DGLSASAVEHHAVPLFKACMKRL--G---D-FSVAPVILGEQARVAFGDEAAAAFGAEVA
IVLIGERPGLSVPDSLGTYITFRPQSG-RRDSERNCISNIH-ADGLGYEVAADKIVWIVR
EALRLQLTGVDLKENAE--------GAIEALPHQES------------------------
>gi|54024157|ref|YP_118399.1| ethanolamine ammonia-lyase small subunit [Nocardia
farcinica IFM 10152]
------------------------------------------------------------
----------------------------------MEIDNAADSPQDVWAPLRRTTQARIG
LGRTGNALPTRRVLEFRAAHAAARDAVHLPFDAADFAERIA----A-VGLGAP----SVV
RSNAGDRGEYLRRPDLGRTPADLSA------------VPRTDA----------DIGIVLA
DGLSPRALDEHGPGLLEALAAELRPH-----YRLAPPVLAVQARVALGDHIGAALGVGTL
IVLIGERPGLSVADSLGIYLTHLPRPG-RTDADRNCVSNIHPPEGLGYQRAAAITAALVA
GARRLGRSGVALKDTSG-----------DELAGTESLVLD--------------------
>gi|218530188|ref|YP_002421004.1| Ethanolamine ammonia-lyase [Methylobacterium
chloromethanicum CM4]
------------------------------------------------------------
------------------------------------MST---QTDTLWQRLARLTPARIG
LGRAGAGLPTREVLKFGLAHAQARDAVHTPMDAAAIAGAVE----A-LG-MPT----VTV
TSGAEDRATYLRRPDYGRRLSPESLKALSDSAAD---SAAEPV----------DLAIVVA
DGLSARAVHEGAAALLAAFKPHAEAA---S-WRLAPVTIATQARVALGDAAGAALRARAV
VVVIGERPGLSSPDSLGLYVTFDPKPG-RSDAERNCISNVR-PAGLSFELAAFKLNWLLT
QAFSRGLTGVNLKDESD-----------RLLEAAAPDP------AIGGF-----------
>gi|183980688|ref|YP_001848979.1| ethanolamine ammonia-lyase light chain, EutC
[Mycobacterium marinum M]
------------------------------------------------------------
-----------------------------------MNAPDARAADEVWALLRDVTQARIG
LGRAGNSLPTRRVLEFQAAHAAARDAVHDPLDVAGLTEQVR----D-LGLGAP----LVV
RSQASSRSEYLRRPDLGRAPADLSI------------LPNTGA----------DIGIVLA
DGLSPRALTDHGAGLLGALVREFHDR-----YRIAPPVIATQARVALGDHVGQALGVRTL
LVIIGERPGLSVADSLGIYLTHLPRPG-LTDADRNCISNIHPPDGLDYQTAAGIAAALVT
GARKLGRSGVALKDTSR-----------TELTADDTLGIG--------------------
>gi|91977450|ref|YP_570109.1| ethanolamine ammonia-lyase small subunit
[Rhodopseudomonas palustris BisB5]
------------------------------------------------------------
-------------------------------MMDDNTNDRPPVTESPWSEWRKVSPARLA
LGRVGTGLPTDEVLRFGWAHAMARDAIHAALDAPKLAATLQ----Q-LG-WVT----AQT
RSHAPDRVTYLRRPDLGRVLDPHEAGKLRA-------LDVAAG----------NICIVIG
DGLSSIAVERHAAPLLAALQPLLPAE-----LAGSPVVIATQARVALADEVADVLKSRLS
IMLIGERPGLSSPDSLGIYITHAPFSG-RSDADRNCISNVR-PEGLSYAAAAFKLAWLVR
EALGRGLTGVNLKDESD-----------LTLLNGSVADLD----RLPGPTK---------
>gi|118616009|ref|YP_904341.1| ethanolamine ammonia-lyase small subunit
[Mycobacterium ulcerans Agy99]
------------------------------------------------------------
-----------------------------------MNAPDARAADEVWALLRDVTQARIG
LGRAGNSLPTRRVLEFQAAHAAGRDAVHDPLDVAGLTEQVR----D-LGLGAP----LVV
RSQASSRSEYLRRPELGRAPADLSI------------LPNTGA----------DIGIVLA
DGLSPRALTDHGAGLLGALVREFHHR-----YRIAPPVIATQARVALGDHIGQALGVRTL
LVIIGERPGLSVADSLGVYLTHLPRPG-LTDADRNCISNIHPPDGLDYQTAAGIAAALVT
GARKLGRSGVALKDTSR-----------TELTVDDTLGIG--------------------
>gi|148253762|ref|YP_001238347.1| ethanolamine ammonia-lyase light chain
[Bradyrhizobium sp. BTAi1]
------------------------------------------------------------
-----------------------------------------------------MTRARVA
LGRCGDGLPTQARLEFQMAHALARDAVWGKVNFDSIADALA----P----REV----IKV
ASAAPDRASYLRRPDLGRRLAAGAASQLPS----------GPF----------DLVFVIA
DGLSADAVERHAADVVIATEARLP-----G-LAIGPVVLASQARVALGDDVGAAMRARLV
AVLIGERPGLSAADSLGVYLTLHPAPG-LRDSARNCISNIH-DHGLSAERAGEKLAWLVR
EALRIGVTGIGLKEAAP----------DGAIETTHSTAEITHHKPTGARGHE--------
>gi|169630907|ref|YP_001704556.1| ethanolamine ammonia-lyase, small subunit
[Mycobacterium abscessus]
------------------------------------------------------------
----------------------------------MSHIANNVAAQNIWDTLRRSTQSRIG
```

```
LGRSGDALPTTRVLEFGTAHAAARDAVHTPLDAQALAGRID----G-LGLGAP----LLV
TSRATDRSEYLRRPDLGRAPADGALDVLP----------GSGG----------DIGIVLA
DGLSPRALDDHGVPLLQALHRRLR-----G-YAIAPLVVATQARVALGDHIGAALGVDTV
LVLIGERPGLSVADSVGIYLTHNPVVG-CTDAQRNCVSNIHPPEGLGYDQAAQVVAALVA
GARQIGRSGVDLKDMTG-----------AGNQIEGAGP------ALPT-----------
>gi|171059483|ref|YP_001791832.1| ethanolamine ammonia-lyase [Leptothrix cholodnii
SP-6]
------------------------------------------------------------
--------------------------------------MTPPVTPARWDTLRRYTDARIA
LGRAGHSLPTAAHLAFQLAHAQARDAVHLPFDVRGVSAALQ------ALGLES----LSL
HSAAIDRAVYLQRPDLGRRLDEPSRQALAQWRA----GQSGRF----------DLAFVIA
DGLSALAVHQNAVALISATLARLRSDPVQT-WSVAPIALVEEGRVAIGDEAGHGLRADAV
VVLIGERPGLSSPDSLGIYITWAPGPG-LTDASRNCISNVR-PAGLSIDAAATRLHRLLA
QARLRQLTGVALKDDVD--------EQPSALAPGQPKGDESDSFLLAPTGPGRPGSQPD
>gi|119944062|ref|YP_941742.1| ethanolamine ammonia-lyase small subunit
[Psychromonas ingrahamii 37]
------------------------------------------------------------
-------------------------------MNKVVPSSEEMVHKDPWEKLRQFTNARIG
LGRVGTSIPTAELLRFQLSHAQAIDAVHVPLDVEQLDQQFA----A-SDVLQPYLPIQKL
HSKVRDRMEYLQRPDLGRQLDDASIYKLQQK------NTGESY----------DVVFVVA
DGLSSYAISNHAKPFLDILINSLNQDPNKE-WKIAPLCLVLQGRVAVGDDVCEALNAKAV
VLLIGERPGLSSPDSMGLYLTWNAKRG-IEDSQRNCVSNIR-PEGLQYQAAAHKCRYLLN
ESQRMKLSGVSLKDRSE------------DLQLESTTT------QQFCLTI--------
>gi|118473833|ref|YP_885935.1| ethanolamine ammonia-lyase small subunit
[Mycobacterium smegmatis str. MC2 155]
------------------------------------------------------------
-----------------------------------MTVSNDIAVQQFWDELRKTTQARIG
LGRAGNSLPTQQVLELAAAHAAARDAVHVPLDVEALAAQVR----E-VGIGEP----IVV
TSRATSRDEYLRRPDLGRQPAEGTE------------VPESGA----------DIGFVLA
DGLSPMGLNHHGAALLKALVERLKDR-----HTLAPPIIATQARVGLGDHIGAQARVRTL
LVIIGERPGLSVADSLGIYLTHLPQPG-RTDADRNCISNIHPPDGLGYAEAARVASTLVD
GAVALGRSGVDLKDTSR----------DAALGPLSPHELA-------------------
>gi|169629873|ref|YP_001703522.1| ethanolamine ammonia-lyase, light subunit
[Mycobacterium abscessus]
------------------------------------------------------------
------------------------------------MTAGDVARQRFWKDLRLNTQARIG
LDRAGNALHTRDVLDLAAAHAIARDAVHVPLDIDRFAADVG----A-LGLGVP----VVV
TSQVGSRAEYLRRPDLGRLPADLSA------------VARRPA----------DIGFVLA
DGLSPTALMRHGVPLLRELALRLGNA-----YTLAAPVIATQARVALGDHVAEQGRYRTL
IVIIGERPGLSVVDSLGIYLTHLPRSG-CTDADRNCISNIHPPDGLSYSEAARIAASLVG
GALQLGRSGVELKDTSR----------ASAIDDPGLESLG-------------------
========================================

%%  EutG [targeting tail implicated]

>gi++|16765781|ref|NP_461396.1| putative transport protein [Salmonella typhimurium
LT2]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQAE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-LGALGACGQEAQARGVSHLFVMVDSFLHQA
GMTAPLARSLAMKGVAMTVWPCPPGEPCITDVCAAVAQLREAACDGVVAFGGGSVLDAAK
AVALLVTNP--DQTLSAM----TEHSTLRPRLPLIAVPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAV
TEGVPPNVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----NMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGQA---NAMLLPTVMG
FNRMVCRERFSQIGRA---------------------LTNKKSDDRDAIAAVCELIAEVG
QSKRLADAGAKPEH----YSAWAQAALE-DI-------CLRSNPRTATQAQIIDLYAAAG
--------------------
>gi++|62181027|ref|YP_217444.1| paral putative transport protein in ethanolamine
utilization [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
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------------------------------------------------------------
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------------------------------------------------------------
--------------------------------------------------------MQAE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-LGALGACGQEAQARGVSHLFVMVDSFLHQA
GMTAPLARSLAMKGVAMTVWPCPPGEPCITDVCAAVAQLREAACDGVVAFGGGSVLDAAK
AVALLVTNP--DQTLSAM----TERSTLRPRLPLIAVPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAV
TEGVPPNVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----NMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGQA---NAMLLPTVMG
FNRMVCRERFSQIGRA---------------------LTNKKSDDRDAIAAVSELIAEVG
QSKRLADAGAKPEH----YSAWAQAALE-DI-------CLRSNPRTATQAQIIDLYAAAG
--------------------
>gi++|16761379|ref|NP_456996.1| putative alchohol dehydrogenase [Salmonella enterica
subsp. enterica serovar Typhi str. CT18]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQAE
LQTALFQAFNTLNLQRVKTFSVPPVTLCG-LGALGACGQEAQARGVSHLFVMVDSFLHQA
GMTAPLARSLAMKGVAMTVWPCPPGEPCITDVCAAVAQLREAACDGVVAFGGGSVLDAAK
AVALLVTNP--DQTLSAM----TERSTLRPRLPLIAVPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAV
TEGVPPNVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGQDLAARE-----NMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGQA---NAMLLPTVMG
FNRMVCRERFSQIGRA---------------------LTNKKSDDRDAIAAVCELIAEVG
QSKRLADAGAKPEH----YSAWAQAALE-DI-------CLRSNPRTATQAQIIDLYAAAG
--------------------
>gi++|197249493|ref|YP_002147415.1| ethanolamine utilization protein EutG
[Salmonella enterica subsp. enterica serovar Agona str. SL483]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQAE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-LGALGACGQEAQARGVSHLFVMVDSFLHQA
GMTAPLARSLAMKGVAMTVWPCPPGEPCITDVCAAVAQLREAACDGVVAFGGGSVLDAAK
AVALLVTNP--DQTLSAM----TERSTLRPRLPLIAVPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAV
TEGVPPNVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----NMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGQA---NAMLLPTVMG
FNRMVCRERFSQIGRA---------------------LTNKKSDDRDAIAAVSELIAEVG
QSKRLADAGAKPEH----YSAWAQAALE-DI-------CLRSNPRTATQAQIIDLYVAAG
--------------------
>gi++|161612793|ref|YP_001586758.1| hypothetical protein SPAB_00492 [Salmonella
enterica subsp. enterica serovar Paratyphi B str. SPB7]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQAE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-LGALGACGQEAQARGVSHLFVMVDSFLHQA
GMTAPLVRSLAMKGVAMTVWPCPPGEPCITDVCAAVAQLREAACDGVVAFGGGSVLDAAK
AVALLVTNP--DQTLSAM----TERSTLRPRLPLIAVPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAV
TEGVPPNVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----NMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGQA---NAMLLPTVMG
FNRMVCRERFSQIGRA---------------------LTNKKSDDRDAIAAVSELIAEVG
QSKRLADAGAKPEH----YSAWAQAALE-DI-------CLRSNPRTATQAQIIDLYAAAG
--------------------
>gi++|56412655|ref|YP_149730.1| putative alchohol dehydrogenase [Salmonella enterica
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subsp. enterica serovar Paratyphi A str. ATCC 9150]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQAE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-LGALGACGQEAQARGVSHLFVMVDSFLHQA
GMTAPLARSLAMKGVAMTVWPCPPGEPCITDVCAAVAQLREAACDGVVAFGGGSVLDAAK
AVALLVTNP--DQTLSAM----TERSTLRPRLPLIAVPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAV
TEGVPPNVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----NMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGQA---NAMLLPTVMG
FNRMVCRERFSQIGRA---------------------LTNKKSDDRDAIAAVSELIAEVG
QSKRLADAGTKPEH----YSAWAQAALE-DI-------CLRSNPRTATQAQIIDLYAAAG
--------------------
>gi++|207857873|ref|YP_002244524.1| putative alchohol dehydrogenase [Salmonella
enterica subsp. enterica serovar Enteritidis str. P125109]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQAE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-LGALGACGQEAQARGVSHLFVMVDSFLHQA
GMTAPLARSLAMKGVAMTVWPCPPGEPCITDVCAAVAQLREAACDGVVAFGGGSVLDAAK
AVALLVTNP--DQTLSAM----TERSTLRPRLPLIAVPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAV
TEGVPPNVTAMT-----------------------------GIDALTHAIEAYSAL-SAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----NMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGQA---NAMLLPTVMG
FNRMVCRERFSQIGRA---------------------LTNKKSDDRDAIAAVSELIAEVG
QSKRLADAGAKPEH----YSAWAQAALE-DI-------CLRSNPRTATQAQIIDLYAAAG
--------------------
>gi++|161502389|ref|YP_001569501.1| hypothetical protein SARI_00423 [Salmonella
enterica subsp. arizonae serovar 62:z4,z23:--]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQAE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-LGALSACGQEAQSRGLSHLFVMVDSFLHQA
GMTAPLARSLAMKGVAMTVWPCPPGEPCITDVCAAVAQLREAACDGVVAFGGGSVLDAAK
AVALLVTNP--DQTLSAM----TERSTLRPRLPLIAVPTTAGTG----------------
---SETTNVTVIIDAASGRKQVLAHASLMPDV---------------------AILDAAV
TEGVPPNVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLTARE-----NMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGLA---NAMLLPTVMG
FNRMVCRERFSQIGRA---------------------LTNKKSDDRDAIAAVSELIAEVG
QSKRLADAGARPEH----YSAWAQAAQD-DI-------CMRTNPRTASQVQIIELYVAAQ
--------------------
>gi++|218559389|ref|YP_002392302.1| putative alcohol dehydrogenase in ethanolamine
utilization; ethanolaminosome [Escherichia coli S88]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQSE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-PGAVSSCGQQAQTRGLKHLFVMADSFLHQA
GMTAGLTRSLAVKGIAMTLWPCPVGEPCITDVCAAVAQLRESGCDGVIAFGGGSVLDAAK
AVALLVTNP--DSTLAEM----SETSVLQPRLPLIAIPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAL
TEGVPSHVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----SMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGLA---NAMLLPTVME
FNRMVCRDRFSQIGRA---------------------LRTKKSDDRDAINAVSELIAEVG
IGKRLGDVGATSAH----YGAWAQAALE-DI-------CLRSNPRTASLEQIVGLYAAAQ
--------------------
```

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>gi++|74312978|ref|YP_311397.1| hypothetical protein SSON_2533 [Shigella sonnei
Ss046]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------------MGERKRRGYMQNE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-PGSVSSCGQQAQTRGLKHLFVMADSFLHQA
GMTAGLTRSLAVKGIAMTLWPCPVGEPCITDVCAAVAQLRESGCDGVIAFGGGSVLDAAK
AVALLVTNP--DSTLAEM----SETSVLQPRLPLIAIPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAL
TEGVPSHVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----SMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGLA---NAMLLPTVME
FNRMVCRERFSQIGRA---------------------LRTKKSDDRDAINAVSELIAEVG
IGKRLGDVGATSAH----YGAWAQAALE-DI-------CLRSNPRTASLEQIVGLYAAAQ
--------------------
>gi++|26248820|ref|NP_754860.1| ethanolamine utilization protein eutG [Escherichia
coli CFT073]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------------MGERKRRGSMQSE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-PGAVSSCGQQAQTRGLKHLFVMADSFLHQA
GMTAGLTRSLAVKGIAMTLWPCPVGEPCITDVCAAVAQLRESGCDGVIAFGGGSVLDAAK
AVALLVTNP--DSTLAEM----SETSVLQPRLPLIAIPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAL
TEGVPSHVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----SMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGLA---NAMLLPTVME
FNRMVCRDRFSQIGRA--------------L--RTKKSDDRDA-----INAVSELIAEVG
IGKRLGDVGATSAH----YGAWAQAALE-DI-------CLRSNPRTASLEQIVGLYAAAQ
--------------------
>gi++|157161912|ref|YP_001459230.1| ethanolamine utilization protein EutG
[Escherichia coli HS]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQNE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-PGAVSSCGQQAQTRGLKHLFVMADSFLHQA
GMTAGLTRSLAVKGIAMTLWPCPVGEPCITDVCAAVAQLRESGCDGVIAFGGGSVLDAAK
AVALLVTNP--DSTLAEM----SETSVLQPRLPLIAIPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAL
TEGVPSHVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----SMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGLA---NAMLLPTVME
FNRMVCRERFSQIGRA--------------LRTKKSD-------DRDAINAVSELIAEVG
IGKRLGDVGATSAH----YGAWAQAALE-DI-------CLRSNPRTASLEQIVGLYAAAQ
--------------------
>gi++|38704087|ref|NP_311342.2| hypothetical protein ECs3315 [Escherichia coli
O157:H7 str. Sakai]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQNE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-PGSVSSCGQQAQTRGLKHLFVMADSFLHQA
GMTAGLTRSLAVKGIAMTLWPCPVGEPCITDVCAAVAQLRESGCDGVIAFGGGSVLDAAK
AVALLVTNP--DSTLAEM----SETSVLQPRLPLIAIPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAL
TEGVPSHVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----SMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGLA---NAMLLPTVME
FNRMVCRERFSQIGRA--------------LRTKKSD-------DRDAINAVSELIAEVG
IGKRLGDVGATSAH----YGAWAQAALE-DI-------CLRSNPRTASLEQLVGLYAAAQ
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>gi++|15802975|ref|NP_289005.1| iron-containing alcohol dehydrogenase [Escherichia
coli O157:H7 EDL933]
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------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------------MGERKRRGYMQNE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-PGSVSSCGQQAQTRGLKHLFVMADSFLHQA
GMTAGLTRSLAVKGIAMTLWPCPVGEPCITDVCAAVAQLRESGCDGVIAFGGGSVLDAAK
AVALLVTNP--DSTLAEM----SETSVLQPRLPLIAIPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAL
TEGVPSHVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----SMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGLA---NAMLLPTVME
FNRMVCRERFSQIGRA--------------L--RTKKSDDRDA-----INAVSELIAEVG
IGKRLGDVGATSAH----YGAWAQAALE-DI-------CLRSNPRTASLEQLVGLYAAAQ
--------------------
>gi++|218700909|ref|YP_002408538.1| putative alcohol dehydrogenase in ethanolamine
utilization; ethanolaminosome [Escherichia coli IAI39]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQNE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-LGAVSSCGQQAQSRGLKHLFVMADSFLHQA
GMTAGLTRSLAVKGIAMTLWPCPVGEPCITDVCAAVAQLRESGCDGVIAFGGGSVLDAAK
AVALLVTNP--DSTLAEM----SETSVLQPRLPLIAIPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAL
TEGVPSHVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----SMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGLA---NAMLLPTVME
FNRMVCRDRFSQIGRA--------------LRTKKSD-------DRDAINAVSELIAEVG
IGKRLGDVGATSVH----YGAWAQAALE-DI-------CLRSNPRTASLEQIVGLYAAAQ
--------------------
>gi++|215487754|ref|YP_002330185.1| predicted alcohol dehydrogenase in
ethanolamineutilization [Escherichia coli O127:H6 str. E2348/69]
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------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQSE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-PGAVSSCGQQAQTRGLKHLFVMADSFLHQA
GMTAGLTRSLAVKGIAMTLWPCPVGEPCITDVCAAVAQLRESGCDGVIAFGGGSVLDAAK
AVALLVTNP--DSTLAEM----SETSVLQPRLPLIAIPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAVL
TEGVPSHVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----SMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGLA---NAMLLPTVME
FNRMVCRDRFSQIGRA--------------LRTKKSD-------DRDAINAVSELIAEVG
IGKRLGDVGATSAH----YGAWAQAALE-DI-------CLRSNPRTASLEQIVGLYAAAQ
--------------------
>gi++|89109258|ref|AP_003038.1| predicted alcohol dehydrogenase in ethanolamine
utilization [Escherichia coli str. K-12 substr. W3110]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQNE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-PGSVSSCGQQAQTRGLKHLFVMADSFLHQA
GMTAGLTRSLTVKGIAMTLWPCPVGEPCITDVCAAVAQLRESGCDGVIAFGGGSVLDAAK
AVTLLVTNP--DSTLAEM----SETSVLQPRLPLIAIPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAL
TEGVPSHVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----SMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGLA---NAMLLPTVME
FNRMVCRERFSQIGRA--------------LRTKKSD-------DRDAINAVSELIAEVG
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IGKRLGDVGATSAH----YGAWAQAALE-DI-------CLRSNPRTASLEQIVGLYAAAQ
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>gi++|110642625|ref|YP_670355.1| ethanolamine utilization protein EutG [Escherichia
coli 536]
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------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQSE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-PGAVSSCGQQAQTRGLKHLFVMADSFLHQA
GMTAGLTRSLAVKGIAMTLWPCPVGEPCITDVCAAVAQLRESGCDGVIAFGGGSVLDAAK
AVALLVTNP--DSTLAEM----SETSVLQPRLPLIAIPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAL
TEGVPSHVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLVARE-----SMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGLA---NAMLLPTVME
FNRMVCRERFSQVGRA--------------LRTKKSD-------DRDAINAVSELIAEVG
IGKRMGDVGATSAH----YGAWAQAALE-DI-------CLRSNPRTASLEQIVGLYAAAQ
--------------------
>gi++|218690579|ref|YP_002398791.1| putative alcohol dehydrogenase in ethanolamine
utilization; ethanolaminosome [Escherichia coli ED1a]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQSE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-PGTVSSCGQQAQTRGLKHLFVMADSFLHQA
GMTAGLTRSLAVKGIAMTLWPCPVGEPCITDVCAAVAQLRESGCDGVIAFGGGSVLDAAK
AVALLVTNP--DSTLAEM----SETSVLQPRLPLIAIPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAVL
TEGVPSHVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----SMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGLA---NAMLLPTVME
FNRMVCRDRFSQIGRA--------------LRTKKSD-------DRDAINAVSELIAEVG
INKRLADVGATTGH----YGAWAQAAQE-DI-------CLRSNPRTASLEQIVGLYAAAQ
--------------------
>gi++|218696079|ref|YP_002403746.1| putative alcohol dehydrogenase in ethanolamine
utilization; ethanolaminosome [Escherichia coli 55989]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQNE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-PGSVSSCGQQAQTRGLKHLFVMADSFLHQA
GMTAGLTRSLAVKGIAMTLWPCPVGEPCITDVCAAVAQLRESGCDGVIAFGGGSVLDAAK
AVALLVTNP--DSTLAEM----SETSVLQPRLPLIAIPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAL
TEGVPSHVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----SMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGLA---NAMLLPTVME
FNRMVCRERFSQIGRA---------------------LRTKKSDDRDAINAVSELIAEVG
IGKRLGDVGATSAH----YGAWAQAAQE-DI-------CLRSNPRTASLEQIVGLYAAAQ
--------------------
>gi++|170681253|ref|YP_001744635.1| ethanolamine utilization protein EutG
[Escherichia coli SMS-3-5]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQNE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-PGAVSSCGQQAQTRGLKHLFVMADSFLHQA
GMTAGLTRSLAVKGIAMTLWPCPVGEPCITDVCAAVAQLRESGCDGVIAFGGGSVLDAAK
AVALLVTNP--DSTLAEM----SETSVLQPRLPLIAIPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAL
TEGVPSHVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGQSLPKAVG--------YGHDLAARE-----SMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGLA---NAMLLPTVME
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FNRMVCRDRFSQIGRA--------------LRTKKSD-------DRDAINAVSELIAEVG
IGKRLGDIGATSAH----YGAWAQAALE-DI-------CLRSNPRTASLEQIIGLYAAAQ
--------------------
>gi++|218548114|ref|YP_002381905.1| putative alcohol dehydrogenase in ethanolamine
utilization; ethanolaminosome [Escherichia fergusonii ATCC 35469]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQNE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-PGAVSSCGQQAQTRGLKHLFVMADSFLHQA
GMTAGLTRSLAVKGIAMTLWPCPVGEPCITDVCAAVAQLRESGCDGVIAFGGGSVLDAAK
AVALLVTNP--DSTLAEM----SETSVLQPRLPLIAIPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAL
TEGVPSHVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----SMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGLA---NAMLLPTVME
FNRMVCRERFSQIGRA--------------LRTKKSD-------DRDAINAVSELIAEVG
IGKRLGDVGATSAH----YGAWAQAAQD-DI-------CLRSNPRTASLEQIVGLYAAAQ
--------------------
>gi++|209919925|ref|YP_002294009.1| ethanolamine utilization protein EutG
[Escherichia coli SE11]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQNE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-PGSVSSCGQQAQTRGLKHLFVMADSFLHQA
GMTAGLTRSLAVKGIAMTLWPCPVGEPCITDVCAAVAQLRESGCDGVIAFGGGSVLDAAK
AVALLVTNP--DSTLAEM----SETSVLQPRLPLIAIPTTAGTG----------------
---SETTNVTVIIDTVSGRKQVLAHASLMPDV---------------------AILDAAL
TEGVPSHVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----SMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGLA---NAMLLPTVME
FNRMVCRERFSQIGRA--------------L--RTKKSDDRDA-----INAVSELIAEVG
IGKRLGDVGATSAH----YGAWAQAAQE-DI-------CLRSNPRTASLEQIVGLYAAAQ
--------------------
>gi++|218554976|ref|YP_002387889.1| putative alcohol dehydrogenase in ethanolamine
utilization; ethanolaminosome [Escherichia coli IAI1]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQNE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-PGSVSSCGQQAQTRGLKHLFVMADSFLHQA
GMTAGLTRSLAVKGIAMTLWPCPVGEPCITDVCAAVAQLRESGCDGVIAFGGGSVLDAAK
AVALLVTNP--DSTLAEM----SETSVLQPRLPLIAIPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAL
TEGVPSHVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----SMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGLA---NAMLLPTVME
FNRMVCRERFSQIGRA--------------LRTKKSD-------DHDAINAVSELIAEVG
IGKRLGDVGATSAH----YGAWAQAAQE-DI-------CLRSNPRTASLEQIVGLYAAAQ
--------------------
>gi++|218705951|ref|YP_002413470.1| putative alcohol dehydrogenase in ethanolamine
utilization; ethanolaminosome [Escherichia coli UMN026]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQNE
LQAALFQAFDTLNLQRVKTFSVPPVTLCG-PGAVSSCGQQAQTRGLKHLFVMADSFLHQA
GMTAGLTRSLAVKGIAMTLWPCPVGEPCITDVCAAVAQLRESGCEGVIAFGGGSVLDAAK
AVALLVTNP--DSTLAEM----SETSVLQPRLPLIAIPTTAGTG----------------
---SETTNVTVIIDAVSERKQVLVHASLMPDV---------------------AILDAAL
TEGVPSHVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----SMLLAS
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CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGLA---NAMLLPTVME
FNRMVCRERFSQIGRA--------------LRTKKSD-------DRDAINAVSELIAEVG
INKRLADVGATTGH----YGAWAQAALE-DI-------CLRSNPRTASLEQIVGLYAAAQ
--------------------
>gi++|187732023|ref|YP_001881244.1| ethanolamine utilization protein EutG [Shigella
boydii CDC 3083-94]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQNE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-PGSVSSCGQQAQTRGLKHLFVMADSFLHQA
GMTAGLTRSLAVKGIAMTLWPCPVGEPCITDVCAAVAQLRESGCDGVIAFGGGSVLDAAK
AVALLVTNP--DSTLAEM----SETSVLQPRLPLIAIPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAL
TEDVPSHVTAMT-----------------------------GIDALTHAIEAYSAL-NAI
PL---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----SMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGLA---NAMLLPTVME
FNRMVCRERFSQIGRA--------------LRTKKSD-------DRDAINAVSELIAEVG
IGKRLGDVGATSAH----YGAWAQAALE-DI-------CLRSNPRTASLEQIVGLYAAAQ
--------------------
>gi++|157154795|ref|YP_001463773.1| ethanolamine utilization protein EutG
[Escherichia coli E24377A]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQNE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-PGSVSSCGQQAQTRGLKHLFVMADSFLHQA
GMTAGLTRSLAVKGIAMTLWPCPVGEPSITDVCAAVAQLRESGCDGVIAFGGGSVLDAAK
AVALLVTNP--DSTLAEM----SETSVLQSRLPLIAIPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAL
TEGVPSHVTAMT-----------------------------GIDALTHAIEAYSAL-NAT
PF---------TDSLAIGAIAMIGKSLPKAVG--------YGHDLAARE-----SMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGLA---NAMLLPTVME
FNRMVCRERFSQIGRA--------------LRTKKSD-------DRDAINAVSELIAEVG
IGKRLGDVGATSAH----YGAWAQAAQE-DI-------CLRSNPRTASLEQIVGLYAAAQ
--------------------
>gi++|206578622|ref|YP_002237210.1| ethanolamine utilization protein EutG
[Klebsiella pneumoniae 342]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQAE
LQTALFHAFDTLNLQQVKSFNVPPVTLHG-VGALAACGPQAQARGLKHLFVMVDRFLHQA
GMTAGLERSLAMKGVAMTLWPCPAGEPCVTDVCAAVAKLRDARCDGVVAFGGGSVLDAAK
AVALLVANP--EQTLGEM----TEHSELQPRLPLIAVPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAL
TEGVPPSVTAMT-----------------------------GIDALTHAVEAYSAR-HAT
PF---------TDSLAMGAIAMIGEALPKAVG--------CGQDLAARE-----NMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGLA---NAMLLPTVMG
FNRMVCRGRFSQIGRA------------------LTGRKTDDL---EAIGAVRELIAEVG
LTMRLSDAGATPAH----YATWAQAAQD-DI-------CLRTNPRTATREQIIELYAAAQ
--------------------
>gi++|152971318|ref|YP_001336427.1| ethanolamine utilization enzyme [Klebsiella
pneumoniae subsp. pneumoniae MGH 78578]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQAE
LQTALFHAFDTLNLQQMKSFNVPPVTLHG-VGALAACGPQAQSRGLRHLFVMVDSFLHQA
GMTAGLERSLAMKGIAMTLWPCPAGEPCVTDVCAAVAQLRDARCDGVVAFGGGSVLDAAK
AVALLVANP--EQTLGEM----TEHSELRPRLPLIAVPTTAGTG----------------
---SETTNVTVIIDAVSGRKQVLAHASLMPDV---------------------AILDAAL
TEGVPPHITAMT-----------------------------GIDALTHAVEAYSAR-HAT
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PF---------TDSLAMGAIAMIGEALPKAVG--------CGQDLAARE-----NMLLAS
CMAGMAFSSAG------LGLCHAMAHQPGAALHIP--------HGLA---NAMLLPTVME
FNRMVRRARFSQIGRA------------------LTGKKTD---DREAIAAVRELIAEVG
LTMRLTEAGATSAH----YAAWAQAAQE-DI-------CLRANPRTASREQIIELYAAAR
--------------------
>gi++|120554163|ref|YP_958514.1| iron-containing alcohol dehydrogenase [Marinobacter
aquaeolei VT8]
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------MTTPGQSPDNAL
IESIVTHTVDELAPRGLFNFNAPRQTLMG-EGAILKIGEMLGHLGVTHVLVVADRVVYEK
GLMRSMERSLERAGIEFTIYPAITQEPDESVVTSATELLTRNQADFVLGFGGGSALDAAK
VIALAGSCQ--SSLQQLA----EPGFGGRRVIGLGAVPTTAGTG----------------
---SEVTDISVIMRADRKHKYVIKQVDLMPDL---------------------AIVDPGL
MLNLPPLVTAAT------------------------------GIDALTHAIEAYAAR-SSH
PL---------AKALAICAVQSIAEALPVVVG--------NGGDVAARL-----TMATAA
YKAGLAFSNSG------LGLVHAISHQIGARYRLA--------HGIA---NGILLPYVMR
FNALVCQQEYAAIAHM--------------LGVTRTGMTQREQ-CMASIDAVRQLLSDVG
LPGSLAGTNIHRDD----FAAIAADALE-DV-------CIRDNPRDVTEADIVQLLEEVC
STK-----------------
>gi++|220904637|ref|YP_002479949.1| iron-containing alcohol dehydrogenase
[Desulfovibrio desulfuricans subsp. desulfuricans str. ATCC 27774]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----------------MTQFYGKTKICYG-PYAL----ETLESFPASHAFVVTDPFMVKS
GFADQAVSHLKRKGIGFSIFSGVEPDPTLQAVVEATGHFLRSKADMILALGGGSAIDMAK
AISYF-----------------GHKAARDRKAMLVAIPTTSGTG----------------
---SEVTSIAVITDKVNAVKIPLNDELLIPDA---------------------AILDARF
TRTVPPHVTAST------------------------------GMDVLTHAVEAYTSR-HSN
VF---------TAIYAERAIRNVFTYLHRAYE--------QGDDMVARD-----NMLIGS
CMAGLAFTNSG------LGITHSMAHSLGGQFHIP--------HGLA---NAVLLPIVID
FNSFDAGVKYREIAEM--------------AGL--PAATVEEG-TRNLVAAVRDLNASLG
IPARVRELKVDEGEYRRNLDAMATNALE-DI-------CTQSNPRMPSHDDIVSLFERVW
--------------------
>gi++|83592266|ref|YP_426018.1| Iron-containing alcohol dehydrogenase
[Rhodospirillum rubrum ATCC 11170]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------MTQTAFFIPSINLMG-AGCLATAVNTINERGFKRALIVTDAVLEKL
GVAGKVTELLDDHGVESIVFGGAQPNPTVSNVEAGLAILREAECDCVISLGGGSPHDCAK
GIALCATNG--GVIGDYE----GVDKSAHPQLPLIAINTTAGTA----------------
---SEMTRFCIITDESRLVKMAIVDRHVTPIM---------------------SVNDPEL
MIGKPAALTAAT------------------------------GMDALTHAIEAYVSI-AAT
PI---------TDACALKAVSIIARTLRRAVA--------DGADIKARE-----AMSYAQ
FLAGMAFNNAS------LGFVHAMAHQLGGFYDLP--------HGVC---NAVLLPHVAA
FNASVAGARLKDVAEA--------------MGVDIANLSDDQG-AEACIAAIRTLAADIG
IPAGLTELGVKDGD----VPTLAINALK-DA-------CGLTNPRPATQAEIEAIFRAAA
--------------------
>gi++|82544902|ref|YP_408849.1| ethanolamine ammonia-lyase, heavy chain [Shigella
boydii Sb227]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------------MQNE
LQTALFQAFDTLNLQRVKTFSVPPVTLCG-PGSVSSCGQQAQTRGLKHLFVMADSFLHQA
GMTAGLTRSLAVKGIAMTLWPCPVGEPCITDVCAAVAQLRESGCDGVIAFGGGSVLDAAK
AVALLVTNP--DSTLAEM----SETSVLQPRLPLIAYEDDCVTRLIQDDVNETAYNQIKN
WSISELREY-VLSDETSVDDIAFTRKGLTSEVVAAVAKICSNADLIYGAKKMPVIKKANT
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TIGIPGTFSARLQPNDTRDDVQSIAAQIYEGLSFGVGDAVIGVNPVTDDVENLSRV-LDT
IYGVIDKFNIPTQGCVLAHVTTQIEAIRRGAPGGLIFQSICGSEKGLKEFGVELAMLDEA
RAVGAEFNRIAGENCLYFETGQGSALSAGANFGADQVTMEARNYGLARHYDPFIVNTVVG
FIGPEYLYNDRQIIRAGLEDHFMGKLSGISMGCDCCYTNHADA-DQNLNENLMILLATAG
C-NYIMGMPLGDDI----MLNYQTTAFH-DTATVRQLLNLRPSPEFERWLESMGIMANGR
LTKRAGDPSLFF--------
>gi++|78358307|ref|YP_389756.1| alcetaldehyde dehydrogenase or NADPH-dependent
butanol dehydrogenase [Desulfovibrio desulfuricans subsp. desulfuricans str. G20]
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------------------------------------------------------------
----------------MTQFYGKTKICYG-----EDALETLERLPIKQAFIVTDPFMVKT
GFIDRLISHLDLGGIRHRVFDGVEPDPSLETVTKGTHLYMQDHAEAVIALGGGSAIDAAK
AIAFFASKV----------------DTSRPRPILVAIPTTSGTG----------------
---SEVTAISVVTDKVNEVKIPLNDEQLIPDL---------------------AILDARF
TRTLPPSVTSVT-----------------------------GMDVLTHAIEAYTSR-KAN
AF---------TSIYAEYAIRYVFEYLPRAYR--------CSDDMEARE-----KMLLAS
CMAGMAFNNSG------LGITHSIAHSLGGIFHVP--------HGLA---NAVVLPFVIQ
FNSFDAAVQYREIAQM----------------LSLPAGSVGEG-TQSLIKAVRELNESMG
IPNRIGALKIEESAYRQHADVIARNVLD-DI-------CTAGNPRMPSRADIRMLLEQAW
--------------------
>gi|218551114|ref|YP_002384905.1| alcohol dehydrogenase in rhamnose degradation
pathway [Escherichia fergusonii ATCC 35469]
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------------------------------------------------------------
-----------------------------------------------------------M
GNAVGKMDLNLRRVIMSFMLALPKISLHG-AGAIGDMVNLVANKQWGKALIVTDGQLVKL
GLLDSLFAALDQHEMSYHLFDEVFPNPTEELVQKGYAAFQDAACDYIIAFGGGSPIDTAK
AVKILTANP--APSTAYS----GVGKVTNPGVPLVAINTTAGTA----------------
---AEMTSNAVIIDTARQVKEVIIDPNIIPDI---------------------AVDDASV
MLEIPASVTAAT-----------------------------GMDALTHAVEAYVSV-GAH
PL---------TDANALEAIRLITLWLPKAVD--------DGHNLEARE-----QMAFAQ
YLAGMAFNSAG------LGLVHALAHQPGATHNLP--------HGVC---NAILLPVIEN
FNRPNAIARFARIAQA--------------MGVDTRDMSDEAA-SIEAINAIRALSHRVG
IPAGFSQLGITKED----IEGWLDKALA-DP-------CAPCNPRTASRDEVRELYLEAL
--------------------
>gi|104782026|ref|YP_608524.1| alcohol dehydrogenase II ( [Pseudomonas entomophila
L48]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------MSSTFFIPAVNIMG-IDCLDEAMTAIAGYGLRKALIVTDQGLAKA
GVAERIAGMLAMRDIDSVVFDGAKPNPSIANVEAGLALLRQSRCDCVVSLGGGSPHDCAK
GIALCATNG--GHISDYE----GVDRSSKPQLPLIAINTTAGTA----------------
---SEMTRFCIITDEARHVKMAIVDRNVTPIL---------------------SVNDPAL
MVGMPKGLTAAT-----------------------------GMDALTHAIEAYVST-AAT
PI---------TDACALKAISLISDNLRQAVA--------DGSNLQARE-----NMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NAVLLPHVQR
FNAKVSAARLRDVAKA--------------MGTKVCGLDAEQG-AGAAISAIEHLAAAIG
IPDGLAELGVKVED----VPVLAANALK-DA-------CGLTNPRVASQVEIEAIFKAAF
--------------------
>gi|16762388|ref|NP_458005.1| alcohol dehydrogenase [Salmonella enterica subsp.
enterica serovar Typhi str. CT18]
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
---------------MSFMLALPKISLHG-AGAIADMVNLVANKQWGKALIVTDGQLVKL
GLLDSLFSALDEHQMSYHLFDEVFPNPTEELVQKGFAAYQSAECDYIIAFGGGSPIDTAK
AVKILTANP--GPSTAYS----GVGKVKNAGVPLVAINTTAGTA----------------
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---AEMTSNAVIIDSARKVKEVIIDPNIIPDI---------------------AVDDASV
MLEIPASVTAAT-----------------------------GMDALTHAVEAYVSV-GAH
PL---------TDANALEAIRLINVWLPKAVD--------DGHNLEARE-----QMAFGQ
YLAGMAFNSAG------LGLVHALAHQPGATHNLP--------HGVC---NAILLPIVEN
FNRPNAVARFARIAQA--------------MGVETRGMSDEVA-SQEAINAIRTLSKRVG
IPEGFSKLGVTKED----IEGWLDKALA-DP-------CAPCNPRTASRDEVRELYLEAL
--------------------
>gi|90423471|ref|YP_531841.1| iron-containing alcohol dehydrogenase
[Rhodopseudomonas palustris BisB18]
------------------------------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
--------------MTETTFFIPSLNMMG-AGCLTGAVSSVSRYGFKRALIVTDQMLFKL
GMADKLASQLEQQGIAASIFPGAQPNPTVGNVESGLAQLQADGCDCVISLGGGSSHDCAK
GIALTATNG--GNIRDYE----GVDRSAKPQLPLIAINTTAGTA----------------
---SEMTRFCIITDEKRLVKMAIVDRNVTPLL---------------------SVNDPEL
MLGKPQMLTAAT-----------------------------GMDALTHAIEAYVSV-AAT
PI---------TDACALKAIAIIANNLRTAVA--------EGSNLAARE-----AMAYAG
FMAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NAVLLPHVEA
FNAEVSAARLRDVAHA--------------LGVDTNGMSDQQG-AEACIHAIQRLSTDIG
IPTGLAQLGVKEED----IPTLAANALK-DA-------CGLTNPRRASQADIEAIFRVAA
--------------------
>gi|197250003|ref|YP_002148972.1| lactaldehyde reductase [Salmonella enterica subsp.
enterica serovar Agona str. SL483]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------MSFMLALPKISLHG-AGAIADMVNLVANKQWGKALIVTDGQLVKL
GLLDSLFSALDEHQMSYHLFDEVFPNPTEELVQKGFAAYQTAECDYIIAFGGGSPIDTAK
AVKILTANP--GPSTAYS----GVGKVKNAGVPLVAINTTAGTA----------------
---AEMTSNAVIIDSARKVKEVIIDPNIIPDI---------------------AVDDASV
MLEIPASVTAAT-----------------------------GMDALTHAVEAYVSV-GAH
PL---------TDANALEAIRLINVWLPKAVD--------DGHNLEARE-----QMAFGQ
YLAGMAFNSAG------LGLVHALAHQPGATHNLP--------HGVC---NAILLPIVEN
FNRPNAVARFARIAQA--------------MGVETRGMSDEVA-SQEAINAIRTLSKRVG
IPEGFSKLGVTKED----IEGWLDKALA-DP-------CAPCNPRTASRDEVRELYLEAL
--------------------
>gi|206580570|ref|YP_002241222.1| lactaldehyde reductase [Klebsiella pneumoniae 342]
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------------------------------------------------------------
------------------------------------------------------------
---------------MSFMLALPKISLHG-AGAIGDMVKLVAGKQWGKALIVTDGQLVKL
GLLDSLFSALDKQQMAYQLFDGVYPNPTEALVQQGYAAYQAARCDYLIAFGGGSPIDTAK
AIKILTANP--GPSTAYS----GVGKVKNAGVPLVAINTTAGTA----------------
---AEMTSNAVIIDSERQVKEVIIDPNLIPDI---------------------AVDDASV
MLDIPPAVTAAT-----------------------------GMDALTHAIEAFVSV-GAH
PL---------TDANALEAIRLINLWLPKAVD--------DGHDLQARE-----QMAFGQ
YLAGMAFNSAG------LGLVHALAHQPGATHNLP--------HGVC---NAILLPIIEN
FNRPNAVARFARVAQA--------------MGVDTRGMNDEAA-SMEAINAIRTLSKRVG
IPQGFSQLGVSKAD----MEGWLDKALA-DP-------CAPCNPRPASRDEVRELYLEAL
--------------------
>gi|161617169|ref|YP_001591134.1| hypothetical protein SPAB_05010 [Salmonella
enterica subsp. enterica serovar Paratyphi B str. SPB7]
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------------------------------------------------------------
------------------------------------------------------------
----------------------------------------MRLCLIRPTGRCAFYRRPDK
RSAIGQQGIFLRRIVMSFMLALPKISLHG-AGAIADMVNLVANKQWGKALIVTDGQLVKL
GLLDSLFSALDEHQMSYHLFDEVFPNPTEELVQKGFAAYQSAECDYIIAFGGGSPIDTAK
AVKILTANP--GPSTAYS----GVGKVKNAGVPLVAINTTAGTA----------------
```

```
---AEMTSNAVIIDSARKVKEVIIDPNIIPDI---------------------AVDDASV
MLEIPASVTAAT-----------------------------GMDALTHAVEAYVSV-GAH
PL---------TDANALEAIRLINLWLPKAVD--------DGHNLEARE-----QMAFGQ
YLAGMAFNSAG------LGLVHALAHQPGATHNLP--------HGVC---NAILLPIVEN
FNRPNAVARFARIAQA--------------MGVETRGMSDEAA-SQEAINAIRTLSKRVG
IPEGFSKLGVTKED----IEGWLDKALA-DP-------CAPCNPRTASRDEVRGLYLEAL
--------------------
>gi|152972706|ref|YP_001337852.1| putative alcohol dehydrogenase [Klebsiella
pneumoniae subsp. pneumoniae MGH 78578]
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------------------------------------------------------------
------------------MLALPKISLHG-AGAIGDMVKLVAGKQWGKALIVTDGQLVKL
GLLDSLFAALDEQQMAYQLFDEVFPNPTEALVQQGYAAYQAARCDYLIAFGGGSPIDTAK
AIKILTANP--GSSTAYS----GVGKVKNAGVPLVAINTTAGTA----------------
---AEMTSNAVIIDSERQVKEVIIDPNLIPDI---------------------AVDDASV
MLDIPPAVTAAT-----------------------------GMDALTHAIEAFVSV-GAH
PL---------TDANALEAIRLINLWLPKAVD--------DGHDLQARE-----QMAFGQ
YLAGMAFNSAG------LGLVHALAHQPGATHNLP--------HGVC---NAILLPIIEN
FNRPNAVARFARVAQA--------------MGVDTRGMSDEAA-SMEAINAIRTLSKRVG
IPQGFSQLGVRKAD----IEGWLDKALA-DP-------CAPCNPRPASRDEVRELYLEAL
--------------------
>gi|146313706|ref|YP_001178780.1| lactaldehyde reductase [Enterobacter sp. 638]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------MSFMLALPKISLHG-AGAIGDMVNLVANKQWGKALIVTDGQLVKM
GLLDSLFTALDAHQMSYHLFDDVFPNPTEALVQKGFAAYQDADCDYLIAFGGGSPIDTAK
AIKILTANP--GPSTAYS----GVGKVKNTGVPLVAINTTAGTA----------------
---AEMTSNAVIIDTARQVKEVIIDSNIIPDI---------------------AVDDASV
MLDIPASVTAAT-----------------------------GMDALTHAIEAYVSV-GAH
PL---------TDANALEAIRLIALWLPKAVD--------DGHNLHARE-----QMAFGQ
YLAGMAFNSAG------LGLVHALAHQPGATHNLP--------HGVC---NAILLPIIEN
FNRPNAVARFALVAQA--------------MGVETRGMSDDAA-SQSAIQAIRDLSTRVG
IPSGFSQLGVTKAD----IEGWLDKALA-DP-------CAPCNPRTASRDEVRELYLEAL
--------------------
>gi|16767310|ref|NP_462925.1| putative alcohol dehydrogenase [Salmonella typhimurium
LT2]
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------------------------------------------------------------
---------------MSFMLALPKISLHG-AGAIADMVNLVANKQWGKALIVTDGQLVKL
GLLDSLFSALDEHQMSYHLFDEVFPNPTEELVQKGFAAYQSAECDYIIAFGGGSPIDTAK
AVKILTANP--GPSTAYS----GVGKVKNAGVPLVAINTTAGTA----------------
---AEMTSNAVIIDSARKVKEVIIDPNIIPDI---------------------AVDDASV
MLEIPASVTAAT-----------------------------GMDALTHAVEAYVSV-GAH
PL---------TDANALEAIRLINLWLPKAVD--------DGHNLEARE-----QMAFGQ
YLAGMAFNSAG------LGLVHALAHQPGATHNLP--------HGVC---NAILLPIVEN
FNRPNAVARFARIAQA--------------MGVETRGMSDEAA-SQEAINAIRTLSKRVG
IPEGFSKLGVTKED----IEGWLDKALA-DP-------CAPCNPRTASRDEVRGLYLEAL
--------------------
>gi|207859235|ref|YP_002245886.1| alcohol dehydrogenase [Salmonella enterica subsp.
enterica serovar Enteritidis str. P125109]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------MSFMLALPKISLHG-AGAIADMVNLVANKQWGKALIVTDGQLVKQ
GLLDSLFSALDEHQMSYHLFDEVFPNPTEELVQKGFAAYQSAECDYIIAFGGGSPIDTAK
AVKILTANP--GPSTAYS----GVGKVKNAGVPLVAINTTAGTA----------------
```

```
---AEMTSNAVIIDSSRKVKEVIIDPNIIPDI---------------------AVDDASV
MLEIPASVTAAT-----------------------------GMDALTHAVEAYVSV-GAH
PL---------TDANALEAIRLINLWLPKAVD--------DGHNLEARE-----QMAFGQ
YLAGMAFNSAG------LGLVHALAHQPGATHNLP--------HGVC---NAILLPIVEN
FNRPNAVARFARIAQA--------------MGVETRGMSDEAA-SQEAINAIRTLSKRVG
IPEGFSKLGVTKED----IEGWLDKALA-DP-------CAPCNPRTASRDEVRGLYLEAL
--------------------
>gi|62182504|ref|YP_218921.1| putative iron-containing alcohol dehydrogenase
[Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
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------------------------------------------------------------
---------------MSFMLALPKISLHG-AGAIADMVNLVANKQWGKALIVTDGQLVKL
GLLDSLFSALDKHQMSYHLFDEVFPNPTEELVQKGFAAYQSAECDYIIAFGGGSPIDTAK
AVKILTANP--GPSTAYS----GVGKVKNAGVPLVAINTTAGTA----------------
---AEMTSNAVIIDSARKVKEVIIDPNIIPDI---------------------AVDDASV
MLEIPASVTAAT-----------------------------GMDALTHAVEAYVSV-GAH
PL---------TDANALEAIRLINVWLPKAVD--------DGHNLEARE-----QMAFGQ
YLAGMAFNSAG------LGLVHALAHQPGATHNLP--------HGVC---NAILLPIVEN
FNRPNAVERFARIAQA--------------MGVETRGMSDEAA-SQEAINAIRTLSKRVG
IPEGFSKLGVTKED----IEGWLDKALA-DP-------CAPCNARTASRDEVRGLYLEAL
--------------------
>gi|77457538|ref|YP_347043.1| Iron-containing alcohol dehydrogenase [Pseudomonas
fluorescens Pf0-1]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------MSSTFFIPAVNIMG-SGCLDEAMNAIRNYGFRKALIVTDAGLAKA
GVATMIAEKLAMQDIDSVVFDGAKPNPSIANVEAGLALLKESRCDFVVSLGGGSPHDCAK
GIALCATNG--GQIRDYE----GVDQSTKPQLPLIAINTTAGTA----------------
---SEMTRFCIITDETRHVKMAIVDRNVTPLL---------------------SVNDPAL
MVAMPKSLTAAT-----------------------------GMDALTHAIEAYVST-AAN
PI---------TDACALKAMTLISNNLRLVVR--------DGSDLAARE-----NMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NAVLLPHVQT
FNAQVCAGRLTDVAHA--------------MGADIRGFSPEEG-AQAAIAAIRCLARDVE
IPGGLRDLGAKCTD----IPVLAANALK-DA-------CGFTNPRVADQRQIEEIFRSAF
--------------------
>gi|161505445|ref|YP_001572557.1| hypothetical protein SARI_03603 [Salmonella
enterica subsp. arizonae serovar 62:z4,z23:--]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------MFMSFMLALPKISLHG-AGAIGDMVKLIANKQWGKALIVTDSQLVKL
GLLDNLFSALDAHNMHYHLFDKVFPNPTEALVQKGYAAYQAEACDYIIAFGGGSPIDTAK
AVKILTANP--GPSTAYS----GVGKVKNAGVPLVAINTTAGTA----------------
---AEMTSNAVIIDTERQVKEVIIDPNIIPDI---------------------AVDDASV
MLEIPASVTAAT-----------------------------GMDALTHAVEAYVSV-GAH
PL---------TDANALEAVRLINLWLPKAVD--------DGHNLEARE-----QMAFGQ
YLAGMAFNSAG------LGLVHALAHQPGATHNLP--------HGVC---NAILLPIIEN
FNRPNAVARFARLAQA--------------MGVDTRGMSDEAA-SQEAINAIRALSKRVG
IPEGFSQLGVTKDD----IEGWLDKALA-DP-------CAPCNPRTASRDEVRELYLEAL
--------------------
>gi|157371893|ref|YP_001479882.1| iron-containing alcohol dehydrogenase [Serratia
proteamaculans 568]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------MAASTFFIPPVNMIG-SGCLDEAAKTMKQQGLRHALIVTDKVLNNI
GVVAQVQQLLAVQQIESCVYDGTHPNPTTLNVKQGLALLQEHRCDCVVSLGGGSPHDCAK
```

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GIALVATNG--GEIKDYE----GVDRSAKPQLPMIAINTTAGTA----------------
---SEMTRFCIITDEARHIKMAIVDKHVTPIL---------------------SVNDPHL
MAGMPKGLTAAT-----------------------------GMDALTHAIEAYVSS-AAN
PI---------TDACALKAVTMIAESLRDAVA--------DGSNMQARE-----NMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NAVLLPHVQE
FNARVCAPRLKDIAVA--------------MGLDVKHLNDPQG-AAACIAAIRLLAKDVG
IPAGLLDLKVKEQD----FDTLAANALK-DA-------CGFTNPIQATHEQIVAIFRAAM
--------------------
>gi|56478056|ref|YP_159645.1| alcohol dehydrogenase II [Aromatoleum aromaticum EbN1]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------MSTTTFFIPPVNLMG-AGCLADAMAAIRSYGFRHALIVTDAGLARA
GVADKVAALLAEQDIQATVFDGAKPNPTVGNVEAGLALLRDKQCDCVISLGGGSPHDCAK
GIALVATNG--GRIGDYE----GVDRSAKPQLPLVAINTTAGTA----------------
---SEMTRFCIITDEARHIKMAIVDRNVTPIL---------------------SVNDPTL
MVAKPAALTAAT-----------------------------GMDALTHAVEAYVST-AAT
PI---------TDACALKAVTLIAANLRRAVA--------DGNDLDARE-----QMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NAVLLPHVEA
FNASFSATRLADVARA--------------MGADVDALDDAAA-AEGCLAAIRRLAADVG
IPAGLTQLGVKAED----IPTLAANALN-DA-------CGLTNPRPATQADIEAIFRGAL
--------------------
>gi|52425857|ref|YP_088994.1| EutG protein [Mannheimia succiniciproducens MBEL55E]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----------MGVVLMSTYYFLPTRNVFG-ENAVEEVGELMRSLGGNRPLIVTDGFLAQS
GMAEQLATILRGAGLEPIIFGGAEPNPTDKNVESGIAFYHDHNCDCIISLGGGSSHDCAK
GIGLIASNG--GRIQDYE----GVDRSTNPMVPLMAVNTTAGTA----------------
---SEITRFCIITDTARKVKMAIVDWRVTPQI---------------------AVNDPLL
MKGMPAGLTAAT-----------------------------GMDALTHAIEAYVST-AAN
PL---------TDAAALMAISMIQQYLPKAVA--------NGDYMKARD-----KMAYAQ
YLAGIAFNNAS------LGYVHAMAHQLGGFYNLP--------HGVC---NAILLPYVEE
FNLIGNLNRFRDIANA--------------MGENIQGLSTDDA-ALKAIAAIRRLSKQVG
IPANLKELGVKPED----FDVMAENAMK-DV-------CMLTNPRKATKQQVIEIFQRAY
DGN-----------------
>gi|197284552|ref|YP_002150424.1| probable alcohol dehydrogenase [Proteus mirabilis
HI4320]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------MASSTFYIPSVNKLG-AGCLADAINSMKDFGFHKALIVTDSVLNQL
GVVNKVSELLAKSGIASVTYDGTAPNPTVENVEAGLALLKEHQCDCVISLGGGSPHDCAK
GIALVAANG--GKIADYE----GVDRSEHPQLPLIAINTTAGTA----------------
---SEMTRFCIITDTARHIKMAIVDKNVTPIL---------------------SVNDSEL
MIGMPKGLTAAT-----------------------------GMDALTHAVEAYVST-AAN
PI---------TDACALKAVTMISESLRKVVE--------NGGDTAARE-----NMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYNLP--------HGVC---NAVLLPHVQA
YNIQAAAGRLKDIAQA--------------MGVDVSAMNDEQG-AQACIEEIRKIAKDVG
IPAGLKELGVKEED----FKTLAENALK-DA-------CAITNPVQGSESDVIEIFRQAM
--------------------
>gi|117618598|ref|YP_856001.1| 1,3-propanediol dehydrogenase [Aeromonas hydrophila
subsp. hydrophila ATCC 7966]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------MATFKFYIPAINLMG-AGCLQEAAADIKGYGHRKALIVTDKILNQI
GVVAKVAGLLAEHGIESAVFDETKPNPTMTNVEAGLAMLKANGCDCVISLGGGSPHDCAK
GIALVAANG--GSIKDYE----GVDRSAKPQLPLIAINTTAGTA----------------
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---SEMTRFCIITDEARHVKMAIVDKHVTPLM---------------------SVNDPEL
MLAKPAGLTAAT-----------------------------GMDALTHAIEAYVST-IAT
PV---------TDASAIMAIQLIAKHLRTAVN--------QGDDLHARE-----QMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NAVLLPHVQA
YNAQVCAARLKDVARH--------------MGVDVSAMNDEQG-AAAAIAAIQQLAHDVK
IPAGLEQLGVKADD----FNLLAENALK-DA-------CGFTNPKQASHAEIVAIFRAAM
--------------------
>gi|51594736|ref|YP_068927.1| alcohol dehydrogenase [Yersinia pseudotuberculosis IP
32953]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------MSFMLALPKISLHG-TGAIGDMVKLLSDKQWGKALIVTDGQLVEL
GLLDSLFAALAQYQLPYGLFGEVFPNPTEELVQAGFAAFTQHQCDYLIAFGGGSPIDTAK
AIKILTANP--GPSTAYS----GVGKVKQTGVPLIAINTTAGTA----------------
---AELTSNAVIIDSQRQVKEVIIDTNLIPDI---------------------AVDDPSV
MLNIPASVTAAT-----------------------------GMDALTHAIEAYVSL-GAH
TL---------TDHSALESIRLISQWLPLAVA--------DGKNLQARE-----MMACGQ
YLAGMAFNSAG------LGLVHALAHQPGATHNLP--------HGVC---NAILLPVIEE
YNRPQATRRFARIAQA--------------MGVDTQDMSDEQA-SHQAIAAIRQLSLQVG
IPAGFSALGIEESD----IEGWLDKALA-DP-------CAPCNPRSADREQIRTLYLQAL
--------------------
>gi|170026061|ref|YP_001722566.1| lactaldehyde reductase [Yersinia
pseudotuberculosis YPIII]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------MSFMLALPKISLHG-TGAIGDMVKLLSDKQWGKALIVTDGQLVEL
GLLDSLFAALAQYQLPYGLFGEVFPNPTEELVQAGFAAFTQHQCDYLIAFGGGSPIDTAK
AIKILTANP--GPSTAYS----GVGKVKQTGVPLIAINTTAGTA----------------
---AELTSNAVIIDSQRQVKEVIIDTNLIPDI---------------------AVDDPSV
MLNIPASVTAAT-----------------------------GMDALTHAVEAYVSL-GAH
TL---------TDHSALESIRLISQWLPLAVA--------DGKNLQARE-----MMACGQ
YLAGMAFNSAG------LGLVHALAHQPGATHNLP--------HGVC---NAILLPVIEE
YNRPQATRRFARIAQA--------------MGVDTQDMSDEQA-SHQAIAAIRQLSLQVG
IPAGFSALGIEESD----IEGWLDKALA-DP-------CAPCNPRSADREQIRTLYLQAL
--------------------
>gi|126452408|ref|YP_001066362.1| EutG protein [Burkholderia pseudomallei 1106a]
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------MDRAFSFPGITGGSTRDA
PTQPGDDMSNLSSAERTDSFFIPRVTLIG-PGCARETGARAKSLGAKKALIVTDAGLHKM
GVSEIVAGHIREAGLQAAIFPGAQPNPTDVNVHDGVELYRREGCDFIVSLGGGSSHDCAK
GIGLVTAGG--GHIRDYE----GIDKSTVPMTPLISINTTAGTA----------------
---AEMTRFCIITNSSNHVKMAIVDWRCTPLI---------------------AIDDPSL
MVAMPPALTAAT-----------------------------GMDALTHAVEAYVST-AAT
PI---------TDACAEKAIALIGEWLPKAVA--------NGESMQARA-----AMCYAQ
YLAGMAFNNAS------LGYVHAMAHQLGGFYNLP--------HGVC---NAILLPHVCE
FNLIAAPERFAAIAPL--------------LGVRTAGMSTPDA-ARAAIAAIRALSASIG
IPSGLAALGVKAED----HEVMAGNAQK-DA-------CMLTNPRKATLAQVIAIFAAAM
--------------------
>gi|59711795|ref|YP_204571.1| Fe-containing alcohol dehydrogenase [Vibrio fischeri
ES114]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----------------MSAFFIPTVNLMG-AGCLTEAMDSIKSQGYKKGLIVTDNVLVAI
GMVKQVSDLLAERGVEVAVFDGTQPNPTIGNVNAGLKILKDNECDFVISLGGGSPHDCAK
GIALVAANG--GEIADYE----GVDQSAKPQLPLIAINTTAGTA----------------
```

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---SEMTRFCIITDEARHIKMAIVDKHTTPLM---------------------SVNDPEL
MLAKPASLTAAT-----------------------------GMDALTHAIEAYVSI-AAT
PV---------TDAVAIKAMELIQAHLRTAVN--------DGQNLEARE-----QMAYAQ
FMAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NAILLPHVQS
YNAKVCPERLKDVAKA--------------MGVNVEGMTNEEG-AQAALEAIKQLSQDVG
IPSGLTELNAKEED----FDTLAENALK-DA-------CGFTNPKQATHEEIVSIFKAAM
--------------------
>gi|21228871|ref|NP_634793.1| Iron-containing alcohol dehydrogenase [Methanosarcina
mazei Go1]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------MQSKTLLLAGKKSVLLIFCIFIIAPGR
FEQNLSRGVEGMIEKMTYTYLNPKIALMG-PGCVNGIGTHAKDLGGTKALIVSGKSRHGK
ELAADIRRILERAGIEAAIFPGADPNPTDTSVMEGADIYRKENCNMIVAVGGGSPMDCAK
AIGIVVYNG--GRINDYE----GVGKVTRGIPPLITVNTTAGTA----------------
---SEMTSFTIITDTERHIKMAIVDPRITPDV---------------------AVNDPEL
MVSMPPALTAAT-----------------------------GMDALTHAVEAYVST-MAT
PT---------TDAAAIKAIELISKYLPEAVL--------HGEDIRARD-----MMAHAE
YLAGIAFNNAS------LGYVHSMAHQLGGFYDLP--------HGVC---NAILLPYVEM
YNKQVCPERFADIAKA--------------MGEKVEGLSPDEA-ADKAIDAIKKLAAEIG
IPSGLKELGAREED----LELLAENAMQ-DV-------CRLTNPRELSKEDIIEIYRKAL
--------------------
>gi|22124498|ref|NP_667921.1| oxidoreductase [Yersinia pestis KIM]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------MSFMLALPKISLHG-TGAIGDMVKLLSDKQWGKALIVTDGQLVEL
GLLDSLFAAMAQYQLPYGLFGEVFPNPTEELVQAGFAAFTQHQCDYLIAFGGGSPIDTAK
AIKILTANP--GPSTAYS----GVGKVKQTGVPLIAINTTAGTA----------------
---AELTSNAVIIDSQRQVKEVIIDTNLIPDI---------------------AVDDPSV
MLNIPASVTAAT-----------------------------GMDALTHAVEAYVSL-GAH
TL---------TDHSALESIRLISQWLPLAVA--------DGKNLQARE-----MMACGQ
YLAGMAFNSAG------LGLVHALAHQPGATHNLP--------HGVC---NAILLPVIEE
YNRPQATRRFARIAQA--------------MGVDTQDMSDEQA-SHQAIAAIRQLSLQVG
IPAGFSALGIEESD----IEGWLDKALA-DP-------CAPCNPRSADREQIRTLYLQAL
--------------------
>gi|126439344|ref|YP_001059078.1| EutG protein [Burkholderia pseudomallei 668]
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------------------------------------------------------------
------------------------------------------MDRAFSFPGITGGSTRDA
PTQPGDDMSNLSSAERTDSFFIPCVTLIG-PGCARETGARAKSLGAKKALIVTDAGLHKM
GVSEIVAGHIREAGLQAAIFPGAQPNPTDVNVHDGVELYRREGCDFIVSLGGGSSHDCAK
GIGLVTAGG--GHIRDYE----GIDKSTVPMTPLISINTTAGTA----------------
---AEMTRFCIITNSSNHVKMAIVDWRCTPLI---------------------AIDDPSL
MVAMPPALTAAT-----------------------------GMDALTHAVEAYVST-AAT
PI---------TDACAEKAIALIGEWLPKAVA--------NGESMQARA-----AMCYAQ
YLAGMAFNNAS------LGYVHAMAHQLGGFYNLP--------HGVC---NAILLPHVCE
FNLIAAPERFAAIAPL--------------LGVRTAGMSTPDA-ARAAIAAIRALSASIG
IPSGLAALGVKAED----HEVMAGNAQK-DA-------CMLTNPRKATLAQVIAIFAAAM
--------------------
>gi|76812055|ref|YP_333632.1| EutG protein [Burkholderia pseudomallei 1710b]
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------------------------------------------------------------
---------------------------MAAFGVGRNGAAQSAESDAVRFIGARPRAAPRG
QRRASPGPRPIAPKWSRMCLIRTGVARRAAGRSSARGLPADGMDRAFSFPGITGGSTRDA
PTQPGDDMSNLSSAERTDSFFIPCVTLIG-PGCARETGARAKSLGAKKALIVTDAGLHKM
GVSEIVAGHIREAGLQAAIFPGAQPNPTDVNVHDGVELYRREGCDFIVSLGGGSSHDCAK
GIGLVTAGG--GHIRDYE----GIDKSTVPMTPLISINTTAGTA----------------
---AEMTRFCIITNSSNHVKMAIVDWRCTPLI---------------------AIDDPSL
MVAMPPALTAAT-----------------------------GMDALTHAVEAYVST-AAT
```

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PI---------TDACAEKAIALIGEWLPKAVA--------NGESMQARA-----AMCYAQ
YLAGMAFNNAS------LGYVHAMAHQLGGFYNLP--------HGVC---NAILLPHVCE
FNLIAAPERFAAIAPL--------------LGVRTAGMSTPDA-ARAAIAAIRALSASIG
IPSGLAALGVKAED----HEVMAGNAQK-DA-------CMLTNPRKATLAQVIAIFAAAM
--------------------
>gi|28900421|ref|NP_800076.1| alcohol dehydrogenase [Vibrio parahaemolyticus RIMD
2210633]
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------------------------------------------------------------
------------------------------------------------------------
---------------MTSTFFIPTVNLMG-AGCLKDAANSIQSQGFKKGLIVTDKILNQI
GVVKQVQDLLTERGVATVVFDGTQPNPTITNVNDGLALLKENECDFVISLGGGSPHDCAK
GIALVASNG--GKIGDYE----GVDQSAKPMLPLIAINTTAGTA----------------
---SEMTRFCIITDEERHIKMAIVDKHTTPLI---------------------SVNDPEL
MLAKPASLTAAT-----------------------------GMDALTHAIEAYVSI-AAT
PI---------TDAVAIKAIELIQAHLRTAVK--------NGENLEARE-----QMAYAQ
FMAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NAILLPHVQR
YNAQVCPERLRDVAKA--------------MGVDVEGMSAEHG-AAAAIDAIVALAKDVG
IPAGIKELGAKLED----IPTLADNALK-DA-------CGFTNPKQATHEEISAIFEAAM
--------------------
>gi|197335936|ref|YP_002155987.1| 1,3-propanediol dehydrogenase [Vibrio fischeri
MJ11]
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------------------------------------------------------------
----------------MSAFFIPTVNLMG-AGCLTEAMDSIKSQGYKKGLIVTDNVLVAI
GMVKQVSDLLSERGVEVAVFDGTQPNPTIGNVNAGLKILKDNECDFVISLGGGSPHDCAK
GIALVAANG--GEIADYE----GVDQSAKPQLPLIAINTTAGTA----------------
---SEMTRFCIITDEARHIKMAIVDKHTTPLM---------------------SVNDPEL
MLAKPASLTAAT-----------------------------GMDALTHAIEAYVSI-AAT
PV---------TDAVAIKAMELIQAHLRTAVN--------DGQNLEARE-----QMAYAQ
FMAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NAILLPHVQS
YNAKVCPERLKDVAKA--------------MGVNVEGMTNEEG-AQAALEAIKQLSQDVG
IPSGLTELNAKEED----FDTLAENALK-DA-------CGFTNPKQATHEEIVSIFKAAM
--------------------
>gi|152978087|ref|YP_001343716.1| iron-containing alcohol dehydrogenase
[Actinobacillus succinogenes 130Z]
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------------------------------------------------------------
------------------------------------------------------------
---------------MSTYYFLPTRNVFG-ENAVEEVGTLMKSLGGNNPLIVTDAFLAKN
GMADQLAAVLSNAGLKPVIFGGAEPNPTDKNVEEGIVFYNEHGCDSIISLGGGSSHDCAK
GIGLIASNG--GRIQDYE----GVDRSHNAMVPLMAVNTTAGTA----------------
---SEITRFCIITDTARKVKMAIVDWRITPQI---------------------AVNDPLL
MKGMPPSLTAAT-----------------------------GMDALTHAIEAYVST-AAN
PL---------TDAAALMAITMIQQYLPKAVA--------NGDYMKARD-----KMAYAQ
YLAGIAFNNAS------LGYVHAMAHQLGGFYNLP--------HGVC---NAILLPYVEE
FNLIGNLNRFRDIAKA--------------MGENIDGLCTDDA-ALKAIGAIRRLSKQVG
IPANLQLLGVKPED----FDVMAENAMK-DV-------CMLTNPRKATKQQVIEIFQRAY
DGD-----------------
>gi|56552492|ref|YP_163331.1| alcohol dehydrogenase II [Zymomonas mobilis subsp.
mobilis ZM4]
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------------------------------------------------------------
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------------------------------------------------------------
--------------MASSTFYIPFVNEMG-EGSLEKAIKDLNGSGFKNALIVSDAFMNKS
GVVKQVADLLKAQGINSAVYDGVMPNPTVTAVLEGLKILKDNNSDFVISLGGGSPHDCAK
AIALVATNG--GEVKDYE----GIDKSKKPALPLMSINTTAGTA----------------
---SEMTRFCIITDEVRHVKMAIVDRHVTPMV---------------------SVNDPLL
```

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MVGMPKGLTAAT-----------------------------GMDALTHAFEAYSST-AAT
PI---------TDACALKAASMIAKNLKTACD--------NGKDMPARE-----AMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGYYNLP--------HGVC---NAVLLPHVLA
YNASVVAGRLKDVGVA--------------MGLDIANLGDKEG-AEATIQAVRDLAASIG
IPANLTELGAKKED----VPLLADHALK-DA-------CALTNPRQGDQKEVEELFLSAF
--------------------
>gi|83720772|ref|YP_442856.1| alcohol dehydrogenase, iron-containing [Burkholderia
thailandensis E264]
MIFTVIMQFGVIAVNGRIENFARRTSRPGNAGARVGRASGRKRCGSPAPPAPPAPPAPPG
SAPSRSAPGRRAARSASVMLVLFLRSVMRHNALNLYCAVLAAITSARRFAYRRAPTAKAR
AVVSVAILPVCRHAAISSARAFASAAGRRGDSARLSGRGEDRQNRTPHGAARPASAALGD
ARRRKRRRARSLRNGAACAEFEQAMRAIQSAVHESTAFSRDGTVRAFSFPGQTGDFTRDA
LTQPGDDMSYLNIAQRTDSFFIPCVTLIG-PGCARETGVRAKSLGAKKALIVTDAGLHKM
GLSEIVAGHIRDAGLQAVIFAGAEPNPTDVNVHDGVERFQREGCDFIVSLGGGSSHDCAK
GIGLVTAGG--GHIRDYE----GIDKSTVPMTPLISINTTAGTA----------------
---AEMTRFCIITNSSNHVKMAIVDWRCTPLI---------------------AIDDPCL
MVAMPPALTAAT-----------------------------GMDALTHAVEAYVST-AAT
PI---------TDACAEKAIALIGEWLPKAVA--------NGESMEARA-----AMCYAQ
YLAGMAFNNAS------LGYVHAMAHQLGGFYNLP--------HGVC---NAILLPHVCE
FNLIAAPERFATIASL--------------LGVNTAGSSTVDA-ARAAIAAIRGLSASIG
IPAGLAALGVKAED----HEVMASNAQK-DA-------CMLTNPRKATLAQVIAIFAAAM
--------------------
>gi|110807737|ref|YP_691257.1| putative alcohol dehydrogenase [Shigella flexneri 5
str. 8401]
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------------------------------------------------------------
--------------MASSTFFIPSVNVIG-ADSLTDAMNMMADYGFTRTLIVTDNMLTKL
GMAGDVQKALEERNIFSVIYDGTQPNPTTENVAAGLKLLKENNCDSVISLGGGSPHDCAK
GIALVAANG--GDIRDYE----GVDRSAKPQLPMIAINTTAGTA----------------
---SEMTRFCIITDEARHNKMAIVDKHVTPLL---------------------SVNDSSL
MIGMPKSLTAAT-----------------------------GMDALTHAIEAYVSI-AAT
PI---------TDACALKAVTMIAENLPLAVE--------DGSNAKARE-----AMVYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYNLP--------HGVC---NAVLLPHVQV
FNSKVAAARLRDCAAA--------------MGVNVTGKNDAEG-AEACINAIRELAKKVD
IPAGLRDLNVKEED----FAVLATNALK-DA-------CGFTNPIQATHEEIVVIYRAAM
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>gi|87200808|ref|YP_498065.1| iron-containing alcohol dehydrogenase [Novosphingobium
aromaticivorans DSM 12444]
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------------------------------------------------------------
----------------MAAINLPRVIRAG-GGALAELPDAMAQCGLSRPFVVTDAFLVQS
GMVARMLEVLDGAGIAATVFDATVPDPTVAVVEQALGALREAECDCVIGFGGGSPIDTSK
AIAALALEP--RAVQSMK----APATTDVPGLPIIAVPTTAGTG----------------
---SEATKFTIVTDEATSEKMLCAGLAFLPTI---------------------AIVDFEL
TMGKPARLTADT-----------------------------GIDSLTHAIEAYVSK-KAN
PF---------SDAMAISAMKLIAPNIRTACA--------EPGNRAARE-----AMMIGA
HHAGIAFSNAS------VALVHGMSRPIGAFFHVP--------HGLS---NAMLLPAITA
FSAPSALPRYADCARA--------------MGVALESEGDQSA-VARLLDELAALNADLS
VPTP-QSHGISADRWFEVVPEMARQAIA-SG-------SPGNNPRVPDAAEIERLYAEVF
G-------------------
>gi|15804130|ref|NP_290169.1| putative alcohol dehydrogenase [Escherichia coli
O157:H7 EDL933]
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------------------------------------------------------------
--------------MASSTFFIPSVNVIG-ADSLTDAMNMMADYGFTRTLIVTDSMLTKL
GMAGDVQKALEERNIFSVIYDGTQPNPTTENVAAGLKLLKENNCDSVISLGGGSPHDCAK
GIALVAANG--GDIRDYE----GVDRSAKPQLPMIAINTTAGTA----------------
```

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---SEMTRFCIITDEARHIKMAIVDKHVTPLL---------------------SVNDSSL
MIGMPKSLTAAT-----------------------------GMDALTHAIEAYVSI-AAT
PI---------TDACALKAVTMIAENLPLAVE--------DGSNAKARE-----AMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYNLP--------HGVC---NAVLLPHVQV
FNSKVAAARLRDCAAA--------------MGVNVTGKNDAEG-AEACINAIRELAKKVD
IPAGLRDLNVKEED----FAVLAANALK-DA-------CGFTNPIQATHEEIVAIYRAAM
--------------------
>gi|147678976|ref|YP_001213191.1| alcohol dehydrogenase [Pelotomaculum
thermopropionicum SI]
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------------------------------------------------------------
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------------------------------------------------------------
-------------MSSICKHVAPEI-IFG-RGALSQVGESAVRLGANKVFIVSDQGVVNA
GWVERVLSYLKAAGLQYEIFSSVTSNPKHTEITEGLKRYLESECDSIMAVGGGSPTDVAK
SIATMATNG--GVIQDFE----GINKITKPLPPMLAVPTTAGAG----------------
---SEVTQFAIIVDKERKLKMAIISKSLVPDI---------------------AIIDPEV
LQTKSARLTAAT-----------------------------GIDALSHAIEAYVSL-AAT
PL---------TEVHSLSALRLIAQNLRESVA--------CRTNMEAKT-----SMAMAS
LQAGIAFSNAI------LGAAHAMVHQVDGFLDTH--------HGES---NACILPYVME
FNLIACPGKFKQIAEA--------------LGEDVTGLSTWAA-AKKAIKAVRALVSDVG
LAEGLAELGMKEEY----IPSFSRNALK-DA-------CLVTNPRDADENDIAEIYRMAM
--------------------
>gi|24114857|ref|NP_709367.1| putative alcohol dehydrogenase [Shigella flexneri 2a
str. 301]
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------------------------------------------------------------
------------------------------------------------------------
--------------MASSTFFIPSVNVIG-ADSLTDAMNMMADYGFTRTLIVTDNMLTKL
GMAGDVQKALEERNIFSVIYDGTQPNPTTENVAAGLKLLKENNCDSVISLGGGSPHDCAK
GIALVAANG--GDIRDYE----GVDRSAKPQLPMIAINTTAGTA----------------
---SEMTRFCIITDEARHNKMAIVDKHVTPLL---------------------SVNDSSL
MIGMPKSLTAAT-----------------------------GMDALTHAIEAYVSI-AAT
PI---------TDACALKAVTMIAENLPLAVE--------DGSNAKARE-----AMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYNLP--------HGVC---NAVLLPHVQV
FNSKVAAARLRDCAAA--------------MGVNVTGKNDAEG-AEACINAIRELAKKVD
IPAGLRDLNVKEED----FAVLATNALK-DA-------CGFTNPIQATHEEIVVIYRAAM
--------------------
>gi|218707226|ref|YP_002414745.1| putative alcohol dehydrogenase [Escherichia coli
UMN026]
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------------------------------------------------------------
------------------------------------------------------------
--------------MAASTFFIPSVNVIG-ADSLNDAMNMMADYGFTRTLIVTDNMLTKL
GMAGDVQKALEERNIFSVIYDGTQPNPTTENVAAGLKLLKENNCDSVISLGGGSPHDCAK
GIALVAANG--GDIRDYE----GVDRSAKPQLPMIAINTTAGTA----------------
---SEMTRFCIITDEARHIKMAIVDKHVTPLL---------------------SVNDSSL
MIGMPKSLTAAT-----------------------------GMDALTHAIEAYVSI-AAT
PI---------TDACALKAVTMIAENLPLAVE--------DGSNAKARE-----AMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYNLP--------HGVC---NAVLLPHVQV
FNSKVAAARLRDCAAA--------------MGVNVTGKNDAEG-AEACINAIRELAKKVN
IPAGLRDLNVKEED----FAVLATNALK-DA-------CGFTNPIQATHEEIVAIYRAAM
--------------------
>gi|147677186|ref|YP_001211401.1| alcohol dehydrogenase [Pelotomaculum
thermopropionicum SI]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------MKISYFWTSGTIITG-RGSLKRIADEAKGLGATRVLIVTDPVLLKT
GLIERVKEALAPAGLETGIFSGVEPEPRLQIVTECLKAVKEGGYDLIVAVGGGSSMDVSK
```

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AASVLMTNP--GTINDYL----GVNLIPRPGIPVIAVPTTAGTG----------------
---SEVTPIAILSDVEEQLKKGVVSPYLLPRV---------------------AIVDPEL
TVTMPPAITAAT-----------------------------GMDALTHAVESYISV-NAT
PI---------TDILALEAIRLIALNLRTAVA--------NGQDIEARS-----NMSMAS
LLAGIAFANAG------VGAVHALAYPLGAQFHVP--------HGVA---NAVLLPYVME
SNLLGALPRFKTMALA--------------MGEKVEDLSDRLA-ADKFNEAIKLLAADIR
IPLHLRELGVTAES----IPGMAEGAAKVTR-------LLANNPRILSVSDIREIYERAF
--------------------
>gi|110643834|ref|YP_671564.1| putative alcohol dehydrogenase [Escherichia coli 536]
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------------------------------------------------------------
--------------MAASTFFIPSVNVIG-ADSLNDAMNMMADYGFTRTLIVTDNMLTKL
GMAGDVQKALEERNIFSVIYDGTQPNPTTENVAAGLKLLKENNCDSVISLGGGSPHDCAK
GIALVAANG--GDIRDYE----GVDRSAKPQLPMIAINTTAGTA----------------
---SEMTRFCIITDEARHIKMAIVDKHVTPLL---------------------SVNDSSL
MVGMPKSLTAAT-----------------------------GMDALTHAIEAYVSI-AAT
PI---------TDACALKAVTMIAENLPLAVE--------DGSNAKARE-----AMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYNLP--------HGVC---NAVLLPHVQV
FNSKVAAARLRDCAAA--------------MGVNVTGKNDAEG-AEACINAIRELAKKVD
IPAGLRDLNVKEED----FAVLATNALK-DA-------CGFTNPIQATHEEIVAIYRAAM
--------------------
>gi|215488872|ref|YP_002331303.1| putative alcohol dehydrogenase [Escherichia coli
O127:H6 str. E2348/69]
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------------------------------------------------------------
--------------MAASTFFIPSVNVIG-ADSLNDAMNMMADYGFTRTLIVTDNILTKL
GMAGDVQKALEERNIFSVIYDGTQPNPTTENVAAGLKLLKENNCDSVISLGGGSPHDCAK
GIALVAANG--GDIRDYE----GVDRSAKPQLPMIAINTTAGTA----------------
---SEMTRFCIITDEARHIKMAIVDKHVTPLL---------------------SVNDSSL
MIGMPKSLTAAT-----------------------------GMDALTHAIEAYVSI-AAT
PI---------TDACALKAVTMIAENLPLAVE--------DGSNAKARE-----AMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYNLP--------HGVC---NAVLLPHVQV
FNSKVAAARLRDCAAA--------------MGVNVTGKNDAEG-AEACINAIRELAKKVD
IPAGLRDLNVKEED----FAVLATNALK-DA-------CGFTNPIQATHEEIVAIYRAAM
--------------------
>gi|157154897|ref|YP_001465066.1| putative alcohol dehydrogenase [Escherichia coli
E24377A]
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------------------------------------------------------------
--------------MASSTFFIPSVNVIG-ADSLTDAMNMMADYGFTRTLIVTDNMLTKL
GMAGDVQKALEERNIFSVIYDGTQPNPTTENVAAGLKLLKENNCDSVISLGGGSPHDCAK
GIALVAANG--GDIRDYE----GVDRSAKPQLPMIAINTTAGTA----------------
---SEMTRFCIITDEARHIKMAIVDKHVTPLL---------------------SVNDSSL
MIGMPKSLTAAT-----------------------------GMDALTHAIEAYVSI-AAT
PI---------TDACALKAVTMIAENLPLAVE--------DGSNAKARE-----AMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYNLP--------HGVC---NAVLLPHVQV
FNSKVAAARLRDCAAA--------------MGVNVTGKNDAEG-AEACINAIRELAKKVD
IPAGLRDLNVKEED----FAVLATNALK-DA-------CGFTNPIQATHEEIVAIYRAAM
--------------------
>gi|91213104|ref|YP_543090.1| putative alcohol dehydrogenase [Escherichia coli
UTI89]
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------------------------------------------------------------
------------------------------------------------------------
--------------MAASTFFIPSVNVIG-ADSLNDAMNMMADYGFTRTLIVTDNMLTKL
GMAGDVQKALEERNIFSVIYDGTQPNPTTENVAAGLKLLKENNCDSVISLGGGSPHDCAK
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GIALVAANG--GDIRDYE----GVDRSAKPQLPMIAINTTAGTA----------------
---SEMTRFCIITDEARHIKMAIVDKHVTPLL---------------------SVNDSSL
MIGMPKSLTAAT-----------------------------GMDALTHAIEAYVSI-AAT
PI---------TDACALKAVTMIAENLPLAVE--------DGSNAKARE-----AMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYNLP--------HGVC---NAVLLPHVQV
FNSKVAAARLRDCAAA--------------MGVNVTGKNDAEG-AEACINAIRELAKKVD
IPAGLRDLNVKEED----FAVLATNALK-DA-------CGFTNPIQATHEEIVAIYRAAM
--------------------
>gi|49176377|ref|YP_026233.1| predicted Fe-containing alcohol dehydrogenase
[Escherichia coli str. K-12 substr. MG1655]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------MAASTFFIPSVNVIG-ADSLTDAMNMMADYGFTRTLIVTDNMLTKL
GMAGDVQKALEERNIFSVIYDGTQPNPTTENVAAGLKLLKENNCDSVISLGGGSPHDCAK
GIALVAANG--GDIRDYE----GVDRSAKPQLPMIAINTTAGTA----------------
---SEMTRFCIITDEARHIKMAIVDKHVTPLL---------------------SVNDSSL
MIGMPKSLTAAT-----------------------------GMDALTHAIEAYVSI-AAT
PI---------TDACALKAVTMIAENLPLAVE--------DGSNAKARE-----AMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYNLP--------HGVC---NAVLLPHVQV
FNSKVAAARLRDCAAA--------------MGVNVTGKNDAEG-AEACINAIRELAKKVD
IPAGLRDLNVKEED----FAVLATNALK-DA-------CGFTNPIQATHEEIVAIYRAAM
--------------------
>gi|37676187|ref|NP_936583.1| alcohol dehydrogenase, class IV [Vibrio vulnificus
YJ016]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------MASAFFIPTVNLMG-AGCLKDAADSIKAQGFTKGLIVTDKILNQI
GVVKQVQDLLSERHVEAVVFDGTQPNPTIGNVNAGLALLKQNECDFVISLGGGSPHDCAK
GIALVAANG--GEIADYE----GVDKSAKPMLPLIAINTTAGTA----------------
---SEMTRFCIITDEERHIKMAIVDKHTTPLI---------------------SVNDPEL
MLAKPASLTAAT-----------------------------GMDALTHAVEAYVSI-AAT
PI---------TDAVAIKAIELIQAHLRTAVA--------HGDDIEARE-----QMAYAQ
FMAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NAILLPHVQR
YNAQVCPERLRDVAKA--------------MGVNVEGMSAEQG-AEAAIDAIVALAKDVG
IPAGIRELGAKSED----IPTLADNALK-DA-------CGFTNPKQATHEEISAIFEAAM
--------------------
>gi|27366481|ref|NP_762008.1| alcohol dehydrogenase, class IV [Vibrio vulnificus
CMCP6]
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------------------------------------------------------------
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------------------------------------------------------------
--------------------------MG-AGCLKDAADSIKAQGFTKGLIVTDKILNQI
GVVKQVQDLLSERHVETVVFDGTQPNPTIGNVNAGLALLKQNECDFVISLGGGSPHDCAK
GIALVAANG--GEIADYE----GVDKSAKPMLPLIAINTTAGTA----------------
---SEMTRFCIITDEERHIKMAIVDKHTTPLI---------------------SVNDPEL
MLAKPASLTAAT-----------------------------GMDALTHAVEAYVSI-AAT
PI---------TDAVAIKAIELIQAHLRTAVA--------HGDDIEARE-----QMAYAQ
FMAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NAILLPHVQR
YNAQVCPERLRDVAKA--------------MGVNVEGMSAEQG-AEAAIDAIVALAKDVG
IPAGIRELGAKSED----IPTLADNALK-DA-------CGFTNPKQATHEEISAIFEAAM
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>gi|39934280|ref|NP_946556.1| putative alcohol dehydrogenase [Rhodopseudomonas
palustris CGA009]
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------------------------------------------------------------
--------------MTATTFFIPSLNLFG-AGCVSSAADHAKARGFKRALIVTDSGLHKL
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GVADQIASMLIERNVTSVVFPGAKPNPTIKNVEDGLALLKQENCDCVISLGGGSAHDCAK
GIALTATNG--GSIKDYE----GVDRSAHAQLPLIAINTTAGTA----------------
---SEMTRFCIITDEERQVKMAIVDRHTTPLL---------------------SVNDPVL
MLGKPPALTAAT-----------------------------GMDALTHAIEAYVSI-AAT
PI---------TDACALKAMSIISNSLRTVVA--------EGQNLVARE-----AMSYAG
FLAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NAVLLPHVQA
YNAQVAAGRLKDVAHA--------------LGVDTTGMTDAQG-ADAAIHAIQRLSADVG
IPPGLGGLGMKETD----VPILAANALK-DA-------CGFTNPKQATQTEIETIFRAAA
--------------------
>gi|209695265|ref|YP_002263194.1| alcohol dehydrogenase 2 [Aliivibrio salmonicida
LFI1238]
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------------------------------------------------------------
------------------------------------------------------------
----------------MSAFFIPSINLMG-AGCLAEAMDSIKSQGYKKALIVTDNVLVAI
GMVKQVSDLLAERGVEVAVFDGTQPNPTIGNVNAGLKILQENQCDLVISLGGGSPHDCAK
GIALVAANG--GEIADYE----GVDQSPKPQMPLVAINTTAGTA----------------
---SEMTRFCIITDEARHIKMAIVDKHTTPLM---------------------SVNDPEL
MLAKPASLTAAT-----------------------------GMDALTHAIEAYVSI-AAT
PI---------TDAVAIKAMELIQAHLRTAVE--------DGQNLEARE-----QMAYAQ
FMAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NAILLPHVQS
YNAKVCPERLKDVAKA--------------MGVNVEGMTNEEG-AQAALDAIKVLSKDVG
IPSGLTALNAKEED----FDTLAENALK-DA-------CGFTNPKQATHDEIVNIFKAAM
--------------------
>gi|54309683|ref|YP_130703.1| putative alcohol dehydrogenase [Photobacterium
profundum SS9]
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------------------------------------------------------------
------------------------------------------------------------
---------------MSSAFFIPSVNLMG-AGCLTEAADAVKAHGFKKALIVTDKVLNQI
GVVKQVVDLLAERNVEAVVFDGTQPNPTMGNVEAGLALLKANECDFVISLGGGSPHDCAK
GVALVASNG--GSISDYE----GVDVSAKPQLPLVAINTTAGTA----------------
---SEMTRFCIITDEARHIKMAIVDKNTTPLM---------------------SVNDPEL
MLAKPASLTAAT-----------------------------GMDALTHAIEAYVST-AAT
PI---------TDAVAIKAMELIQAHLRTAVN--------DGQNLEARE-----QMAYAQ
FMAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NAVLLPHVQR
YNAKVCPERLRDVAKA--------------MGVNVESMTAEQG-ADAALEAIQVLSKDVG
IPAGLKDLGAKNED----ISILADNALK-DA-------CGFTNPKQATHEEISEIFAAAM
--------------------
>gi|82545951|ref|YP_409898.1| putative alcohol dehydrogenase [Shigella boydii Sb227]
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------------------------------------------------------------
------------------------------------------------------------
--------------MASSTFFIPSVNVIG-ADSLTDAMNMMADYGFTRTLIVTDSMLTKL
GMAGDVQKALEERNIFSVIYDGTQPNPTTENVAAGLKLLKENNCDSVISLGGGSPHDCAK
GIALVAANG--GDIRDYE----GVDRSAKPQLPMIAINTTAGTA----------------
---SEMTRFCIITDEARHIKMAIVDKHVTPLL---------------------SVNDSSL
MIGMPKSLTAAT-----------------------------GMDALTHAIEAYVSI-AAT
PI---------TDACALKAVTMIAENLPLAVE--------DGSNAKARE-----AMAYAQ
FLAGMAFNNAS------LGYVHAMAYQLGGFYNLP--------HGVC---NAVLLPHVQV
FNSKVAAARLRDCAAA--------------MGVNVTGKNDAEG-AEACINAIRELAKKVD
IPAGLRDLNVKEED----FAVLATNALK-DA-------CGFTNPIQATHEEIVAIYRAAM
--------------------
>gi|56459904|ref|YP_155185.1| alcohol dehydrogenase [Idiomarina loihiensis L2TR]
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------------------------------------------------------------
------------------------------------------------------------
---------------MSSTFYIPAVNIIG-ENALKDAATQMDNYGFKQALIVTDPGMTKL
GVTAEIEALLKEHGIDSLIYDGVQPNPTVTNVKAGLDVLQKHQCDCVISLGGGSAHDCAK
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GIALVATNG--GHISDYE----GVDVSKKPQLPLISINTTAGTA----------------
---SEMTRFCIITDPERHIKMAIVDQNVTPIL---------------------SVNDPRL
MVGMPASLTAAT-----------------------------GMDALTHAVEAYVST-DAT
PI---------TDACAIKAIEIIRDNLHEAVH--------NGANMEARE-----QMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NAVLLPHVQR
YNSQVVAPRLKDIGKA--------------LGAEVQGLTEKEG-ADAAIAAIVKLSQSVN
IPAGLEELGAKEED----FNTLADNAMK-DA-------CGLTNPIQPSHEDIVTIFKAAF
--------------------
>gi|34498183|ref|NP_902398.1| alcohol dehydrogenase [Chromobacterium violaceum ATCC
12472]
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------------------------------------------------------------
--------------MSTSAFFIPSLNLMG-AGCLQQAVDAMRGHGFRRALIVTDQGLVKA
GLAAKVADMLGKADIEPVIFDGVHPNPSCANVNAGLALLKEKQCDVVVSLGGGSPHDCAK
GIALVAVNG--GKIQDYE----GVDKSAKPQLPLVAINTTAGTA----------------
---SEMTRFCIITDESRHIKMAIVDKHTTPIL---------------------SVNDPET
MAGMPASLTAAT-----------------------------GMDALTHAVEAYVST-IAT
PI---------TDACALKAVELIAGFLRRAVK--------DGKDMEARE-----QMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NAVLLPHVQA
FNAASAGERLGDVAIA--------------LGEKTRS-------AQAAIAAIKRLAADVG
IPAGLRELGVKEAD----IPTLADNALK-DA-------CGFTNPRKGSHEDVCAIFRAAM
--------------------
>gi|218550867|ref|YP_002384658.1| putative alcohol dehydrogenase [Escherichia
fergusonii ATCC 35469]
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------------------------------------------------------------
------------------------------------------------------------
--------------MAASTFFIPSVNVIG-ADSLNDAMNMMAEYGFRRTLIVTDSMLTQL
GMAGDVQKALQERDIFSVIYDGTQPNPTTENVAAGLKLLTENNCDSVISLGGGSPHDCAK
GIALVAANG--GDIRDYE----GVDRSAKPQLPMIAINTTAGTA----------------
---SEMTRFCIITDEARHIKMAIVDKHVTPLL---------------------SVNDSSL
MIGMPKSLTAAT-----------------------------GMDALTHAIEAYVSI-AAT
PI---------TDACALKAVTMIAENLPLAVE--------DGSNAKARE-----AMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYNLP--------HGVC---NAVLLPHVQV
FNSKVAAARLRDCAAA--------------MGVNVTGKNDAEG-AEACINAIRELAKKVN
IPAGLRDLNVKEED----IPVLATNALK-DA-------CGFTNPIQATHEEIMAIYRAAM
--------------------
>gi|145299820|ref|YP_001142661.1| alcohol dehydrogenase [Aeromonas salmonicida
subsp. salmonicida A449]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------MATFKFYIPAINLMG-AGCLQEAAADIKGYGYRKALIVTDKILNQI
GVVAKLTTLLAEHGIESVVFDETKPNPTMTNVESGLAMIRANGCDCVISLGGGSPHDCAK
GIALVAANG--GSIQDYE----GVDRSAKPQLPLIAINTTAGTA----------------
---SEMTRFCIITDEARQVKMAIIDKHVTPLM---------------------SVNDPEL
MLAKPAGLTAAT-----------------------------GMDALTHAIEAYVST-IAT
PV---------TDASAIMAIQLIAKHLRTAVN--------QGDDLHARE-----QMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NAVLLPHVQA
YNAQVNAARLKDVARY--------------MGVDVSTMNDEQG-AAAAIAAIKQLALDVK
IPAGLEQLGVKADD----FDVLASNALK-DA-------CGFTNPKQASHEEIVAIFRAAM
--------------------
>gi|20091453|ref|NP_617528.1| alcohol dehydrogenase [Methanosarcina acetivorans C2A]
------------------------------------------------------------
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------------------------------------------------------------
---------------------------------------------------------MLN
EAVVKQSCCQKELRSMTYTYLNPKVALMG-AGCVKEIGKHAKELGGTKALIVSGRSRHGE
ELAGDIRKILETAGLKIAIFPGADPNPTDSSVMEGAIIYEKENCDLIVAVGGGSPMDCAK
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AIGIVAKNG--GEINDYE----GIGKVTKGVPPLITVNTTAGTA----------------
---SEMTSFTIITDTKRHIKMAIVDPRITPDV---------------------AVNDPEL
MVSMPPALTAAT-----------------------------GMDALTHAVEAYVST-IAT
PT---------TDAAAIKAIELISKYLPEAVA--------HGGDVRTRD-----MMAHAE
YLAGIAFNNAS------LGYVHSMAHQLGGLYDLP--------HGIC---NAILLPYVEM
YNKEVCPERFADIAKA--------------MGEKVEGLSPEEA-ADKAIAAIKKLAADIG
IPSGLKELGAREED----LELLAENAMQ-DV-------CHLTNPRELSKEEVIEIYRKAM
--------------------
>gi|26250232|ref|NP_756272.1| putative alcohol dehydrogenase [Escherichia coli
CFT073]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------MAASTFFIPSVNVIG-ADSLNDAMNMMADYGFTRTLIVTDNILTKL
GMAGDVQKALEERNIFSVIYDGTQPNPTTENVAAGLKLLKENNCDSVISLGGGSPHDCAK
GIALVAANG--GDIRDYE----GVDRSAKPQLPMIAINTTAGTA----------------
---SEMTRFCIITDEARHIKMAIVDKHVTPLL---------------------SVNDSSL
MIGMPKSLTAAT-----------------------------GMDALTHAIEAYVSI-AAT
PI---------TDACALKAVTMIAENLPLAVE--------DGSNAKARE-----AMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYNLP--------HGVC---NAVLLPHVQV
FNSKVAAARLRDCAAA--------------MGVNVTGKNDAEG-AEACINAIRELAKKVN
IPAGLRDLNVKEED----IPVLATNALK-DA-------CGFTNPIQATHEEIMAIYRAAM
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>gi|126173559|ref|YP_001049708.1| iron-containing alcohol dehydrogenase [Shewanella
baltica OS155]
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------------------------------------------------------------
---------------MAAKFFIPSVNVLG-QGAVDDAIGDIKTLGFKHALIVTDKPLVKI
GLVGEVAEKLGQNGITSTIYDGVQPNPTVTNVEAGLALLKANKCDFVISLGGGSPHDCAK
GIALVATNG--GSIKDYE----GLDQSAKPQLPLVAINTTAGTA----------------
---SEMTRFCIITDEARHIKMAIVDKHTTPLL---------------------SVNDPEL
MLKKPASLTAAT-----------------------------GMDALTHAVEAYVSI-AAN
PI---------TDACAIKAMELIQANLVNAVE--------NGQDINARE-----QMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NALLLPHVQE
YNAQVVPARLKDIAKA--------------MGVDVSSMTDEQG-ASAAIAAIKKLSFAVK
IPENLTLLGVKAED----IPTLADNALK-DA-------CGFTNPKQATQAEICQIFTNAL
--------------------
>gi|169829620|ref|YP_001699778.1| NAD-dependent methanol dehydrogenase
[Lysinibacillus sphaericus C3-41]
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------------------------------------------------------------
------------MSDVLKQFVMPKKNLFG-PGAIQEVGKHLNDLEVKKTLIVTDEGLHKL
GLSEQIANIITAAGIDVAIFPKAEPNPTDQNIEDGIADYHAESCDSIVSLGGGSAHDAAK
GIGLIASNG--GRIQDYE----GVDKSQNPLVPLIAINTTAGTA----------------
---SEMTRFTIITDTARKVKMAIVDKHVTPLL---------------------SINDSEL
MIGLPPALTAAT-----------------------------GVDALTHAIESFVST-NAT
PI---------TDACAEKVLQLVPEFLPRAYA--------NGADLEARE-----QMVYAQ
FLAGMAFNNAS------LGYVHAIAHQLGGYYNLP--------HGVC---NAILLPHVCR
FNVTARTERFARIAEL--------------LGENVTGLSKRDA-AEKAISAIEKLSKDLN
IPSGFRELGAKDED----IEILAKNAML-DV-------CAETNPRKATLDDIKQIITNAM
GPIVKKEESLEAVAALS---
>gi|77920437|ref|YP_358252.1| alcohol dehydrogenase, class IV [Pelobacter
carbinolicus DSM 2380]
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------------------------------------------------------------
---------MRALAEQTFAFNIPTVSLLG-VGAAKQAGEQAKKLGGQKALLVTDKGLVKL
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GMAGDIQANIEQAGLQVVLFDGAEPNPTDKNVEAGLKVYRENGCDLIVSLGGGSSHDCAK
AIGVVAANG--GSIRDYE----GLGKITKATPPKIAINTTAGTA----------------
---SEMTFFCVITNTDTHVKMPIAGSQVTPSV---------------------AINDPVL
MLGLPPALTAAT-----------------------------GMDALTHAVEAYVSV-IAT
PA---------TDACGLQAIELIAKWLRKAVA--------NGQDLEARE-----RMAFAE
YLAGMAFNNAS------VGHVHAMAHQLGGFYNLP--------HGVC---NAVLLPVVEQ
FNLIACPERFRDIAIA--------------MGEDVEGLSVMDA-AEKAIAAIRRLSADVG
IPDGLAELGVKEDD----IPVLAENASK-DI-------CTLTNPRITTINDIISLYKTAM
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>gi|161505791|ref|YP_001572903.1| putative alcohol dehydrogenase [Salmonella
enterica subsp. arizonae serovar 62:z4,z23:--]
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------------------------------------------------------------
--------------MAASTFFIPSVNVIG-ADSLKDAMNTMAEYGFRRTLIVTDAMLTKL
GMAGDIQKALQKRDIFSVIYDGTQPNPTTSNVAAGLKLLKENGCDSVISLGGGSPHDCAK
GIALVAANG--GDIRDYE----GVDRSAKPQLPMIAINTTAGTA----------------
---SEMTRFCIITDEERHIKMAIVDKHVTPLL---------------------SVNDSSL
MVGMPKSLTAAT-----------------------------GMDALTHAIEAYVSI-AAT
PI---------TDACALKAVTMIAENLIVAVE--------EGSNVQARE-----AMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYNLP--------HGVC---NAVLLPHVQV
FNSQVAAARLRDCAAA--------------MGVDVSGMNEAEG-AQACVAAIRQLSQKVN
IPAGLRELNVKEED----IPVLATNALK-DA-------CGLTNPIQATHDEIVEIYRAAM
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>gi|160874467|ref|YP_001553783.1| iron-containing alcohol dehydrogenase [Shewanella
baltica OS195]
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------------------------------------------------------------
---------------MAAKFFIPSVNVLG-QGAVDDAIGDIKTLGFKHALIVTDKPLVKI
GLVGEVAEKLGQNGITSTIYDGVQPNPTVTNVEAGLALLKANKCDFVISLGGGSPHDCAK
GIALVATNG--GSIKDYE----GLDQSAKPQLPLVAINTTAGTA----------------
---SEMTRFCIITDEARHIKMAIVDKHTTPLL---------------------SVNDPEL
MLKKPASLTAAT-----------------------------GMDALTHAVEAYVSI-AAN
PI---------TDACAIKAMELIQANLVNAVE--------NGQDINARE-----QMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NALLLPHVQE
YNAQVVPARLKDIAKA--------------MGVDVSNMTDEQG-ASAAIAAIKKLSVAVK
IPENLTLLGVKAED----IPTLADNALK-DA-------CGFTNPKQATHAEICQIFTNAL
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>gi|222053378|ref|YP_002535740.1| iron-containing alcohol dehydrogenase [Geobacter
sp. FRC-32]
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------------------------------------------------------------
------------------------------------------------------------
----------MALAEQTYGFFIPTVSLMG-IGCSKETGAQAKALGATNLLIVTDAGLSKM
GVADKIKAQLVEAGLKAVIFDGAEPNPTDKNVHDGVKVYLDSKCDGIVSLGGGSSHDCGK
GIGLVIGNG--GNIRDFE----GVNKSTKPMPPFLAINTTAGTA----------------
---SEMTRFCIITNTDTHVKMAIVDWRCTPNI---------------------AINDPVL
MVGKPPALTAAT-----------------------------GMDALTHAVEAYVST-IAT
PI---------TDACAIKAIELVAANLSVAVA--------NGDNLEARD-----AMAYAE
YLAGMAFNNAS------LGYVHSMAHQLGGFYNLP--------HGVC---NAILLPAVSQ
FNLIACPKRFADIAVA--------------LGENIAGLSVTEA-AEKAISAIRKLSASIG
IPAGLKELNVKEED----LKIMAENAKK-DA-------CQLTNPRKATLEQVIDIYKAAM
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>gi|77917873|ref|YP_355688.1| alcohol dehydrogenase, class IV [Pelobacter
carbinolicus DSM 2380]
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--------------MSIRKFVTPEI-IFG-QGALSQIGESAARSGASKVFVVTDQGLIDA
GWVDKALYYLRNAGLQYEIFSSITSNPKDLEVTEGVAHYLRSGCDALVAVGGGSPADTAK
AIATLATNG--GELQDYE----GVNKIRHPLPPMVIVPSTAGTG----------------
---SEVSQFAIIVDHQRRLKMSIISKSLIPDI---------------------AIIDPDL
LNTKSARLAAAT-----------------------------GMDALSHAIESYVSL-AAT
PL---------TDIHALNAIRLIFANLKQSVF--------DRQDAVANN-----NMAMAS
LNAGIAFSNAI------LGAGHAMTHQIDGLLDTH--------HGET---NATLLPHIMQ
FNLPVCRDKFNAIARQ--------------IDEAASQAGPKQDLAEKAIEAVSTLTKEIG
LHNRLASVGLKKEN----IKTLSQNALN-DA-------CLVTNPRDATAEDIEKLFLKAY
--------------------
>gi|218676223|ref|YP_002395042.1| Alcohol dehydrogenase II [Vibrio splendidus LGP32]
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------------------------------------------------------------
------------------------------------------------------------
---------------MSTAFYIPTINFMG-TGCLKDAADSIQSQGFKKGLIVTDKILNQI
GVVKQVQDLLSQRGVDAVVFDGTQPNPTITNVNDGLELLTDNDCDFVVSLGGGSPHDCAK
GIALVASNG--GKIADYE----GVDQSEKPMMPLIAINTTAGTA----------------
---SEMTRFCIITDEARHIKMAIVDKHTTPLI---------------------SVNDPEL
MLAKPASLTAAT-----------------------------GMDALTHAIEAYVSI-AAT
PI---------TDAVAIKAIELVQAHLRTAVA--------HGEDIEARE-----QMAYAQ
FMAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NAILLPHVQR
YNAQVCPDRLRDVAKA--------------MGVNVEGMTAEQG-AEAAINAIVQLANDVN
IPTGIAQLGAKLED----IPTLSDNALK-DA-------CGFTNPKQATHEEISAIFEAAM
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>gi|30064145|ref|NP_838316.1| L-1,2-propanediol oxidoreductase [Shigella flexneri 2a
str. 2457T]
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------------------------------------------------------------
---------------MANRMILNETAWFG-RGAVGALTDEVKRRGYQKALIVTDKTLVQC
GVVAKVTDKMDAAGLAWAIYDGVVPNPTITVVKEGLGVFQNSGADYLIAIGGGSPQDTCK
AIGIISNNPEFADVRSLE----GLSPTNKPSVPILAIPTTAGTA----------------
---AEVTINYVITDEEKRRKFVCVDPHDIPQV---------------------AFIDADM
MDGMPPALKAAT-----------------------------GVDALTHAIEGYITR-GAW
AL---------TDALHIKAIEIIAGALRGSVA----------GDKDAGE-----EMALGQ
YVAGMGFSNVG------LGLVHGMAHPLGAFYNTP--------HGVA---NAILLPHVMR
YNADFTGEKYRDIARV--------------MGVKVEGMSLEGA-RNAAVEAVFALNRDVG
IPPHLRDVGVRKED----ISALAQAALD-DV-------CTGGNPREATLEDIVELYHTAW
--------------------
>gi|152999844|ref|YP_001365525.1| iron-containing alcohol dehydrogenase [Shewanella
baltica OS185]
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------------------------------------------------------------
---------------MAAKFFIPSVNVLG-QGAVDDAIGDIKTLGFKHALIVTDKPLVKI
GLVGEVAEKLGQNGITSTIYDGVQPNPTVTNVEAGLALLKANNCDFVISLGGGSPHDCAK
GIALVATNG--GSIKDYE----GLDQSAKPQLPLVAINTTAGTA----------------
---SEMTRFCIITDEARHIKMAIVDKHTTPLL---------------------SVNDPEL
MLKKPASLTAAT-----------------------------GMDALTHAVEAYVSI-AAN
PI---------TDACAIKAMELIQANLVNAVE--------NGQDINARE-----QMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NALLLPHVQE
YNAQVVPARLKDIAKA--------------MGVDVSGMTDEQG-ASAAIAAIKKLSVAVK
IPENLTLLGVKAED----IPTLADNALK-DA-------CGFTNPKQATHAEICQIFTNAL
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>gi|148264466|ref|YP_001231172.1| iron-containing alcohol dehydrogenase [Geobacter
uraniireducens Rf4]
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----------MALGEQTYGFYIPTVSLMG-IGCSKETGAQAKALGATNLLIVTDAGLSKM
GVADKIKAQLEEAGLKAVIFDGAEPNPTDKNVHDGVKVYQDNKCDGIVSLGGGSSHDCGK
GVGLVIGNG--GHIRDFE----GVNKSAKPMPPFLAINTTAGTA----------------
---SEMTRFCIITNTDTHVKMAIVDWRVTPNI---------------------AINDPLL
MVGKPSALTAAT-----------------------------GMDALTHAVEAYVST-IAT
PI---------TDACAIKAIELIAQNLSTAVA--------NGENLEARD-----AMAYAE
YLAGMAFNNAS------LGYVHSMAHQLGGFYNLP--------HGVC---NAILLPAVSQ
FNIIACPKRFADIAAA--------------LGENITGLSVVEA-ADKAIAAIRRLSASIG
IPAGLKSLNVKEED----LKVMAENAKK-DA-------CQLTNPRKATLEQVIDIFKAAM
--------------------
>gi|197118368|ref|YP_002138795.1| iron-containing alcohol dehydrogenase [Geobacter
bemidjiensis Bem]
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------------------------------------------------------------
--------------MEISKFVAPEI-IFG-RGSLSQIGESVVRLGVSKVFMVSDDHVIAA
GWVDQAVEYLRAAGLETVIFSSLTTNPKDREVTEGTAKYLSSGCDGIVSVGGGSPTDVAK
AIAIIASNG--GKLQDYE----GVNKISLPLPPMVIVPSTAGAG----------------
---SEVSQFAIIVDTKRKLKMSIISRSLIPDI---------------------AIVDPEL
LKTKDAKLAAAT-----------------------------GVDALTHGIESYVSL-AAT
PL---------TDIHALKAIQLISKNLRRAVA--------VRSDMDANT-----NMAMAS
LTAGLAFSNAI------LGAAHAMTHQVDGLLDQH--------HGET---NASILPHVMR
FNLQACPERFRDIAVA--------------MGEDVTGLELMAA-AERSIDAVKALIAEIG
LDQGLSELGLREEF----IPLLSENATK-DA-------CLLTNPRSATREQIEEIYRNAM
--------------------
>gi|89901502|ref|YP_523973.1| iron-containing alcohol dehydrogenase [Rhodoferax
ferrireducens T118]
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------------------------------------------------------------
--------------MSQFSFETAPRIICE-QGGANRLGEIAKGMGISRLFLVTDAGLIKA
KLIDGALASLTAAGVAATVFSDVLADPPELSVQAAVDAARAAGADGVLGFGGGSSLDTAK
LVALLACTP--QALPDIY----GIGLARGPRLPLIQVPTTAGTG----------------
---SEVTPISILT-TPSHEKKGVVSPLLYPDV---------------------ALLDSRL
TLGLPPTVTAMT-----------------------------GVDAMVHAIESFSTRLKKN
PL---------SDALAIKALQLLYANLPAAVN--------DGKDPTVRE-----NMLLGS
LFAGMAFANAP------VGAVHALAYPLGGHYGLP--------HGLT---NSLVFVAVLR
FNLAAAQGLYAELGRA--------------ILPELAAAGDSEA-AASFVAAISARVAAMP
YAQSLRDAGVKQDD----LPMLARDAMNVQR-------LLVNNPRDVSFDDALAMYQAAY
--------------------
>gi|89901636|ref|YP_524107.1| iron-containing alcohol dehydrogenase [Rhodoferax
ferrireducens T118]
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------------------------------------------------------------
---------------MSTTFFIPAVNIMG-AGCLQEAILAIRGYGFHKALIVTDTVLNKL
GVAGQIQSLLTAQEIESVVFDGAKPNPTVGNVKAGLTQLKEHQCDFVISLGGGSPHDCAK
GIALCASNG--GEISDYE----GVDRSAKPQLPLVSINTTAGTA----------------
---AEMTRFCIITDEVRHIKMAIVDRNVTPLM---------------------SVNDPNL
MLAKPKGLTAAT-----------------------------GMDALTHAVEAYVST-AAT
PI---------TDACALKAVELISRNLRTAVA--------HGDNLQARE-----QMAYAQ
FLAGMAFNNAS------LGYVHAMSHQLGGFYDLP--------HGVC---NALLLPHVQA
FNAATSAERLRDVARA--------------MGVSVDGMDAAAG-AQACLSAIRKLSMDIG
IPASLSELGVKEKD----IPLLTENALK-DA-------CGLTNPRKASQAEIEAIFRGAM
HAPVAAGQAQHKATRESAPA
>gi|148264435|ref|YP_001231141.1| iron-containing alcohol dehydrogenase [Geobacter
uraniireducens Rf4]
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------------------------------------------------------------
--------------MNISKFVAPEI-IFG-RGSLSQLGESVVRIGASKVFLVSDDGVINA
GWVDQAVYYLRAAGVEAEIFSSLTTNPKDFEVTEGVIRYREARCDGIVAVGGGSPTDVAK
AVAMLAANG--GRLQDYE----GINKISRPLPPMVIAPSTAGAG----------------
---SEVSQFTIIVDTVRKLKMSIISKSLVPDI---------------------AIVDPEL
LKSKDAKLAAAT-----------------------------GIDALTHGIESYVSL-AAT
PL---------TDIHALKAIQLISYNLVRAVA--------DRLDMEANA-----NMAMAA
LTAGLAFSNAI------LGAAHAMTHQVDGLIDQH--------HGET---NASILPHVME
FNLHTCPDRFRDIAIA--------------MGKDVAGLDTLAA-AELSIEAVKRLIADIG
LDKGLAQIGLKEEF----IPLLSRNAMK-DA-------CLVTNPRSATCEEIEAIFRKAM
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>gi|206580795|ref|YP_002236838.1| lactaldehyde reductase [Klebsiella pneumoniae 342]
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------------------------------------------------------------
---------------MANRMILNETAWFG-RGAINALTDEVARRGYRKALIVTDSTLARC
GVAAKVTDKLDAAGLAWDMFSDVIPNPTIAVVQQGLQAFQRSGADYLIAIGGGSPQDTCK
AIGIIQRNPEFADVRSLE----GLSPTRQPSVPIFAVPTTAGTA----------------
---AEVTINYVITDEEQRRKFVCVDPHDIPQV---------------------AFIDADM
MDAMPPALKAAT-----------------------------GVDALTHAIEGYLTR-GAW
AL---------TDALHLKAIEIIAGALRGSVA----------GDAGAGE-----AMALGQ
YVAGMGFSNVG------LGLVHGMAHPLGAFYNTP--------HGVA---NAILLPHVMR
FNAEATGEKYRDIARS--------------MGVRVEALSLTAA-RQAAVEAVCQLNRDVG
IPGHLREVGVRKED----IPALAQAALE-DV-------CTGGNPREASLADIVGLYQAAW
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>gi|170682829|ref|YP_001744963.1| lactaldehyde reductase [Escherichia coli SMS-3-5]
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------------------------------------------------------------
--------------MMANRMILNETAWFG-RGAVGALTDEVKRRGYQKALIVTDKTLVQC
GVVAKVTDKMDAAGLAWAIYDGVVPNPTITVVKEGLGVFQNSGADYLIAIGGGSPQDTCK
AIGIISNNPEFADVRSLE----GLSPTNKPSVPILAIPTTAGTA----------------
---AEVTINYVITDEEKRRKFVCVDPHDIPQV---------------------AFIDADM
MDGMPPALKAAT-----------------------------GVDALTHAIEGYITR-GAW
AL---------TDALHIKAIEIIAGALRGSVA----------GDKDAGE-----EMALGQ
YVAGMGFSNVG------LGLVHGMAHPLGAFYNTP--------HGVA---NAILLPHVMR
YNADFTGEKYRDIARV--------------MGLKVEGMSLEEA-RNAAVEAVFALNRDVG
IPPHLRDVGVRKED----IPALAQAALD-DV-------CTGGNPREATLEDIVELYHTAW
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>gi|157159169|ref|YP_001464122.1| L-1,2-propanediol oxidoreductase [Escherichia coli
E24377A]
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------------------------------------------------------------
---------------MANRMILNETAWFG-RGAVGALTDEVKRRGYQKALIVTDKTLVQC
GVVAKVTDKMDAAGLAWAIYDGVVPNPTITVVKEGLGVFQNSGADYLIAIGGGSPQDTCK
AIGIISNNPEFADVRSLE----GLSPTNKPSVPILAIPTTAGTA----------------
---AEVTINYVITDEEKRRKFVCVDPHDIPQV---------------------AFIDADM
MDGMPPALKAAT-----------------------------GVDALTHAIEGYITR-GAW
AL---------TDALHIKAIEIIAGALRGSVA----------GDKDAGE-----EMALGQ
YVAGMGFSNVG------LGLVHGMAHPLGAFYNTP--------HGVA---NAILLPHVMR
YNADFTGEKYRDIARV--------------MGVKVEGMSLEEA-RNAAVEAVFALNRDVG
IPPHLRDVGVRKED----IPALAQAALD-DV-------CTGGNPREATLEDIVELYHTAW
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>gi|146295466|ref|YP_001179237.1| alcohol dehydrogenase [Caldicellulosiruptor
saccharolyticus DSM 8903]
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--------------MKTYRFYMPPISLMG-RGCLKDVGQEIKALGYKKALIVTDKSLVKI
GLVKKVTDMLDEANINYVIFDETKPNPTVKNVEDGLKMLKDNNCDFLISIGGGSPHDCAK
GIGLVATNG--GSIKDYE----GVNKSQKPILPLVAINTTAGTG----------------
---SEVTRFAIITDEDRHVKMAIVDWHVTPLI---------------------AVNDPEL
MIEMPKSLTAAT-----------------------------GMDALTHAIEAYLST-DAT
PV---------TDASALMAIELIFKYLKKAVE--------NGNDIEARE-----KMAYAE
YLAGVAFNNAG------LGYVHAMAHQLGGFYDLP--------HGVC---NAVLLPHVLA
YNFKAVPHRFIDIAKA--------------LGIDVQGASQEKV-GEMVIEGIKDLSTGIG
IPAGLKELGAKDED----IRTLAENALK-DA-------CGLTNPRQATVEEIMEIYKAAF
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>gi|170018955|ref|YP_001723909.1| L-1,2-propanediol oxidoreductase [Escherichia coli
ATCC 8739]
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------------------------------------------------------------
------------------------------------------------------------
--------------MMANRMILNETAWFG-RGAVGALTDEVKRRGYQKALIVTDKTLVQC
GVVAKVTHKMDAAGLAWAIYDGVVPNPTITVVKEGLGVFQNSGADYLIAIGGGSPQDTCK
AIGIISNNPEFADVRSLE----GLSPTNKPSVPILAIPTTAGTA----------------
---AEVTINYVITDEEKRRKFVCVDPHDIPQV---------------------AFIDADM
MDGMPPALKAAT-----------------------------GVDALTHAIEGYITR-GAW
AL---------TDALHIKAIEIIAGALRGSVA----------GDKDAGE-----EMALGQ
YVAGMGFSNVG------LGLVHGMAHPLGAFYNTP--------HGVA---NAILLPHVMR
YNADFTGEKYRDIARV--------------MGVKVEGMSLEEA-RNAAVEAVFALNRDVG
IPPHLRDVGVRKED----IPALAQAALN-DV-------CTGGNPREATLEDIVELYHTAW
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>gi|108757039|ref|YP_633768.1| alcohol dehydrogenase, iron-containing [Myxococcus
xanthus DK 1622]
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------------------------------------------------------------
-----MKPFDIPSEPRVTEMAWPTRIVFG-AGALLRLPAQAQRLGIQRPLLVTDAGVVKA
GLAARVADVLNTAGLACEVFDRVEPNPTERDVFAGLEAYRSHSCDGIVALGGGSALDAGK
LIQLLTTHE--PPLSRYDDAKGGDQYVRDDLPPLIAIPTTAGTG----------------
---SEVGRSGVVTLEDTGRKTVIFSPYLLPRA---------------------AICDPEL
TLGLPPGITAAT-----------------------------GMDAFTHCLEAYLAN-GFH
PL---------ADAVAIDGIYRVGRSLETAVR--------DGKDLAART-----DMMVAA
MEGAMAFQK-G------LGACHALAHALTPVSNVH--------HGLA---NAIVLPVVME
FNRAVCTARLARVAVA--------------LGDTTQAREEVL--AGNAIDRVRKLNAAVG
IPSRLRDAGVQEKD----LERIAEKAFQ-DA-------SHLSNPRKVSQADLLALAREAY
--------------------
>gi|74313371|ref|YP_311790.1| L-1,2-propanediol oxidoreductase [Shigella sonnei
Ss046]
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------------------------------------------------------------
--------------MMANRMILNETAWFG-RGAVGALTDEVKRRGYQKALIVTDKTLVQC
GVVAKVTDKMDAAGLAWAIYDGVVPNPTITVVKEGLGVFQNSGADYLIAIGGGSPQDTCK
AIGIISNNPEFADVRSLE----GLSPTNKPSVPILAIPTTAGTA----------------
---AEVTINYVITDEEKRRKFVCVDPHDIPQV---------------------AFIDADM
MDGMPPALKAAT-----------------------------GVDALTHAIEGYITR-GAW
AL---------TDALHIKAIEIIAGALRGSVA----------GDKDAGE-----EMALGQ
YVAGMGFSNVG------LGLVHGMAHPLGAFYNTP--------HGVA---NAILLPHVMH
YNADFTGEKYRDIARV--------------MGVKVEGMSLEEA-RNAAVEAVFALNRDVG
IPPHLRDVGVRKED----IPALAQAALD-DV-------CTGGNPREATLEDIVELYHTAW
--------------------
>gi|77461342|ref|YP_350849.1| Iron-containing alcohol dehydrogenase [Pseudomonas
fluorescens Pf0-1]
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------------------------------------------------------------
--------------MSLSSFKIAHKLITG-AGAIEQLAAELTRLDIDNPLIVTDAALVKS
GTVELALAQIGER--EYEIFDRVLPDPEIAIVEDCMRVYREGGHDGLIGLGGGSAIDIAK
SVAAYAGYH--GALEDLF----GVDQVPRKGPPLIAIPTTAGTG----------------
---SEVTNVAILSDKVAQLKKGIVSDYLLPDV---------------------ALVSPQM
TLTCPRSVTAAS-----------------------------GVDALVHAIESYLSL-NAS
PI---------TDSLAIGAIKLIARSLPKAYA--------NPSNLQARE-----DMATAS
LMAGMAFGNAG------VGAVHALAYPLGGRFNIA--------HGVS---NALLLPYVMT
WNKMACVERMQDIAEA--------------MGVKTAHLSLNEA-ADSAVAAMTELCAAVE
IPLGLRSFGVPEEA----IPAMAVEAAGIER-------LMRNNPRKLSAADIEKIYRAAY
--------------------
>gi|118580417|ref|YP_901667.1| iron-containing alcohol dehydrogenase [Pelobacter
propionicus DSM 2379]
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
----------MALAEQVYNFYIPAITKMG-IGAVKELGPCAQFLKGTKALLVTDKGMADL
GVADRMKQLLEVDGVQCVIFSGAEPNPTDLNVRAGIKVYRENNCDMLVSLGGGSSHDCAK
GIGIVATND--GDIRDFA----GVDTFKNALPPFIAINTTAGTA----------------
---SEMTSFAVITNSDIHVKMIFASPRITATI---------------------AINDPAL
MVGLPAPLTAST-----------------------------GMDALTHAVEAYVAA-LAN
PV---------TDACIAAAIKLIAEYLPQAVA--------NGSNLEARD-----KMAYAE
YLAGMAFSNAG------IGIVHAMAHQPGALLNKP--------HGVC---NAILLPHGCS
FNLIACPQRYADIAQA--------------MGVDTTGLMPMEA-AERGVEAIRKLSAAVG
IPAGLSEIGVKTSD----IPTLAENAIK-DI-------CCLFNPRTIKLDDLTRLYTEAM
--------------------
>gi|89893311|ref|YP_516798.1| hypothetical protein DSY0565 [Desulfitobacterium
hafniense Y51]
------------------------------------------------------------
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------------------------------------------------------------
----------MSVVHQVYGYYMPTVNLMG-AGAAQEAGKQAKILGGKTALLVTDAFLNQS
GLAKQIAEIIEAEGVKVVIYPGAEPNPTDKNVHDGVAVFEKENCNMIVSLGGGSAHDCAK
GVGLVAGNG--GNIRDFE----GVDKSAKPMVPMIAVNTTAGTA----------------
---SEMTRFCIITDTDRHIKMAIVDWHATPNV---------------------SINDPLL
MIGKPAPLTAAT-----------------------------GMDALTHAVEAYVST-AAT
PI---------TDSAALMAIKLISKYLRRAVA--------NGQDFEARD-----QMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYNLP--------HGVC---NAILLPRVSR
FNLIGNLERFVDIAEA--------------LGEEIKNLSARDA-AEKALTAMTTLSQDIS
IPSGLTELGVKEED----LQTMAVNAMK-DA-------CSLTNPRLAKLEDIIQIYKNSL
--------------------
>gi|15803321|ref|NP_289354.1| L-1,2-propanediol oxidoreductase [Escherichia coli
O157:H7 EDL933]
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------------------------------------------------------------
--------------MMANRMILNETAWFG-RGAVGALTDEVKRRGYQKALIVTDKTLVQC
GVVAKVTDKMDAAGLAWAIYDGVVPNPTITVVKEGLGVFQNSGADYLIAIGGGSPQDTCK
AIGIISNNPEFADVRSLE----GLSPTNKPSVPILAIPTTAGTA----------------
---AEVTINYVITDEEKRRKFVCVDPHDIPQV---------------------AFIDADM
MDGMPPALKAAT-----------------------------GVDALTHAIEGYITR-GAW
AL---------TDALHIKAIEIIAGALRGSVA----------GDKDAGE-----EMALGQ
YVAGMGFSNVG------LGLVHGMAHPLGAFYNTP--------HGVA---NAILLPHVMR
YNADFTGEKYRDIARV--------------MGVKVEGMSLEEA-RNAAVEAVFALNRDVG
IPPHLRDVGVRKED----IPALAQAALD-DV-------CTGGNPREATLEDIVELYHTAW
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>gi|82778178|ref|YP_404527.1| L-1,2-propanediol oxidoreductase [Shigella dysenteriae
Sd197]
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------------------------------------------------------------
--------------MMANRMILNETAWFG-RGAVGALTDEVKRRGYQKALIVTDKTLVQC
GVVAKVTDKMDAAGLAWAIYDGVVPNPTITVVKEGLGVFQNSGADYLIAIGGGSPQDTCK
AIGIISNNPEFADVRSLE----GLSPTNKPSVPILAIPTTAGTA----------------
---AEVTINYVLTDEEKRRKFVCVDPHDIPQV---------------------AFIDADM
MDGMPPALKAAT-----------------------------GVDALTHAIEGYITR-GAW
AL---------TDALHIKAIEIIAGALRGSVA----------GDKDAGE-----EMALGQ
YVAGMGFSNVG------LGLVHGMAHPLGAFYNTP--------HGVA---NAILLPHVMR
YNADFTGEKYRDIARV--------------MGVKVEGMSLEEA-RNAAVEAVFALNRDVG
IPPHLRDVGVRKED----IPALAQAALD-DV-------CTGGNPREATLEDIVELYRTAW
--------------------
>gi|66047214|ref|YP_237055.1| Iron-containing alcohol dehydrogenase [Pseudomonas 
syringae pv. syringae B728a]
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------------------------------------------------------------
---------------MISTFFIPAVNIIG-TGCIDEAMLAIRKYGFRKALIVTDAGLARA
GVASQVAGLLVEQGIDSVVYDGARPNPTIANVENGLALLQERQCDFVISLGGGSPHDCAK
GIALCASNG--GHISDYE----GVDRSAKPQLPLIAINTTAGTA----------------
---SEMTRFCIITDEARHVKMAIIDRNVTPLL---------------------SVNDPDM
MVAMPRSLTAAT-----------------------------GMDALTHAIEAYVST-AAN
PI---------TDACALQAMALIANNLRDAFN--------NGANITARE-----NMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NAVLLPHVQR
FNASVSAARLTDVAHA--------------MGSNIRGLSPEEG-AQAAIDAIRALSAAVE
IPAGLATLGVKEED----FPMLASNALK-DA-------CGLTNPRPADLEQIQDIFRQAL
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>gi|218701516|ref|YP_002409145.1| L-1,2-propanediol oxidoreductase [Escherichia coli 
IAI39]
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------------------------------------------------------------
--------------MMANRMILNETAWFG-RAAVGALTDEVKRRGYQKALIVTDKTLVQC
GVVAKVTDKMDAAGLAWAIYDGVVPNPTITVVKEGLDVFQNSGADYLIAIGGGSPQDTCK
AIGIISNNPEFADVRSLE----GLSPTNKPSVPILAIPTTAGTA----------------
---AEVTINYVITDEEKRRKFVCVDPHDIPQV---------------------AFIDADM
MDGMPPALKAAT-----------------------------GVDALTHAIEGYITR-GAW
AL---------TDALHIKAIEIIAGALRGSVA----------GDKDAGE-----EMALGQ
YVAGMGFSNVG------LGLVHGMAHPLGAFYNTP--------HGVA---NAILLPHVMR
YNADFTGEKYRDIARV--------------MGVKVEGMSLEEA-RNAAVEAVFALNRDVG
IPPHLRDVGVRKED----IPALAQAALD-DV-------CTGGNPREATLEDIVELYHTAW
--------------------
>gi|113866887|ref|YP_725376.1| alcohol dehydrogenase, class IV [Ralstonia eutropha 
H16]
------------------------------------------------------------
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------------------------------------------------------------
MRARPARAPKRKAQERPSSSRMPACTRWGYPKPSRGTSAR--------------------
------------QGFRPLIFPGAEPNPTDVNVHDGVKLFEQEGCDFIVSLGGGSSHDCAK
GIGLVTAGG--GHIRDYE----GIDKSTVPMTPLISINTTAGTA----------------
---AEMTRFCIITNSSNHVKMAIVDWRCTPLI---------------------AIDDPRL
MVAMPPALTAAT-----------------------------GMDALTHAVEAYVST-AAT
PI---------TDACAEKAIALIGEWLPKAVA--------NGNSLEARA-----AMCYAQ
YLAGMAFNNAS------LGYVHAMAHQLGGLYNLP--------HGVC---NAILLPHVSE
FNLIAAPERFAKIAEL--------------LGENVASLSTSDA-AKAAISAIRALAASIG
IPAGLASLGVKAED----HEVMAHNAQK-DA-------CMLTNPRRATTAQVIAIFAAAM
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>gi|77917867|ref|YP_355682.1| alcohol dehydrogenase, class IV [Pelobacter 
carbinolicus DSM 2380]
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-------MPIVNLAETTYGFFIPSVTLMG-PGCAKEVGPKANELGAKKALLVTDAGLMKM
GVADTIAGYIKDAGVEVTIYPGAEPNPTDKNVHDGVKVYEDEGCDFIVSLGGGSSHDCAK
GIGLVTAGG--GNIRDYE----GVNKSTVPMTPLIAINTTAGTA----------------
---SEMTRFCIITNLETHVKMAIVDWRCTPLI---------------------AVDDPVL
MLGKPPALTAAT-----------------------------GMDALTHAVEAYVST-IAT
PI---------TDACAEKAIRLIAEWLRPAVA--------MGANIEARD-----AMCYAQ
YLAGMAFNNAS------LGYVHAMAHQLGGFYNLP--------HGVC---NAILLPSVCD
YNMIACPDRFADIADF--------------MGVDTTGMPVTEA-AAAGIEAIRELSASIG
IPAGLTELNVKEED----LKTMAENAQK-DA-------CMLTNPRTATLDQVIDIYKAAM
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>gi|218690922|ref|YP_002399134.1| L-1,2-propanediol oxidoreductase [Escherichia coli
ED1a]
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
--------------MMANRMILNETAWFG-RGAVGSLTDEVKRRGYQKALIVTDKTLVQC
GVVAKVIDKMDAAGLAWAIYDGVVPNPTITVVKEGLDVFQNSGADYLIAIGGGSPQDTCK
AIGIISNNPEFADVRSLE----GLSPTNKPSVPILAIPTTAGTA----------------
---AEVTINYVITDEEKRRKFVCVDPHDIPQV---------------------AFIDADM
MDGMPPALKAAT-----------------------------GVDALTHAIEGYITR-GAW
AL---------TDALHIKAIEIIAGALRGSVA----------GDKDAGE-----EMALGQ
YVAGMGFSNVG------LGLVHGMAHPLGAFYNTP--------HGVA---NAILLPHVMR
YNADFTGEKYHDIARV--------------MGVKVEGMSLEEA-RNAAVEAVFALNRDVG
IPPHLRDVGVRKED----IPALAQAALD-DV-------CTGGNPREATLEDIVELYHTAW
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>gi|157162253|ref|YP_001459571.1| L-1,2-propanediol oxidoreductase [Escherichia coli
HS]
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------------------------------------------------------------
---------------MANRMILNETAWFG-RGAVGALTDEVKRRGYQKALIVTDKTLVQC
GVVAKVTDKMDAAGLAWAIYDGVVPNPTITVVKEGLGVFQNSGADYLIAIGGGSPQDTCK
AIGIISNNPEFADVRSLE----GLSPTNKPSVPILAIPTTAGTA----------------
---AEVTINYVITDEEKRRKFVCVDPHDIPQV---------------------AFIDADM
MDGMPPALKAAT-----------------------------GVDALTHAIEGYITR-GAW
AL---------TDALHIKAIEIIAGALRGSVA----------GDKDAGE-----EMALGQ
YVAGMGFSNVG------LGLVHGMAHPLGAFYNTP--------HGVA---NAILLPHVMR
YNADFTGEKYRDIARV--------------MGVKVEGMSLEEA-RNAAVEAVFVLNRDVG
IPPHLRDVGVRKED----IPALAQAALN-DV-------CTGGNPREATLEDIVELYHTAW
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>gi|77920438|ref|YP_358253.1| alcohol dehydrogenase, class IV [Pelobacter
carbinolicus DSM 2380]
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------------------------------------------------------------
---------MGAMAEQVYGFFMPTTSLLG-NGAVKEIGNQAKVLGGTKALIVTDIGLVKL
GMVDTLKGYLEQAGLQVAVFDGVEPNPTDVNVRDCLKVWQDNSCDLLVTFGGGSSHDCGK
GMAIMATSG--GDIRDWA----GIDTLQANLPPYISINTTAGTA----------------
---SEMTRFAVVTNTDTHVKMVFCDARLTADV---------------------AINDPAL
MVGLPPALTAAT-----------------------------GMDALTHAIEAYVTTLLSN
PI---------TDAVALQAISLIGKWLRKAVA--------NGADMEARD-----AMAYAE
YLAGMAFNSAG------LGIVHSMAHQPGSLLGKP--------HGVC---NAICLPVVCE
FNLMANAEKYAKVAEG--------------LGEDISGLSVMEA-AEKAVAAIRRLSKDVG
IPSGLAEIGVTEKD----IPIMAENALN-DM-------CTLFNPRNVKVEDIIELYKKAL
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>gi|28871422|ref|NP_794041.1| alcohol dehydrogenase II [Pseudomonas syringae pv.
tomato str. DC3000]
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------------------------------------------------------------
---------------MSSTFFIPAVNIIG-AGCIDEAMLAIRKYGFLKALIVTDAGLAKA
GVASQVAGLLVEQGIDSVVYDGARPNPTIANVENGLALLRKRQCDFVISLGGGSPHDCAK
GIALCASNG--GHISDYE----GVDRSAKPQLPLIAINTTAGTA----------------
---SEMTRFCIITDEARHVKMAIIDRNVTPLL---------------------SVNDPNM
MVAMPKSLTAAT-----------------------------GMDALTHAIEAYVST-AAT
PI---------TDACALQAMSLIANNLREAVS--------NGTNITARE-----NMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NAVLLPHVQR
FNASVSAARLTDVAHA--------------MGASVRGLSPEEG-AHAAIEAIRALSAAVE
IPAGLTALGVKEED----FPVLAANALK-DA-------CGFTNPRPADLEQIQELFRQAL
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>gi|26249204|ref|NP_755244.1| L-1,2-propanediol oxidoreductase [Escherichia coli
CFT073]
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------------------------------------------------------------
--------------MMANRMILNETAWFG-RGAVGSLTDEVKRRGYQKALIVTDKTLVQC
GVVAKVIDKMDAAGLAWAIYDGVVPNPTITVVKEGLDVFQNSGADYLIAIGGGSPQDTCK
AIGIISNNPEFADVRSLE----GLSPTNKPSVPILAIPTTAGTA----------------
---AEVTINYVITDEEKRRKFVCVDPHDIPQV---------------------AFIDADM
MDGMPPALKAAT-----------------------------GVDALTHAIEGYITR-GAW
AL---------TDALHIKAIEIIAGALRGSVA----------GDKDAGE-----EMALGQ
YVAGMGFSNVG------LGLVHGMAHPLGAFYNTP--------HGVA---NAILLPHVMR
YNADFTGEKYRDIARV--------------MGVKVEGMSLEEA-RNAAVEAVFALNRDVG
IPPHLRDVGVRKED----IPALAQAALD-DV-------CTGGNPREATLEDIVELYHTAW
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>gi|219855464|ref|YP_002472586.1| hypothetical protein CKR_2121 [Clostridium
kluyveri NBRC 12016]
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------------------------------------------------------------
--------MSRGVFMNYSMFQCPRDIIYG-EDAVDLTGAKSLKLGKRVLIVTGKHSSKKT
GALDRVSDSLKKSGLEYVIFDKVESDPSVNTVRLGVETAKEKNIDVIVALGGGSALDAAK
AISMVSTNG--GDILDYE-----KKAPEIEGIPIVALPTTAGTG----------------
---SEVTKYSIITDTERKIKMLIGNDFLIPKV---------------------AILDPNL
TKMMPPSVTAAT-----------------------------GMDAFTHAVEAYISK-AAQ
PM---------CDVYAVKAIELITSNLIKAVL--------KEDDMEARS-----NMLLGQ
MYAGLAFSNAS------VALVHAMSRPLGAYYKVP--------HGLA---NALLLPEVMR
FNRAACSEKFKFIAKT--------------MGENIEGKSTREA-SYLAIESIKNLFSETG
LPKSLKEVGVDKDN----FDKMAKDAVE-NK-------STTLNPRKPTLGQLIEIYETIY
--------------------
>gi|215488116|ref|YP_002330547.1| L-1,2-propanediol oxidoreductase [Escherichia coli
O127:H6 str. E2348/69]
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------------------------------------------------------------
--------------MMANRMILNETAWFG-RGAVGALTDEVKRRGYQKALIVTDKTLVQC
GVVAKVTDKMDAAGLAWAIYDGVVPNPTITVVKEGLGVFQNSGADYLIAIGGGSPQDTCK
AIGIISNNPEFADVRSLE----GLSPTNKPSVPILAIPTTAGTA----------------
---AEVTINYVITDEEKRRKFVCVDPHDIPQV---------------------AFIDADM
MDGMPPALKAAT-----------------------------GVDALTHAIEGYITR-GAW
AL---------TDALHIKAIEIIAGALRGSVA----------GDKDAGE-----EMALGQ
YVAGMGFSNVG------LGLVHGMAHPLGAFYNTP--------HGVA---NAILLPHVMR
YNADFTGEKYRDIARV--------------MGVKVEGMSLEEA-RNAAVEAVFALNRDVG
IPPHLRDVGVRKED----IPTLAQAALD-DV-------CTGGNPREATLEDIVELYHTAW
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>gi|153955023|ref|YP_001395788.1| DhaT1 [Clostridium kluyveri DSM 555]
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------------------------------------------------------------
--------------MNYSMFQCPRDIIYG-EDAVDLTGAKSLKLGKRVLIVTGKHSSKKT
GALDRVSDSLKKSGLEYVIFDKVESDPSVNTVRLGVETAKEKNIDVIVALGGGSALDAAK
AISMVSTNG--GDILDYE-----KKAPEIEGIPIVALPTTAGTG----------------
---SEVTKYSIITDTERKIKMLIGNDFLIPKV---------------------AILDPNL
TKMMPPSVTAAT-----------------------------GMDAFTHAVEAYISK-AAQ
PM---------CDVYAVKAIELITSNLIKAVL--------KEDDMEARS-----NMLLGQ
MYAGLAFSNAS------VALVHAMSRPLGAYYKVP--------HGLA---NALLLPEVMR
FNRAACSEKFKFIAKT--------------MGENIEGKSTREA-SYLAIESIKNLFSETG
LPKSLKEVGVDKDN----FDKMAKDAVE-NK-------STTLNPRKPTLGQLIEIYETIY
--------------------
>gi|91212167|ref|YP_542153.1| L-1,2-propanediol oxidoreductase [Escherichia coli
UTI89]
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------------------------------------------------------------
--------------MMANRMILNETAWFG-RGAVGALTDEVKRRGYQKALIVTDKTLVQC
GVVAKVIDKMDAAGLAWAIYDGVVPNPTITVVKEGLDVFQNSGADYLIAIGGGSPQDTCK
AIGIISNNPEFADVRSLE----GLSPTNKPSVPILAIPTTAGTA----------------
---AEVTINYVITDEEKRRKFVCVDPHDIPQV---------------------AFIDADM
MDGMPPALKAAT-----------------------------GVDALTHAIEGYITR-GAW
AL---------TDALHIKAIEIIAGALRGTVA----------GDKDAGE-----EMALGQ
YVAGMGFSNVG------LGLVHGMAHPLGAFYNTP--------HGVA---NAILLPHVMR
YNADFTGEKYRDIARV--------------MGVKVEGMSLEEA-RNAAVEAVFALNRDVG
IPPHLRDVGVRKED----IPALAQAALD-DV-------CTGGNPREATLEDIVELYHTAW
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>gi|77919193|ref|YP_357008.1| alcohol dehydrogenase, class IV [Pelobacter
carbinolicus DSM 2380]
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------------------------------------------------------------
-------MAVVNLAETTYGFFIPSVTLMG-PGCAKEVGPKANELGAKKALLVTDAGLMKM
GVADTIAGYIKDAGVEVVIYPGAEPNPTDKNVHDGVKVYEDEGCDFIVSLGGGSSHDCAK
GIGLVTAGG--GNIRDYE----GVNKSTVPMTPLIAINTTAGTA----------------
---SEMTRFCIITNLETHVKMAIVDWRCTPLI---------------------AVDDPVL
MLGKPPALTAAT-----------------------------GMDALTHAVEAYVST-IAT
PI---------TDACAEKAIRLIAEWLRPAVA--------LGANIAARD-----AMCYAQ
YLAGMAFNNAS------LGYVHAMAHQLGGFYNLP--------HGVC---NAILLPAVCD
YNMIACPDRFADIADF--------------MGVPTEGLSVTEA-AAAGIEAIRELSASIG
IPAGLTELNVKEED----LKTMAENAQK-DA-------CMLTNPRTATLDQVIDIYKAAM
--------------------
>gi|118578993|ref|YP_900243.1| iron-containing alcohol dehydrogenase [Pelobacter
propionicus DSM 2379]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----------MALADQTFGFFIPSVTLLG-LGCSKEAGEQAKALGATKLLIVTDAGLAKM
GVADTIKGYVEAAGLQAAIYPGAEPNPTDKNVHDGVKAYQDNKCDGIISLGGGSSHDCGK
GIGLVIAGG--GNIRDYE----GVNKSTKVMPPFLAINTTAGTA----------------
---SEMTRFCIITNTDTHVKMAIVDWRVTPNI---------------------AIDDPLM
MVGMPPKLTAAT-----------------------------GMDALTHAVEAYVSI-IAN
PI---------TDACAIKAIELIAKNLSPAVA--------NGEDLVARD-----AMAYAE
YLAGMAFNNAS------LGYVHSMAHQLGGFYNLP--------HGVC---NAILLPVVSQ
FNLIACPQRFADIAVA--------------LGECIDGLSVTEA-GQKAIDRIKSLSASIG
IPANLTELGVKEAD----LKIMSENAKK-DA-------CQLTNPRKATLDEVISIFKAAL
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>gi|110806740|ref|YP_690260.1| L-1,2-propanediol oxidoreductase [Shigella flexneri 5
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str. 8401]
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------------------------------------------------------------
---------------MANRMILNETAWFG-RGAVGALTDEVKRRGYQKALIVTDKTLVQC
GVVAKVTDKMDAAGLAWAIYDGVVPNPTITVVKEGLGVFQNSGADYLIAIGGGSPQDTCK
AIGIISNNPEFADVRSLE----GLSPTNKPSVPILAIPTTAGTA----------------
---AEVTINYVITDEEKRRKFVCVDPHDIPQV---------------------AFIDADM
MDGMPPALKAAT-----------------------------GVDALTHAIEGDITR-GAW
AL---------TDALHIKAIEIIAGALRGSVA----------GDKDAGE-----EMALGQ
YVAGMGFSNVG------LGLVHGMAHPLGAFYNTP--------HGVA---NAILLPHVMR
YNADFTGEKYRDIARV--------------MGVKVEGMSLEGA-RNAAVEAVFALNRDVG
IPPHLRDVGVRKED----ISALAQAALD-DV-------CTGGNPREATLEDIVELYHTAW
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>gi|71735079|ref|YP_276126.1| alcohol dehydrogenase II [Pseudomonas syringae pv.
phaseolicola 1448A]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------MISTFFIPAVNIIG-TGCIDEAMLAIRKYGFLKALIVTDAGLAKA
GVASQVAGLLVEQGIDSVVYDGAKPNPTIANVENGLALLRERQCDFVISLGGGSPHDCAK
GIALCASNG--GHISDYE----GVDRSAKPQLPLIAINTTAGTA----------------
---SEMTRFCIITDEARHVKMAIIDRNVTPLL---------------------SVNDPNM
MIAMPKSLTAAT-----------------------------GMDALTHAIEAYVST-AAN
PI---------TDACALQAMALIANNLRDAFT--------NGANITARE-----NMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NAVLLPHVQR
FNASVSAARLTDVAHA--------------MGCNIRGLSPQEG-AQAAIEAIRALSAAVE
IPAGLAVLGVKEED----FPILATNALK-DA-------CGLTNPRRADLEQIQEIFRQAM
--------------------
>gi|110642940|ref|YP_670670.1| L-1,2-propanediol oxidoreductase [Escherichia coli
536]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------MMANRMILNETAWFG-RGAVGSLTDEVKRRGYQKALIVTDKTLVQC
GVVAKVIDKMDAAGLAWAIYDGVVPNPTITVVKEGLDVFQNSGADYLIAIGGGSPQDTCK
AIGIISNNPEFADVRSLE----GLSPTNKPSVPILAIPTTAGTA----------------
---AEVTINYVITDEEKRRKFVCVDPHDIPQV---------------------AFIDADM
MDGMPPALKAAT-----------------------------GVDALTHAIEGYITR-GAW
AL---------TDALHIKAIEIIAGALRGSVV----------GDKDAGE-----EMALGQ
YVAGMGFSNVG------LGLVHGMAHPLGAFYNTP--------HGVA---NAILLPHVMR
YNADFTGEKYRDIARV--------------MGVKVEGMSLEEA-RNAAVEAVFALNRDVG
IPPHLRDVGVRKED----IPALAQAALD-DV-------CTGGNPREATLEDIVELYHTAW
--------------------
>gi|24373064|ref|NP_717107.1| alcohol dehydrogenase II [Shewanella oneidensis MR-1]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------MAAKFFIPSVNVLG-KGAVDDAIGDIKTLGFKRALIVTDKPLVNI
GLVGEVAEKLGQNGITSTVFDGVQPNPTVGNVEAGLALLKANQCDFVISLGGGSPHDCAK
GIALVATNG--GSIKDYE----GLDKSTKPQLPLVAINTTAGTA----------------
---SEMTRFCIITDEARHIKMAIVDKHTTPIL---------------------SVNDPEL
MLKKPASLTAAT-----------------------------GMDALTHAVEAYVSI-AAN
PI---------TDACAIKAIELIQGNLVNAVK--------QGQDIEARE-----QMAYAQ
FLAGMAFNNAS------LGYVHAMAHQLGGFYDLP--------HGVC---NALLLPHVQE
YNAKVVPHRLKDIAKA--------------MGVDVAKMTDEQG-AAAAITAIKTLSVAVN
IPENLTLLGVKAED----IPTLADNALK-DA-------CGFTNPKQATHAEICQIFTNAL
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%%  Pfl2 [targeting tail implicated]

>gi++|150018873|ref|YP_001311127.1| pyruvate formate-lyase [Clostridium beijerinckii
NCIMB 8052]
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------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MIS
KGFSKPTERVE-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------RMI-VD-AIPY-VESERAVLV
TESYKET-EGLSPI-------LR----RAKAVEKIFNNLPITIRED-ELVVGAITKN-PR
STEICPEFS--YDWVAKEFDT---MGARVAD--P--------------------------
---FQIPKETAAELS--EAFKYW-----DGKTTSALADSY---MSQ--------------
-EAKDCM----------------ANGVFTVGN--YFYGGV--------------------
------GHICVDYGKIL--RKGFKGIIAEVIEAMSKMDK-------KDPDYI---KKQQF
YNAVVISYSAAINFAHRYAQKARDMAAAE-LNPTRKAELLQIAANCERVPENGATNFYEA
CQSFWFIQIMVQIESNGHS--ISPGRFDQYMYPYLKED------KNISKEF-----AQEL
VDCIWIKLND-INKT-RDEISAQAFAGYAVFQNLC---VGGQ-NE-EGL--DATNEISYM
CMDATAHV-KLPAPSFSIRVW-QGTPDEFLLRACEVAR-LGLGVPAMYN-DEVIIPALVN
--------R------G---VTLRDARNYCII-GCVE------------------PQCPNK
-TEG-W----HDAAFFNV--AKVLEITLNNGK------VGNKQL----------GP-ITG
DIT--TFKSIDDFYAAFKKQMEYFVYYLVEADNCVDYAHAERAPL--PFLSAMVDDCIGR
GKSVQE----GGAIY-----NFTGPQ-AFGIADTGDSVYAIQKHVFEDKTI-EMDQLK--
----------AALDANFG--------HTGVNTVSTSNNNADVTEMQIYEAVKRILSNSGS
IDISEIQSRISSEFTSPKTTVSGDFDNIRR------------------------------
------------LLES--TPCFGNDIDEVDMVARKCAQIYCFEV-EKY--TNP--R----
--GGQFQAGVYPVSA-NVLFGKDVAALPDGRLAKTPLAD-GVSPRAGKDCAGPTAAANS-
-VAKLDH-FVASN-------------GTLYNQKFLPSAVAGDTG--LQNFASVIRSYFD-
----HKGMHVQFNVIDKQLLLDAQKHPENYKDLVVRVAGYSAQFTVLAKEVQDDIINRTE
HSL------------
>gi++|83592239|ref|YP_425991.1| pyruvate formate-lyase [Rhodospirillum rubrum ATCC
11170]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MIE
KGFSKPTDRVM-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------NEI-LN-AKPY-VESERAVLV
TEAYKET-EGL-PAI------LR----RAKAAEKIFNNLPVTIRND-ELIVGAITKN-PR
STEICPEFS--YDWVEKEFDT---MATRLAD--P--------------------------
---FLIPKETAKELH--DAFLYW-----PGKTTSDLASSY---MSQ--------------
-EAKDCI----------------ASGVFTVGN--YFYGGV--------------------
------GHVCVDYGKVL--KIGFRGIITEVVQAMEKMDR-------MDPDYI---KKQQF
YNAVIIAYTAAINFAHRYAAKALELAQNE-ANPTRKAELLQIAQNCARVPENGATTFYEA
CQSFWFVQCLLQIESSGHS--ISPGRFDQYMYPFLCAD------KSIDKGF-----AQEL
VDCIWIKLND-VNKT-RDEVSAQAFAGYAVFQNLC---VGGQ-TE-GGL--DATNEISYM
CMEATAHV-RLPAPSFSIRVW-QGTPDDFLHRACEVVR-LGLGVPAMYN-DEVIVPALQN
--------R------G---VTLHDARNYGIV-GCVE------------------PQCIHK
-TEG-W----HDAAFFNV--AKVLEITLNNGK-----AGGK-QL----------GP-VTG
EFT--SFRNMDDLYAAFQKQMAYFVHYLVEADNCVDLAHGERCPL--PFVSALVDDCIGR
GKSLQE----GGAIY-----NFTGPQ-AFGVADTGDSVYAIQKNVFEDKKI-TLAEMK--
----------EALDANFG------LPVGGSAPSAGGDFTEEQVFAAVRKVLSSNGSMDVS
ALKGEVYRTLSGQAAPAAGGSSTKYDAIRR------------------------------
------------LLDA--SPAFGNDIDDVDMVARECALIYCREV-EKY--TNP--R----
--GGQFQAGIYPVSA-NVLFGKDVAALPDGRLAKAPLAD-GVSPRPGQDVKGPTAAANS-
-VAKLDH-FIASN-------------GTLYNQKFLPSALAGDAG--LQNFASLVRSYFD-
```

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----HKGMHVQFNVIDRQTLLDAQLEPEKHNDLVVRVAGYSAQFVVLAKEVQDDIISRTE
QTL------------
>gi++|90422675|ref|YP_531045.1| pyruvate formate-lyase [Rhodopseudomonas palustris BisB18]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MIE
KGFSKPTERVM-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------NVI-LN-AKPF-VESERAVLV
TDAYKET-EGL-PAI------LR----RAKAAEKIFNNLPVTIRAD-ELIVGAITKR-PR
STEICPEFS--FDWVEKEFET---MATRVAD--P--------------------------
---FQIPKETAAELH--EAFKYW-----PGKTTSDLASSY---MSQ--------------
-EAKDCI----------------AAGVFTVGN--YFYGGV--------------------
------GHVCVDYGKVL--KIGFRGIITEVVLAMEKLDR-------MDPGYI---KKQQF
YNAVIISYTAAINFAHRYAVKAEELAQTE-SNATRKAELLQIAKNCARVPEYGASNFYEA
CQSFWFLQALLQIESSGHS--ISPGRFDQYMYPFLAAD------KSISREF-----AQEL
IDCIWIKLND-VNKT-RDGGSAQAFAGYAVFQNLC---VGGQ-TE-EGL--DATNDVSFM
CMEATAHV-ALPAPSFSIRVW-QGTPDDFLYRACEVVR-LGLGVPAMYN-DEVIVPSLQN
--------R------G---VSLRDARDYGIV-GCVE------------------PQAIHK
-TEG-W----HDAAFFNV--AKVLEITLNNGR------VGDKQV----------GP-ASG
ELL--SFRCIDDVFAAFQKQIEYFVRYLVEADNCVDLAHGERCPL--PFVSALVEDCIGR
GKSLQE----GGALY-----NFTGPQ-AFGVADTGDSVYAIQKNVFEDKKI-TLGELK--
----------AALDANFGRPVGES---AHADAGTNYTEEQVF------------------
-------------------------AAVKKVLNSSGSTDVSALKGKVYSALAGANGAKSG
GASSSYDALHRLLEA---TPAFGNDIHEVDMVARRCAQIYCLEV-EKY--TNP--R----
--GGQFQAGIYPVSA-NVLFGKDVAALPDGRFAKAPLAD-GVSPRQGKDVNGPTAAANS-
-VAKLDH-FIASN-------------GTLYNQKFLPAALAGDSG--LQNFASLVRSYFD-
----HKGMHVQFNVVDRQTLLDAQREPEKHNDLVVRVAGYSAQFVVLAKEVQDDIISRTE
QTL------------
>gi++|26250357|ref|NP_756397.1| hypothetical protein c4537 [Escherichia coli CFT073]
------------------------------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MLE
KGFSNPTDRVV-------------------------------------------------
------------------------------------------------------------
---------------------------RLR---------NMI-LT-AKPY-VESERAVLA
TEAYKET-EQL-PAI------MR----RAKVVEKIFNQLPVTIRPD-ELIVGAVTIN-PR
STEICPEFS--YDWVEKEFET---MEHRIAD--P--------------------------
---FVIPKKTAQELH--EAFKYW-----PGKTTSALAASY---MSE--------------
-GTKESM----------------ASGVFTVGN--YFFGGV--------------------
------GHVSVDYGKVL--KIGFRGIINEVSRALESLDR-------TEPGYI---KKEQF
YNAVLISYNAAIRFAHRYAEEASRLAQQE-SNPTRKRELEQIAQNCTRVPEYGATTFWEA
CQTFWFIQSMLQIESSGHS--ISPGRFDQYMYPYLESD------KSISREF-----AQEL
VDCCWIKLND-INKT-RDEVSAQAFAGYAVFQNLC---CGGQ-TE-DGR--DATNDLSYM
CMEATAHV-RLPQPSFSIRVW-QGTPDEFLYRACELVR-MGLGVPAMYN-DEVIIPALQN
--------R------G---ISLRDARDYCII-GCVE------------------PQAPHR
-TEG-W----HDAAFFNV--AKVLEITLNNGR------VGNKQL----------GP-VTG
ELT--QFTSMEDFYTAFQKQMAHFVHQLVEACNSVDIAHGERCPL--PFLSALVDDCIGR
GKSLQE----GGAIY-----NFTGPQ-AFGVADTGDSVYAIQKQVFEDRKL-SLSELK--
----------SALDANFG--YPVGANPHTPAAKSSLNEQDIY------------------
-------------------------DVVKRIIEQHGALDPAAIKNEVYRQLTSGSAAPVQ
SGTMSRHEEIRRILEN--TPCFGNDIDDVDLVARKCALIYCQEV-EKY--TNP--R----
--GGQFQAGIYPVSA-NVLFGKDVAALPDGRLAKEPLAD-GVSPRQGKDTLGPTAAANS-
-VAKLDH-FIASN-------------GTLYNQKFLPSSLAGENG--LRNFSGLIRHYFD-
----KKGMHVQFNVIDRNTLIEAQKNPEQHQDLVVRVAGYSAQWVVLAKEVQDDIISRTE
QQLS-----------
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>gi++|28211126|ref|NP_782070.1| formate acetyltransferase 2 [Clostridium tetani E88]
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EIPDGMTERLI-------------------------------------------------
------------------------------------------------------------
---------------------------KLK---------ENY-MK-QVPS-ITTHRARAI
TKIAKEN-PGV-PKS------VL----RGKCFKYCCETAPLVIQDN-ELIVGAPNGK-PR
AGAFSPDIA--WRWMEDEIDT---IANRPQD--P--------------------------
---FYISEEDKKIMR-EELFPYW-----KGKSVDEYCEDQ---YRE--------------
-AGVWEL--------------SGESFVSDCSY--HAVNGG--------------------
------GDSNPGYDVILM-KKGMLDIKREAEEKLASLSY-------ERPEDI---EKIYF
YKSIIDTAEGVMIYAKRMSDYAAELAAKE-TDPKRKAELQKISKVNARVPAHKPSTFWEA
IQAVWTIESLLVVEENQTG--MSIGRVDQYMYPFYKSDIE-S--GRMTDFE-----AFEL
AGCMLIKMSE-MMWI-TSEGGSKFFAGYQPFVNMC---VGGV-TR-EGR--DATNELTYL
LMDAVRHV-KIYQPSLACRIH-KGSPQKYLKKIVDVIR-AGMGFPACHF-DDVHIKMMLA
--------K------G---VSIEDARDYCLM-GCVE------------------PQKSGR
-LYQ-W----TSTGYTQW--PICIELVLNHGV---PLWYGK-QV----------CP-DMG
DLS--QFKTYEQFEGAVREQIKYITKWTAVATTISQRVHRELAPK--PLMSMMYEGCMEK
GRGVEA----GGAMY-----NFGPGVVWSGLATYTDSMAAIKKLVFEEKKY-TLEELS--
----------EALKADFV---------------------G-Y------------------
-------------------------ERLRK------------------------------
------------DCLE--APKYGNDDDYADYIAADLVNFTEQEH-RKY--KTL-------
--YSVLSHGTLSISN-NTPFGQMTGATANGRRAWMPLSD-GISPSQGSDFKGPTSIIKS-
-VSKISC-EDMNI-------------GMVHNFKLMSGLLDTPEG--EQGIIALLRSACA-
----LQLGEIQFNYLDNETLIEAQKHPEQYRDLIVRVAGYSAFFVELCKDVQDEIISRTM
LTHF-----------
>gi++|150391563|ref|YP_001321612.1| formate C-acetyltransferase [Alkaliphilus
metalliredigens QYMF]
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---------MNIREFSIKFVEATKNMSEEERNALKKIFQGITQEIPKEDTDISLYRENHQ
GIPTGITERLK-------------------------------------------------
------------------------------------------------------------
---------------------------TLK---------DNY-LK-WKPS-ISIHRARAI
TKIAKEN-PGM-PKI------LL----RAKSFRYCCETAPLVIQDH-ELIVGAPCGA-PR
AGAFSPDIS--WRWLEEELDT---IANRSQD--P--------------------------
---FYISEEDKKELV-EEIFPYW-----KGKSVDEHSEDQ---FRE--------------
-AGVWEI--------------SGESFVSDCSY--HALNGG--------------------
------GDSNPGYDVILM-KKGMLDIQEEAKEKLNELSY-------ENPEDI---EKIYF
YKSVIQTTEGVMVYARRLSEYAMELAQKE-SNPNRKAELMKIAEVNKRVPAHKPNNFWEA
IQSVWTVESLLVVEENQTG--MSIGRVDQYMHPFFEQDLK-N--GNLSEYE-----AFEL
AGSMLIKMSE-MMWL-TSEGSSKFFAGYQPFINMC---VGGV-TR-EGL--DATNDLTYL
LMDAVRHV-KIYQPSLATRIH-SKSPKKYLRKIVDVVR-SGMGFPACHF-DDVHIKMMLA
--------K------G---VSIEDARDYCLM-GCVE------------------PQKSGR
-LYQ-W----TSTAYTQW--PICIELALNKGI---PLWYGK-KV----------CP-DTG
DVD--GFASYEDFEKAVKEQINYITKLSSIATVITQRVHRELAPK--PLMSIMYEGCMEK
GKDVSS----GGAMY-----NFGPGVVWSGLATYVDSMAAIKKLVFDEKKY-TFKQLN--
----------EALNKDFE---------------------G-H------------------
-------------------------EELRN------------------------------
------------DCLK--APKYGNDDDYADLIAVDLVNYTENEH-RKY--KTL-------
--YSVLSHGTLSISN-NTPFGQLTGASANGRKAWAPLSD-GISPTQGADFKGPTATIKS-
-VSKMAC-DNMNI-------------GMVHNFKLMSGLLDTPEG--EEGIVTLLRTASM-
----LGVGEMQFNYLDNETLIKAQKNPEQYRDLIVRVAGYSAFFVELCKDVQDEIISRTM
LTKI-----------
>gi++|188587680|ref|YP_001920768.1| formate C-acetyltransferase [Clostridium
botulinum E3 str. Alaska E43]
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------------------------------------------------------------
--------MDIREFSNKFVEATQNMSAEERECLMKIFEGVSKEITKEEPVLEHVVCTEGD
KIPDGITQRLL-------------------------------------------------
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---------------------------KLK---------ENY-LK-QVPS-ITTYRARAI
TKIAKEN-PGM-PKI------LL----RAKCFKYCCETAPLVIQDN-ELIVGAPCGA-PR
AGAFSPDIA--WRWMVDEIDT---IGTRAQD--P--------------------------
---FYISEEDKKIMR-EELFPYW-----AGKSVDEYCENQ---YRE--------------
-AGVWEL--------------SGESFVSDCSY--HAINGG--------------------
------GDSNPGYDVILM-KKGMLDIQLEAKEHLEKLDY-------ENPEHI---EKIYF
YKAIIDTTEGVMIYAKRLSKYAAELAEKE-TNPKRKLELQKISEINARVPAHKPSTFWEA
IQAVWTIESLLVVEENQTG--MSIGRVDQYMYEYYKNDIE-S--GRMNDFE-----AFEL
SGCMLIKMSE-MMWI-TSEGGSKFFAGYQPFVNMC---VGGV-DR-QGR--DATNELTYL
LMDAVRHV-KIYQPSLACRIH-NQSPQKYLKKIVDVIR-AGMGFPACHF-DDVHIKMMLA
--------K------G---VSIEDARDYCLM-GCVE------------------PQKSGR
-LYQ-W----TSTAYTQW--PICIELVLNNGI---PLWYEK-QV----------CP-NMG
DIN--SFKNYEEFESAVKEQIKYITKWTSVATVISQRVHKELAPK--PLMSIMYEGCMDN
GRGVEA----GGAMY-----NFGPGVIWSGLATYTDSMAAIKKLVFEEKKY-TLQELN--
----------EALKADFV---------------------G-Y------------------
-------------------------EKLRK------------------------------
------------DCLE--APKYGNDDDYADYIAADLINFTELEH-RKF--KTL-------
--YSVLSHGTLSISN-NTPFGQLTGATANGRRAWMPLSD-GISPSQGSDYKGPTAIIKS-
-VSKMSC-DSMNI-------------GMVHNFKLISGLLDTKEG--EDGIITLLRSACV-
----LGLGEVQFNYLDNDTLIEAQKHPEQYRDLIVRVAGYSAFFVELCKDVQDEIISRTM
LTHF-----------
>gi++|187932408|ref|YP_001885647.1| formate C-acetyltransferase [Clostridium
botulinum B str. Eklund 17B]
------------------------------------------------------------
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--------MDIREFSNKFVEATQNMSAEERECLMKIFEGVSKEITKEEPVLEHVVCTEGD
KIPDGITQRLL-------------------------------------------------
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---------------------------KLK---------ENY-LK-QVPS-ITTYRARAI
TKIAKEN-PGM-PKI------LL----RAKCFKYCCETAPLVIQDN-ELIVGAPCGA-PR
AGAFSPDIA--WRWMVDEIDT---IGTRAQD--P--------------------------
---FYISEEDKKIMR-EELFPYW-----AGKSVDEYCENQ---YRE--------------
-AGVWEL--------------SGESFVSDCSY--HAINGG--------------------
------GDSNPGYDVILM-KKGMLDIQLEAKEHLEKLDY-------ENPEHI---EKIYF
YKAIIDTTEGVMIYAKRLSKYAAELAEKE-TNPKRKSELQKISEINARVPAHKPSTFWEA
IQAVWTIESLLVVEENQTG--MSIGRVDQYMYEYYKNDIE-S--GRMNDFE-----AFEL
SGCMLIKMSE-MMWI-TSEGGSKFFAGYQPFVNMC---VGGV-DR-QGR--DATNELTYL
LMDAVRHV-KIYQPSLACRIH-NQSPQKYLKKIVDVIR-AGMGFPACHF-DDVHIKMMLA
--------K------G---VSIEDARDYCLM-GCVE------------------PQKSGR
-LYQ-W----TSTAYTQW--PICIELVLNNGI---PLWYEK-QV----------CP-NMG
DIN--SFKNYEEFESAVKEQIKYITKWTSVATVISQRVHKELAPK--PLMSIMYEGCMDN
GRGVEA----GGAMY-----NFGPGVIWSGLATYTDSMAAIKKLVFEEKKY-TLQELN--
----------EALKADFV---------------------G-Y------------------
-------------------------EKLRK------------------------------
------------DCLE--APKYGNDDDYADYIAADLINFTELEH-RKF--KTL-------
--YSVLSHGTLSISN-NTPFGQLTGATANGRRAWMPLSD-GISPSQGSDYKGPTAIIKS-
-VSKMSC-DSMNI-------------GMVHNFKLISGLLDTKEG--EDGIITLLRSACV-
----LGLGEVQFNYLDNDTLIEAQKHPEQYRDLIVRVAGYSAFFVELCKDVQDEIISRTM
LTHF-----------
>gi++|160879563|ref|YP_001558531.1| formate C-acetyltransferase [Clostridium
phytofermentans ISDg]
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------MDIREFSNKFVEATKNMSPEERSSLMKMFETVSDEINKKETAPSTSNVCNEEGS
NIPDGITPRLH-------------------------------------------------
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---------------------------KLK---------ENY-LT-HKPT-ITTYRARAI
TKIAKEN-PGM-PKI------ML----RAKCFRYCCETAPLVIQDN-ELIVGAPCGA-PR
AGAFSPDIA--WRWMVDEIDT---IGTRPQD--P--------------------------
---FYISEEDKKIMK-EELFPFW-----AGKSVDEYCEDQ---YRE--------------
-AGVWEL--------------SGESFVSDCSY--HAINGG--------------------
------GDSNPGYDVILM-KKGMLDIQQEAKDHLKELDY-------ENPDDI---EKIYF
YKSIIDTTEGVMIYAKRLSEYAAELAAKE-TNPKRKEELLKISEVNAYVPAHKPRTFWEA
IQAVWTIESLLVVEENQTG--MSIGRVDQYMYPFYKDDIE-S--GRMNDYQ-----AFEL
AGCMLIKMSE-MMWI-TSEGGSKFFAGYQPFVNMC---VGGV-TR-SGR--DATNDLTYL
LMDAVRHV-KIYQPSLACRIH-NKSPKEYLKKIVDVVR-SGMGFPACHF-DDAHIKMMLA
--------K------G---VSIEDARDYCLM-GCVE------------------PQKSGR
-LYQ-W----TSTAYTQW--PICIELVLNNGV---PLWYGK-QV----------CP-DMG
ALS--NFKTYEEFEAAVKEQIKYITKWSDVATVISQRIHRDLAPK--PLMSIMYEGCMES
AKDVSA----GGAMY-----NFGPGVVWSGLATYSDSMAAIKKLVFDEKKY-TLEQLN--
----------EALKADFA---------------------G-Y------------------
-------------------------DQIRT------------------------------
------------DCLN--APKYGNDDDYADLIAADLVDFTEHEH-RKY--KTL-------
--YSILCHGTLSISN-NTPFGQLTGASANGRHAWLPLSD-GISPTQGADFNGPTAIIKS-
-ISKMAN-DSMNL-------------GMVHNFKIMSGLLDTPEG--EESLITLLRTACM-
----FGNGEMQFNYLDNNTLIDAQKHPEKYRDLIVRVAGYSAFFIELCKDVQDEIISRTM
LTHF-----------
>gi++|158321419|ref|YP_001513926.1| formate C-acetyltransferase [Alkaliphilus
oremlandii OhILAs]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
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-----MILDIRDFSNKLTEATKNLSVEERMSLMKIFEGISNEITKKDGTCAPAYRSEEGT
GVPNGITERLS-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------ETY-LK-WQPT-ITTHRARAI
TKIAKEN-PGM-PKV------LL----RAKSFRYCCETAPLLIQED-ELIVGAPCGQ-PR
AGAFSPDIA--WRWMEDEIDT---IGNRPQD--P--------------------------
---FYISEEDKRYMR-EELFPFW-----KGKSVDEYCEDQ---YRD--------------
-AGVWEI--------------SGESFVSDCSY--HALNGG--------------------
------GDSNPGYDVILM-KKGMIDIQKEAQEHLEKLSY-------DNPDDI---EKIYY
YKAVIETTEGVMIYARRLADHAADLAAKE-TNPKRKAELQRISEINRRVPANKPSTFWEA
IQAVWTIESLLVVEENQTG--MSIGRVDQYMYPFYKADIE-S--GRMTEFE-----AFEL
AGAMLIKMSE-MMWV-TSEGGSKFFAGYQPFVNMC---VGGV-TR-EGL--DATNDLTYL
LMDAVRHV-KIYQPSLATRIH-SKSPKKYLKKIVDVVR-SGMGFPACHF-DDVHIKMMLA
--------K------G---VSIEDARDYCLM-GCVE------------------PQKSGR
-LYQ-W----TSTAYTQW--PIAIELVLNNGV---PLWYGK-QV----------TP-NMG
DIN--QYKTYEQFEAAVKEQIQYITKLSNIATVISQRVHRDLAPK--PLMSIMYEGCMES
GKDVSA----GGAMY-----NFGPGVVWSGLATYVDSMAAIKKLVFDDKKY-TLQQLN--
----------EALKADFV---------------------G-Y------------------
-------------------------DQVKS------------------------------
------------DCLK--APKYGNDDDYVDLIAADLVNFTEKEH-RKY--RTL-------
--HSIMCHGTLSISN-NTPFGQLTGATANGRGAWTPLSD-GISPTQGADFKGPTAIIKS-
-VSKMAC-DNMNL-------------GMVHNFKLIAGLLDTPEG--EEGIITLLRTANN-
----IGIGEMQFNYLDNNTLLEAQKHPEKYRDLIVRVAGYSAFFVELCKDVQDEIISRTM
LTHF-----------
>gi++|170760633|ref|YP_001787508.1| formate acetyltransferase [Clostridium botulinum
A3 str. Loch Maree]
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------------------------------------------------------------
--------MDIREFSNKFMEATKNMSDEERAGLMKMFQSVSNEITKEEPATLKVACDNNG
EIPDGMTERLV-------------------------------------------------
------------------------------------------------------------
---------------------------KLK---------ETY-LK-HVPT-ITTHRARAI
TKIAKEN-PGT-PKS------VL----RGKCFKHCCETAPLVIQDN-ELIVGAPNGQ-PR
AGAFSPDIA--WRWMVDEIDT---IGTRPQD--P--------------------------
---FYISEEDKKIMR-EELFPYW-----AGKSVDEYCEDQ---YRE--------------
-AGVWEL--------------SGESFVSDCSY--HAVNGG--------------------
------GDSNPGYDVVLM-KKGMLDIKREAEEKLAELKY-------ENPEDI---DKIYF
YKSLIDTAEGVMIYAKRMSDYAAELAQKE-TNPKRKAELQKISEINARVPAHKPSTYWEA
IQAVWTIESLLVVEENQTG--MSIGRVDQYMYPFYKADIE-A--GRMTDYE-----AFEL
SGCMLIKMSE-MMWI-TSEGGSKFFAGYQPFVNMC---VGGV-TR-EGR--DATNELTYL
LMDAVRHV-KIYQPSLACRIH-KSSPQKYLKKIVDVIR-AGMGFPACHF-DDVHIKIMLA
--------K------G---VSIEDARDYCLM-GCVE------------------PQKSGR
-LYQ-W----TSTGYTQW--PICIELVLNNGV---PLWYGK-QV----------CP-DMG
DLS--QFKTYEQFEAAVKEQIKFITKWTSVATVISQRVHKELAPK--PLMSMMYEGCMEN
GRGVEA----GGAMY-----NFGPGVVWSGLATYADSMAAIKKLVFEEKKY-TLQEMN--
----------EALKADFV---------------------G-Y------------------
-------------------------EQLRK------------------------------
------------DCLE--APKYGNDDDYADLITADLINFTEQEH-RKY--KTL-------
--YSVLSHGTLSISN-NTPFGQMTGATANGRRAWMPLSD-GISPSQGADFKGPTSIIKS-
-VSKMSC-EDMNI-------------GMVHNFKLIAGLLDTKEG--EQGIITLLRSACA-
----LQLGEVQFNYLDNKTLIEAQKHPDQYRDLIVRVAGYSAFFVELCKDVQDEIISRTM
LTHF-----------
>gi++|148380073|ref|YP_001254614.1| formate acetyltransferase [Clostridium botulinum
A str. ATCC 3502]
------------------------------------------------------------
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------------------------------------------------------------
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EIPDGMTERLV-------------------------------------------------
------------------------------------------------------------
---------------------------KLK---------ETY-LK-HVPT-ITTHRARAI
TKIAKEN-PGT-PKS------VL----RGKCFKHCCETAPLVIQDN-ELIVGAPNGQ-PR
AGAFSPDIA--WRWMVDEIDT---IGTRPQD--P--------------------------
---FYISEEDKKIMR-EELFPYW-----AGKSVDEYCEDQ---YRE--------------
-AGVWEL--------------SGESFVSDCSY--HAVNGG--------------------
------GDSNPGYDVVLM-KKGMLDIKREAEEKLAELKY-------ENPEDI---DKIYF
YKSLIDTAEGVMIYAKRMSDYAAELAQKE-TNPKRKAELQKISEINARVPAHKPSTYWEA
IQAVWTIESLLVVEENQTG--MSIGRVDQYMYPFYKADIE-A--GRMTDYE-----AFEL
SGCMLIKMSE-MMWI-TSEGGSKFFAGYQPFVNMC---VGGV-TR-EGR--DATNELTYL
LMDAVRHV-KIYQPSLACRIH-KSSPQKYLKKIVDVIR-AGMGFPACHF-DDVHIKIMLA
--------K------G---VSIEDARDYCLM-GCVE------------------PQKSGR
-LYQ-W----TSTGYTQW--PICIELVLNNGV---PLWYGK-QV----------CP-DMG
DLS--QFKTYEQFEAAVKEQIKFITKWTSVATVISQRVHKELAPK--PLMSMMYEGCMEN
GRGVEA----GGAMY-----NFGPGVVWSGLATYADSMAAIKKLVFEDKKY-TLQEMN--
----------EALKADFV---------------------G-Y------------------
-------------------------EQLRK------------------------------
------------DCLE--APKYGNDDDYADLIAADLINFTEQEH-RKY--KTL-------
--YSVLSHGTLSISN-NTPFGQMTGATANGRRAWMPLSD-GISPSQGADFKGPTSIIKS-
-VSKMSC-EDMNI-------------GMVHNFKLIAGLLDTPEG--EQGIITLLRSACA-
----LQLGEVQFNYLDNKTLIEAQKHPDQYRDLIVRVAGYSAFFVELCKDVQDEIISRTM
LTHF-----------
>gi++|170757740|ref|YP_001781665.1| formate acetyltransferase [Clostridium botulinum
B1 str. Okra]
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------------------------------------------------------------
--------MDIREFSNKFMEATKNMSDEERAGLMKMFQSVSNEITKEEPATSKVACDNNG
EIPDGMTERLV-------------------------------------------------
------------------------------------------------------------
---------------------------KLK---------ETY-LK-HVPT-ITTHRARAI
TKIAKEN-PGT-PKS------VL----RGKCFKHCCETAPLVIQDN-ELIVGAPNGQ-PR
AGAFSPDIA--WRWMVDEIDT---IGTRPQD--P--------------------------
---FYISEEDKKIMR-EELFPYW-----AGKSVDEYCEDQ---YRE--------------
-AGVWEL--------------SGESFVSDCSY--HAVNGG--------------------
------GDSNPGYDVVLM-KKGMLDIKREAEEKLAELKY-------ENPEDI---DKIYF
YKSLIDTAEGVMIYAKRMSDYAAELAQKE-TNPKRKAELQKISEINARVPAHKPSTYWEA
IQAVWTIESLLVVEENQTG--MSIGRVDQYMYPFYKADIE-A--GRMTDYE-----AFEL
SGCMLIKMSE-MMWI-TSEGGSKFFAGYQPFVNMC---VGGV-TR-EGR--DATNELTYL
LMDAVRHV-KIYQPSLACRIH-KSSPQKYLKKIVDVIR-AGMGFPACHF-DDVHIKIMLA
--------K------G---VSIEDARDYCLM-GCVE------------------PQKSGR
-LYQ-W----TSTGYTQW--PICIELVLNNGA---PLWYGK-QV----------CP-DMG
DLS--QFKTYEQFEAAVKEQIKFITKWTSVATVISQRVHKELAPK--PLMSMMYEGCMEN
GRGVEA----GGAMY-----NFGPGVVWSGLATYADSMAAIKKLVFEDKKY-TLQEMN--
----------EALKADFV---------------------G-Y------------------
-------------------------EQLRK------------------------------
------------DCLE--APKYGNDDDYADLIAADLINFTEQEH-RKY--KTL-------
--YSVLSHGTLSISN-NTPFGQMTGATANGRRAWMPLSD-GISPSQGADFKGPTSIIKS-
-VSKMSC-EDMNI-------------GMVHNFKLISGLLDTPEG--EQGIITLLRSACA-
----LQLGEVQFNYLDNKTLIEAQKHPEQYRDLIVRVAGYSAFFVELCKDVQDEIISRTM
LTHF-----------
>gi++|51245675|ref|YP_065559.1| pyruvate formate-lyase 2 [Desulfotalea psychrophila
LSv54]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------MDLQSFSEKLIVATKNLNAAERASLKKIFDGDSTEIAEDKNVPSAHLSVDPC
AIPNGPTDRHI-------------------------------------------------
------------------------------------------------------------
---------------------------KLK---------KKF-LT-HVPT-ITTHRARAI
TKIAQEN-PGL-PKA------IL----RGKSFKYCCETAPLVIQDN-ELIVGSPCGA-PR
AGAFSPDIA--WRWVKDELDT---IGTRPQD--P--------------------------
---FFISEEDKKIMR-EELFPFW-----EGRSIDEYCEQQ---YRE--------------
-AGMWEL--------------SGESYVTDCSY--HATNGG--------------------
------GDSNPGYDVILM-KKGMLDIVRESQEKLAELDY-------ENPDDM---DKIYF
YKSLIDTAEGVMIYAKRLSDYAAQLAASE-KDPQRKAELEKISAVNARVPAHKPETYWEA
IQAVWTVESLLIVEENQTG--MSIGRVDQYMYPFYKADIE-A--GRMTEYE-----AFDL
SGCLLVKCSE-MMWI-TSEDASKFFAGYQPFVNMC---LGGV-TR-EGL--DATNDLTYL
LMDAVRHV-KVYQPSVSTRVH-NQSPQKYLKKIVDVIR-AGMGFPAIHF-DDAHIKIMLA
--------K------G---CSIEDSRDYCLM-GCVE------------------PQKSGR
-LYQ-W----TSTAYTQW--PICIEMALNHGV---PLWYGK-QV----------CP-DLG
ALE--SFDTYEKFDAAVKEQIKYVTKWTSVGTVISQRIHRDLAPK--PLMSMMYEGCMES
GKDVSA----GGAMY-----NFGPGVVWSGLATHADSMAAIKKLVFDDKKY-SLTQLN--
----------EALKAEFK---------------------G-Y------------------
-------------------------DQLKA------------------------------
------------DCLA--APKFGNDDDYADLIVNDLVNFTEREH-RKF--KTL-------
--YSVLSHGTLSISN-NTPFGQLLGASANGRDAWMPLSD-GISPTQGADFKGPTAIIKS-
-VSKMPT-DSMNI-------------GMVHNFKLMSGLLDTPEG--ENGIITLIRTASM-
----MGNGEMQFNYLDNDTLLDAQLHPEKYRDLVVRVAGYSAFFVELCKDVQDEIISRTM
LTEI-----------
>gi++|89893162|ref|YP_516649.1| pyruvate-formate lyase [Desulfitobacterium hafniense
Y51]
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------------------------------------------------------------
-----------------------------------------MSTCCLSPHEERIIDPQKG
KVNYEGRERVF-------------------------------------------------
------------------------------------------------------------
---------------------------KIL---------ESF-QD-LRPK-IDVERAKYF
TESFKAT-EGQ-PLQ------PR----WAKALMHIAQNITVYIDDQ-QLIVGRAGAQ-GR
YGIVFPELD--GDFLGLAIEQ---LPQRVES--P--------------------------
---FNIDPDDAQIII-NDVAPYW-----KGKTFHEELAKA---LPE--------------
-DTLKVT---------YDPADPLASRFIVNET--ASFRSS--------------------
------IQWVHDYEKVL--KRGFKGIKEEAQAKLDQLDPL------SPADNM---EKRPF
LEAVIITCDAIVVWANRHAHLAAQMAKLE-KDPQRKQELSDIAERCAWVPEHPARNFREA
VQSQWFVQMFSRIEQKTGTI-ISNGRMDQYFYPYYQKDVA-E--GILTPQQ-----AIEL
LECMWVGMAQ-FIDLYLSPTGGAFNEGYAHWEAVT---VGGQ-TP-DGV--DATNELTYL
FLESKQKF-PLNYPDLAARIH-SRSPERYLYEVAETVK-EGTGFPKLIN-DEEVVPLLLS
--------K------G---AKFAEALDYAVS-GCAE------------------CRMPNR
DTYT------SGNPYINF--AAAIEMTLYNGR---MLKYGDEQL----------GL-ETG
DPT--QFETWDEFWKAYLAQQTNFLKHAFIQQHIIIRLRAQHFAS--PLGSLMHDLCMEN
CLDLHQPVIKGGI-------DLGYFE-LIGYGTVVDSLAAIKKLVYEEKKL-TMAELL--
----------EAVRNNFE---------------------G-H------------------
-------------------------EVIRE------------------------------
------------MVMH--TPKYGNNDPYSDVIAKEVDRTAVEFT-KKYS-REL-------
--GVHLDLRLVPFTS-HVPFGKVVSATPNGRKAWMPLAD-GSSASHGADVNGPTAVLLSN
FFSKNYG-YRNRA-------------ARLLNIKLSPSCVAGEEG--SEKLVSFIRTWCD-
----LKLWHIQFNIVNRETLLAAKQDPDKYRGLIVRVAGYSAYFVDLSSDLQDDIIARTE
HEML-----------
>gi++|220904625|ref|YP_002479937.1| Formate C-acetyltransferase [Desulfovibrio
desulfuricans subsp. desulfuricans str. ATCC 27774]
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------------------------------------------------------------
------MDLHDFSSKIAEVTKNLSPEEREQLRKIFATVTLPAQSAPSAAAQPSPAAHSGP
GVPEGPTQRHV-------------------------------------------------
------------------------------------------------------------
---------------------------LLK---------ENY-LK-QVPR-ITIHRARTI
TKIDKEN-PGM-PRI------LL----RATAFRHCCESAPLIIQDH-ELIVGAPNGA-PR
AGAFSPEIS--WRWLRDELDT---IDSRAQD--P--------------------------
---FHLAEEDKKILC-EEIFPYW-----AGKSVDEYCEAQ---YRE--------------
-AGLWEL--------------SGESYVSDCSY--HALNGG--------------------
------GDSNPGYDVILM-KKGMLDIQREAREHLEQLSY-------DRPEDI---DKIYF
YKSVIETTEGVMIYARRMSEYAAQLAARE-NDPRRKAELLKIAEVNARVPAHAPTTFWEA
IQAVWTVESLLVVEENQTG--MSIGRVDQYMYPFYKADIE-A--GRMTPYE-----AFDL
AGCMLIKMSE-MMWL-TSEGSSKFFAGYQPFVNMC---VGGV-SR-EGR--DATNDLTYL
LMDAVRHV-RIYQPSLATRVH-NTSPQEYLKKIVSVIR-SGMGFPAVHF-DDTHIKMMLA
--------K------G---VDIEDARDYCLM-GCVE------------------PQKSGR
-LYQ-W----TSTAYTQW--PICIELVLNRGV---PLWYGK-QV----------CP-DLG
DLS--QFDTFEKFDAAVKEQIRYITKWSSVATVISQRVHRDLAPK--PLMSIMYEGCMEK
GRDVAA----GGAMY-----NFGPGVIWSGLATYADSMAAIKKLVYDDRKY-TLQQLN--
----------EALKANFE---------------------G-Y------------------
-------------------------DAILA------------------------------
------------DCLA--APKYGNDDDYADDIAADLIAFTEREH-RKY--RTL-------
--YSILSHGTLSISN-NTPFGQLLGASAGGRKAWQPLSD-GISPTQGADYKGPTAIIKS-
-VSKMSN-DNMNI-------------GMVHNFKLMPGLLDTPEG--EQGIITLIRSASI-
----LGNGEMQFNYLDNKTMLEAQQNPKDYRDLVVRVAGYSAFFVELCKDVQDEIISRTV
LRHF-----------
>gi++|78358322|ref|YP_389771.1| formate C-acetyltransferase [Desulfovibrio
desulfuricans subsp. desulfuricans str. G20]
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--------MDLQDFSHKLAEATKNLTPAERASLKKIFEGVSAEVFSQPAPVSAVATGAES
GIPDGPTPRHV-------------------------------------------------
------------------------------------------------------------
---------------------------KLK---------ENF-LK-QVPS-ITVQRAVAI
TKIAKEN-PGL-PKP------LL----RAKTFRYCCETAPLVIQDH-ELIVGSPNGA-PR
AGAFSPEVA--WRWLQDELDT---IGSRPQD--P--------------------------
---FYISEEDKKVLR-EEVFPFW-----QNKSVDEFCEGQ---YRE--------------
-ADLWEM--------------SGESFVSDCSY--HAVNGG--------------------
------GDSNPGYDVILM-KKGMLDIQREAREKLEQLDY-------ANPEDI---DKIYF
YKSVIETAEGVMIYARRLSAYAAELAARE-TDPRRKAELQKISEVNARVPAHAPSNFWEA
IQAVWTVESLLVVEENQTG--MSIGRVDQYMYPFYRADID-S--GRLTEYE-----AFDL
AGCMLVKMSE-MMWI-TSEGASKFFAGYQPFVNMC---VGGV-TR-EGH--DATNDLTYM
LMDAVRHV-RIYQPTLATRVH-NKSPQKYLKKIVDVIR-SGMGFPAVHF-DDAHIKMMLA
--------K------G---VSIEDARDYCLM-GCVE------------------PQKSGR
-LYQ-W----TSTGYTQW--PICIELVLNHGV---PLWYGK-KV----------TP-DMG
DLS--QYDTYEKFEAAVKEQIRWITKNTSVATVISQRAHRELAPK--PLMSLMYEGCMES
GRDVSA----GGAMY-----NFGPGVVWSGLATYVDSMAAIKKLVYDDRKY-TLAQLN--
----------EALKADFA---------------------G-Y------------------
-------------------------DQILA------------------------------
------------DCLA--APKYGNDDDYADMIAADLVHFTETEH-RKY--KTL-------
--YSVLSHGTLSISN-NTPFGQLLGASANGRRAWMPLSD-GISPTQGADYKGPTAIIKS-
-VSKMAN-DNMNI-------------GMVHNFKLMSGLLDTPEG--ENGLITLIRTACM-
----LGNGEMQFNYLDNELLLDAQKHPEKYRDLVVRVAGYSAFFVELCKDVQDEIISRTM
LHGF-----------
>gi++|219666434|ref|YP_002456869.1| Formate C-acetyltransferase [Desulfitobacterium
hafniense DCB-2]
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------------------------------------------------------------
-----------------------------------------MSACCLSPHEERIIDPQKG
KVNYEGRERVF-------------------------------------------------
------------------------------------------------------------
---------------------------KIL---------ESF--QDLRPK-IDVERAKYF
TESFKAT-EGQ-PLQ------LR----WAKALMHIAQNITVYIDDQ-QLIVGRAGAQ-GR
YGIIFPELD--GDFLGLAIEQ---LPQRVES--P--------------------------
---FNIDPDDAQIII-NDVAPYW-----KGKTFHEELAKA---LPE--------------
-DTLKVT---------YDPADPLASRFIVNET--ASFRSS--------------------
------IQWVHDYEKVL--KRGFKGIKEEAQAKLDQLDPL------SPADNM---EKRPF
LEAVIITCDAIVVWANRHADLAAQMAKLE-KDPQRKQELSDIAERCAWVPAHPARNFREA
VQSQWFVQMFSRIEQKTGTI-ISNGRMDQYFYPYYQKDVA-E--GILNTQQ-----AIEL
LECMWVGMAQ-FIDLYLSPTGGAFNEGYAHWEAVT---VGGQ-TP-DGV--DATNELTYL
FLESKQKF-PLNYPDLAARIH-SRSPERYLYEVAETVK-EGTGFPKLIN-DEEVVPLLLS
--------K------G---AKFAEALDYAVS-GCAE------------------CRMPNR
DTYT------SGNPYINF--AAAIEMTLYNGR---MLKYGDEQL----------GL-ETG
DPT--QFETWDEFWKAYLAQQTNFLKHAFIQQHIIIRLRAQHFAS--PLGSLMHDLCMEN
YTDLHQPVIKGGI-------DLGYFE-LIGYGTVVDSLAAIKKLVYEEKKL-TMAELL--
----------EAVRNNFE---------------------G-H------------------
-------------------------EVIRE------------------------------
------------MVMH--TPKYGNNDPYSDVIAKEVDRTAVEFT-KKYS-REL-------
--GVHLDLRLVPFTS-HVPFGKVVSATPNGRKAWMPLAD-GSSASHGADVNGPTAVLLSN
FFSKNYG-YRNRA-------------ARLLNIKLSPSCVAGEEG--SEKLVSFIRTWCD-
----LKLWHIQFNIVNRETLLAAKQDPDKYRGLIVRVAGYSAYFVDLSSDLQDDIIARTE
HEMI-----------
>gi++|117621288|ref|YP_855870.1| pyruvate formate-lyase [Aeromonas hydrophila subsp.
hydrophila ATCC 7966]
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-MMEGLTPRLQ-------------------------------------------------
------------------------------------------------------------
---------------------------RLR---------NHY-LT-VRPS-VSIYRAQAF
TEVVKAN-PGM-PTI------LL----RAKAFRHACETAPILIQDD-ELIVGHPCGK-PR
AGAFSPDIA--WRWVRDELDT---MSTRPQD--P--------------------------
---FEISEADKKTIR-EEIVPFW-----EGRSLDEICEAQ---YRE--------------
-AGVWAF--------------SGETFVSDLSY--HQINGG--------------------
------GDTCPGYDVLLF-TKGMNGIKADAQAHLDQLSM-------ENPDDI---DRIYY
YKAAIETCEGVVNYARRIAAHARELAAKE-QDAQRRAELLTIAEVNENVPANPPKTLQEA
LQSIWTVESLFEIEENQTG--LSLGRVDQYCYPMFEADIR-E--GRLTHES-----ALEL
MQAFIIKCAE-LMWM-SSELGAKYFAGYQPFINLT---VGGQ-KR-SGG--DACNDLTYL
IMDAVRFV-KVYQPSLACRIH-NQSPQKYMEKIVDVVK-AGMGFPACHF-DDSHIKMMLR
--------K------G---FDFEDARDYCLM-GCVE------------------PQKSGR
-IYQ-W----TSTGYTQW--PIAIEFVLNRGR---MVLFDS-HQ----------GL-DTG
DLR--ELRTFEQFDAAVKQQIAHIVRMSAVGTVISQRVHRDVAPK--PLMSLMVEGCMES
GKDVSA----GGAMI-----NYGPGLIFSGLATYVDSMAAIRKLVFEEQRY-TLEQIR--
----------DALLANFE---------------------G-F------------------
-------------------------EALRR------------------------------
------------DCLN--APKYGNDDNYVDQYALDITEWTEKEC-RKY--KML--Y----
---SRMSHGTLSISN-NTPIGELTNATPNGRLAWMPLSD-GISPTQGADKQGPTAIIKS-
-VSKMNV-ETMNI-------------GMVHNFKFLKGLLDTQEG--RHGLITLLRTASI-
----LGNGQMQFSYVDNEVLKKAQQEPEKYRDLIVRVAGYSAYFVELCKEVQDEIISRTV
IEKF-----------
>gi++|206580147|ref|YP_002240668.1| putative formate C-acetyltransferase [Klebsiella
pneumoniae 342]
------------MAHYNLTPRVKVLADRLLAQKSTLCTEHATTLNALDGDIAGVPAAVKP
ARRFYELMRQLPLTISADELIVGNQTRKPHGAIFHDENATRRPSVFQFLNLNSELDSPDY
KLVVEKGVLAIKHQLEEKTRALGSAVSRSGMDEVNGCRAAIYACDALLALAQNLANSAEQ
LAAAETNAYRKAELLDSAAILHHVPAHPARNFKEACQAFYLFQLALQLDNGSYAVNPQGA
DIALLPYFQRNINSGALNTQQAYEIVECLWFKLAELSEVRAACAIDGYPMLDAMLRGAAF
DH--AEVNELSAMFISAQRNLSAL--NLPVRLFSGVQPV----------SHAPFAACADT
PVMEGLTPRMQ-------------------------------------------------
------------------------------------------------------------
---------------------------RLR---------NHY-LT-VRPS-VSIYRALAF
TEVVKAN-PGM-PTI------LL----RAKAFRHACETAPILIQDD-ELIVGHPCGK-PR
AGAFSPDIA--WRWVRDELDT---MSTRPQD--P--------------------------
---FEISEADKKTIR-EEIVPFW-----EGRSLDEICEAQ---YRE--------------
-AGVWAF--------------SGETFVSDLSY--HQINGG--------------------
------GDTCPGYDVLLF-TKGMNGIKADAEAHLASLSM-------ENPEDI---DRIYY
YKAAIETCEGVVNYARRIAAHARELAAKE-QNAQRRAELLTIADVNENVPANPPKTLQEA
LQSIWTVESLFEIEENQTG--LSLGRVDQYCYPMFEADIR-E--GRLTHDS-----ALEL
LQAFIIKCAE-LMWM-SSELGAKYFAGYQPFINLT---VGGQ-KR-SGG--DACNDLTYL
IMDAVRFV-KVYQPSLACRIH-NQSPQKYMEKIVDVVK-AGMGFPACHF-DDSHIKMMLR
--------K------G---FDFEDARDYCLM-GCVE------------------PQKSGR
-IYQ-W----TSTGYTQW--PIAIEFVLNRGR---MVLFDS-YQ----------GL-DTG
DLR--DLRTFDEFDAAVKQQIAHIVRLSAIGTVISQRVHRDVAPK--PLMSLLVEGCMES
GKDVAA----GGAMV-----NHGPGLIFSGLATYVDSMAAIRKLVFEEKKY-TLEQIR--
----------DALLANFE---------------------G-Y------------------
-------------------------EALRR------------------------------
------------DCLN--APKYGNDDNYVDQYALDITEWTEKEC-RKY--KML--Y----
---STLSHGTLSISN-NTPIGELTNATPNGRLAWMPLSD-GISPTQGADKQGPTAIIKS-
-VSKMNV-ETMNI-------------GMVHNFKFLKGLLDTPEG--RHGLITLLRTASI-
----LGNGQMQFSYVDNEVLKKAQQEPEKYRDLIVRVAGYSAYFVELCKEVQDEIISRTV
IEKF-----------
>gi++|89897752|ref|YP_521239.1| pyruvate-formate lyase [Desulfitobacterium hafniense
Y51]
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------MKLFQEISKELAANSPSPAYQERKSPVYE
GEITGLTPRLN-------------------------------------------------
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------------------------------------------------------------
---------------------------NLR---------TVY-LQ-AKPS-VSIDRARAF
TEVTREN-PGL-PKI------LL----RAKCFRRACETAPLLIQKD-ELIVGHPCGK-PR
AGAFSPDIA--WRWVRDELDT---MATRPQD--P--------------------------
---FQISEEDKRILR-EEIFPFW-----EGKSVDEICQKQ---YED--------------
-AGIWSF--------------SGESFVSDLSY--HQINGG--------------------
------GDTAPGYDVILI-KKGIKGVRQEAEDRLSRLSM-------ENPEDI---DKIYF
YKAEIETCDGILAYARRLSDYARESADRE-VDSVRKQELHKIADVLTWVPANPPRTFHEA
LQSIWTLESLFVVEENQTG--ISLGRLDQYIYPMFKADMD-A--GRLNKLE-----AFEL
MSCFLIKCSE-VMWL-SSEQGAKYFAGYQPFINCT---VGGQ-KR-TGG--DATNELTYL
IMDAVRFT-KMYQPSLACRIH-NQSPQRYLKKIVEVVK-AGLGFPACHF-DDSHIKMMLA
--------K------G---FSIEDSRDYCLM-GCVE------------------PQKSGG
-IYQ-W----TSTGYTQW--PIAIEFVLNRGV---MKWRGTME-----------GL-DTG
DLD--NFKTYEEFDAACKQQIENIIRLSAIGTIISQRVHKELVPK--PLMSLLVEGCMEK
GTDVTS----GGARI-----NFGPGLIFSGLGTYADSMAAIKKLVFEEKKY-TLKQIR--
----------DALNANFE---------------------G-Y------------------
-------------------------EALRT------------------------------
------------DCLN--APKYGNDDDYADLIASDLIVWTERVH-NSF--KML-------
--FSHFTHGTLSISN-NTPIGEITGATPNGRLAWTPLSD-GISPTQGADKFGPTAIIKS-
-VSKLSV-ESMNI-------------GMVHNFKLLRGILETPEG--ENGLITLLRTASI-
----LGNGQMQFSYVDNEVLKRAQIEPDKYRDLIIRVAGYSAYFVELCKEVQDEIISRTV
LEHF-----------
>gi++|219670900|ref|YP_002461335.1| Formate C-acetyltransferase [Desulfitobacterium
hafniense DCB-2]
-------------------MDSKEFSAKFADVTKNLSPEETAIVMKLFQEISKELAANSP
SPAYQ-------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------------------------ERKSPVYEGEI
T---GLTPRLN-------------------------------------------------
------------------------------------------------------------
---------------------------NLR---------TVY-LQ-AKPS-VSIDRARAF
TEVTREN-PGL-PKI------LL----RAKCFRRACETAPLLIQKD-ELIVGHPCGK-PR
AGAFSPDIA--WRWVRDELDT---MATRPQD--P--------------------------
---FQISEEDKRILR-EEIFPFW-----EGKSVDEICQKQ---YED--------------
-AGIWSF--------------SGESFVSDLSY--HQINGG--------------------
------GDTAPGYDVILI-KKGIKGVRQEAEDRLSRLSM-------ENPEDI---DKIYF
YKAEIEACDGILAYARRLSDYARESADRE-VDSVRKQELHKIADVLTWVPANPPRTFHEA
LQSIWTLESLFVVEENQTG--ISLGRLDQYIYPMFKADMD-A--GRLNKLE-----AFEL
MSCFLIKCSE-VMWL-SSEQGAKYFAGYQPFINCT---VGGQ-KR-TGG--DATNELTYL
IMDAVRFT-KMYQPSLACRIH-NQSPQRYLKKIVEVVK-AGLGFPACHF-DDSHIKMMLA
--------K------G---FSIEDSRDYCLM-GCVE------------------PQKSGG
-IYQ-W----TSTGYTQW--PIAIEFVLNRGV---MKWRGT-ME----------GL-DTG
DLD--NFKTYEEFDAACKQQIENIIRLSAIGTIISQRVHKELVPK--PLMSLLVEGCMEK
GTDVTS----GGARI-----NFGPGLIFSGLGTYADSMAAIKKLVFEEKKY-TLKQIR--
----------DALNANFE---------------------G-Y------------------
-------------------------EALRT------------------------------
------------DCLN--APKYGNDDDYADLIASDLIIWTERVH-NSF--KML--F----
---SHFTHGTLSISN-NTPIGEITGATPNGRLAWTPLSD-GISPTQGADKFGPTAIIKS-
-VSKLSV-ESMNI-------------GMVHNFKLLRGILETPEG--ENGLITLLRTASI-
----LGNGQMQFSYVDNEVLKRAQIEPDKYRDLIIRVAGYSAYFVELCKEVQDEIISRTV
LEHF-----------
>gi++|218549330|ref|YP_002383121.1| putative Formate C-acetyltransferase (Pyruvate
formate-lyase) [Escherichia fergusonii ATCC 35469]
MPLITRTGDPYLMANYNLTPRVKVLAERLLAHPSTLCVEHAGILSGLDGDIAGIPAAVKP
ARRFYELMRQLPLAVSPDELIVGNQTHRPHGAIFHDESTAHRPSVFQFLNLNSDLDAPDY
KLVIEKGVLAIKQQLEEKTRSLGSAVSRSGMDEVNACRAAIYACDALMQLAQNLATSAEK
LAATETNAYRKAELSESAAILHHIPAHPARSFKEACQAFYLFQLALQLDNGSYAVNPEGA
DKALLAYYQHDIANGLLTEAQAYEIVECLWFKLAELSEVRAACAIDGYPMFDALLHGASL
EN--AVINPLSEMFLNAQRNLSAL--NLPVRLFHGAHKT----------VTTPFAACSET
PVLEGLTPRIQ-------------------------------------------------
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---------------------------RLR---------NHY-LT-VRPS-VSIYRALAF
TEVVKAN-PGM-PAI------LL----RAKAFRHACETAPILIQND-ELIVGHPCGK-PR
AGAFSPDIA--WRWVRDELDT---MSTRPQD--P--------------------------
---FEISEEDKKTIR-EEIVPFW-----EGRSLDEICEAQ---YRE--------------
-AGVWSF--------------SGETFVSDLSY--HQVNGG--------------------
------GDTCPGYDVLLF-TKGMNGIKADAEAHLAELSM-------ENPEDI---DRIYY
YKAAIETCEGVINYAHRIAARARELAAVE-QNAQRRAELLTIAEVNQNVPANPPKTLQEA
LQSIWTVESLFEIEENQTG--LSLGRVDQYCYPMFEADIR-E--GRLTHEG-----ALEL
MQAFIIKCAE-LMWM-SSELGAKYFAGYQPFINLT---VGGQ-KR-SGG--DACNDLTYL
IMDAVRFV-KVYQPSLACRIH-NQSPQKYMEKIVDVVK-AGMGFPACHF-DDSHIKMMLR
--------K------G---FDFEDARDYCLM-GCVE------------------PQKSGR
-IYQ-W----TSTGYTQW--PIAIEFVLNRGR---MVLFDS-YQ----------GL-DTG
DLK--DLRTFEDFDAAVKKQVAHIIRLSAIGTVISQRVHRDVAPK--PLMSLLVEGCMEK
GKDVSA----GGAMV-----NHGPGLIFSGLATYVDSMAAIRKLVYEDKKY-TLEQIR--
----------DALLANFE---------------------G-Y------------------
-------------------------EGLRR------------------------------
------------DCLN--APKYGNDDNYVDQYALDITEWTEREC-RKY--KML--Y----
---STLSHGTLSISN-NTPIGELTNATPNGRLAWMPLSD-GISPTQGADKHGPTAIIKS-
-VSKMNV-ETMNI-------------GMVHNFKFLKGLLDTPEG--RNGLITLLRTASI-
----LGNGQMQFSYVDNEVLKKAQQEPEKYRDLIVRVAGYSAYFVELCKEVQDEIISRTV
IEKF-----------
>gi++|218702456|ref|YP_002410085.1| putative Formate C-acetyltransferase (Pyruvate
formate-lyase) [Escherichia coli IAI39]
MPLITRTGDPYLMANYNLTPRVKVLAERLLAHPSTLCVEHAGILSGLDGDIAGIPAAVKP
ARRFYELMRQLPLAVSPDELIVGNQTHRPHGAIFHDESTAHRPSVFQFLNLNSDLDAPDY
KLVIEKGVLAIKQQLEEKTRSLGSAVSRSGMDEVNACRAAIYACDALMQLAQNLATSAEK
LAATETNAYRKAELSESAAILHHIPARPARSFKEACQAFYLFQLALQLDNGSYAVNPEGA
DKALLAYYQHDIANGLLTEAQAYEIVECLWFKLAELSEVRAACTIDGYPMFDALLHGASL
EN--AVINPLSEMFLNAQRNLSAL--NLPIRLFHGAHKT----------VTTLCAACNET
PVLEGLTPRIQ-------------------------------------------------
------------------------------------------------------------
---------------------------RLR---------NHY-LT-VRPS-VSIYRALAF
TEVVKAN-PGM-PTI------LL----RAKAFRHACETAPILIQDD-ELIVGHPCGK-PR
AGAFSPDIA--WRWVRDELDT---MSTRPQD--P--------------------------
---FEISEEDKKTIR-EEIVPFW-----EGRSLDEICEAQ---YRE--------------
-AGVWSF--------------SGETFVSDLSY--HQVNGG--------------------
------GDTCPGYDVLLF-TKGMNGIKADAEAHLAELSM-------ENPEDI---DRIYY
YKAAIDTCEGVINYAHRIAARARELAAVE-QNAQRRAELLTIAEVNQNVPANPPKTLQEA
LQSIWTVESLFEIEENQTG--LSLGRVDQYCYPMFEADIR-E--GRLTHEG-----ALEL
MQAFIIKCAE-LMWM-SSELGAKYFAGYQPFINLT---VGGQ-KR-SGG--DACNDLTYL
IMDAVRFV-KVYQPSLACRIH-NQSPQKYMEKIVDVVK-AGMGFPACHF-DDSHIKMMLR
--------K------G---FDFEDARDYCLM-GCVE------------------PQKSGR
-IYQ-W----TSTGYTQW--PIAIEFVLNRGR---MVLFDS-YQ----------GL-DTG
DLK--DLRTFEDFDAAVKKQVAHIIRLSAIGTVISQRVHRDVAPK--PLMSLLVEGCMEK
GKDVSA----GGAMV-----NHGPGLIFSGLATYVDSMAAIRKLVYEDKKY-TLEQIR--
----------DALLANFE---------------------G-Y------------------
-------------------------EGLRR------------------------------
------------DCLN--APKYGNDDNYVDQYALDITEWTEREC-RKY--KML--Y----
---STLSHGTLSISN-NTPIGELTNATPNGRLAWMPLSD-GISPTQGADKHGPTAIIKS-
-VSKMNV-ETMNI-------------GMVHNFKFLKGLLDTPEG--RHGLITLLRTASI-
----LGNGQMQFSYVDNEVLKKAQQEPEKYRDLIVRVAGYSAYFVELCKEVQDEIISRTV
IEKF-----------
>gi++|91213912|ref|YP_543898.1| hypothetical protein UTI89_C4964 [Escherichia coli
UTI89]
MPLITRTGDPYLMANYNLTPRVKVLAERLLAHPSTLCVEHAGILSGLDGDIAGIPAAVKP
ARRFYELMRQLPLAVSPDELIVGNQTHRPHGAIFHDESTAHRPSVFQFLNLNSDLDAPDY
KLVIEKGVLAIKQQLEEKTRSLGSAVSRSGMDEVNACRAAIYACDALMQLAQNLATSAEK
LAATETNAYRKAELSESAAILHHIPARPARSFKEACQAFYLFQLALQLDNGSYAVNPEGA
DKALLAYYQHDIANGLLTEAQAYEIVECLWFKLAELSEVRAACAIDGYPMFDALLHGASL
EN--AVINPLSEMFLNAQRNLSAL--NLPIRLFHGAHKT----------VTTLCAACNET
PVLEGLTPRIQ-------------------------------------------------
------------------------------------------------------------
---------------------------RLR---------NHY-LT-VRPS-VSIYRALAF
```

```
TEVVKAN-PGM-PTI------LL----RAKAFRHACETAPILIQDD-ELIVGHPCGK-PR
AGAFSPDIA--WRWVRDELDT---MSTRPQD--P--------------------------
---FEISEEDKKTIR-EEIVPFW-----EGRSLDEICEAQ---YRE--------------
-AGVWSF--------------SGETFVSDLSY--HQVNGG--------------------
------GDTCPGYDVLLF-TKGMNGIKADAEAHLAELSM-------ENPEDI---DRIYY
YKAAIDTCEGVINYAHRIAARARELAAVE-QNAQRRAELLTIAEVNQNVPANPPKTLQEA
LQSIWTVESLFEIEENQTG--LSLGRVDQYCYPMFEADIR-E--GRLTHEG-----ALEL
MQAFIIKCAE-LMWM-SSELGAKYFAGYQPFINLT---VGGQ-KR-SGG--DACNDLTYL
IMDAVRFV-KVYQPSLACRIH-NQSPQKYMEKIVDVVK-AGMGFPACHF-DDSHIKMMLR
--------K------G---FDFEDARDYCLM-GCVE------------------PQKSGR
-IYQ-W----TSTGYTQW--PIAIEFVLNRGR---MVLFDS-YQ----------GL-DTG
DLK--DLRTFEDFDAAVKKQVAHIIRLSAIGTVISQRVHRDVAPK--PLMSLLVEGCMEK
GKDVSA----GGAMV-----NHGPGLIFSGLATYVDSMAAIRKLVYEDKKY-TLEQIR--
----------DALLANFE---------------------G-Y------------------
-------------------------EGLRR------------------------------
------------DCLN--APKYGNDDNYVDQYALDITEWTEREC-RKY--KML--Y----
---STLSHGTLSISN-NTPIGELTNATPNGRLAWMPLSD-GISPTQGADKHGPTAIIKS-
-VSKMNV-ETMNI-------------GMVHNFKFLKGLLDTPEG--RHGLITLLRTASI-
----LGNGQMQFSYVDNEVLKKAQQEPEKYRDLIVRVAGYSAYFVELCKEVQDEIISRTV
IEKF-----------
>gi++|197286545|ref|YP_002152417.1| propanediol utilization protein (dehydratase) 
[Proteus mirabilis HI4320]
------------MAKYSLTPRVKMLAERLVSRNSSISTERATIFDSLDNNIAGVPQAIKP
AQRFYQFIRHFPSYIAQDELIIGSQSSTPRGAIFHSEEEVRSDSIYRFLSINNSVTSPDY
MLVVNQGFLAIKAQLEDRMRSIGSAVNRSSMDEANFCKSAIYACDAALYFAQLLSAKAEN
LAAMEGNPYRKAELLESAAILRKVPAKPAETFKEAVQVFYLLQLILHLENGSYAINPMGF
DKALYPFYQRDIDQGRLTPAQAYEIVESLWLKLAELSEVRATKEVDGYPMFDAMTQGIDI
NDPRVSINELSEMLLSARANLSALHSSLQVRLYNGRMNTPPQYASPSANVVTPATANGEL
TVMEGLTPRLQ-------------------------------------------------
------------------------------------------------------------
---------------------------RLR---------NRY-LE-ARPS-VSIYRALAF
TEIARNN-PGL-PPI------LL----RAKAFRRACETAPILIQDE-ELIVGHPCGK-PR
AGAFSPDIA--WRWVRDELDT---MSTRPQD--P--------------------------
---FQISEEDKKVIR-EEIVPFW-----EGRSLDEICEAQ---YRE--------------
-AGVWEF--------------SGETFVSDLSY--HQINGG--------------------
------GDTCPGYDVLLF-TKGMNGIKADAQAKLAELSM-------ENPADI---DRIYF
YKASIESCEGVIAYAHRIAEHARELASKE-SDPQRREELLTIAQVNENVPANPPKTLQEA
LQSIWTVESLFEVEENQTG--LSLGRLDQYCFPMYENDIK-T--GRLTREQ-----ALEM
MQAFIIKCAE-LMWM-SSELGAKYFAGYQPFINLT---VGGQ-KR-SGG--DACNDLTYL
IMDAVRFV-KVYQPSLACRIH-NQSPQQYMEKIVDVVK-AGMGFPACHF-DDSHIKMMLR
--------K------G---FDFEDARDYCLM-GCVE------------------PQKSGR
-IYQ-W----TSTGYTQW--PIAIEFVLNRGR---MVLFDS-YQ----------GL-DTG
DLR--DLRTYEDFDRAVKEQVAHIIRLSAIGTVISQRVHRDIAPK--PLMSLLVEGCMEQ
GKDVTA----GGAMV-----NHGPGLIFSGLATYVDSMAAIRKLVYEDKKY-TLEQIR--
----------DGLLANFE---------------------G-H------------------
-------------------------EELLR------------------------------
------------DCLN--APKFGNDDDVVDQYALDITEWTEREC-RKY--KML--Y----
---STFSHGTLSISN-NTPIGELTAATPNGRLAWKPLSD-GISPTQGADKHGPTAIIKS-
-ISKMNV-ETMNI-------------GMVHNFKFLKGLLDTNEG--RQGLITLLRTASI-
----LGNGQMQFSYVDNEVLKKAQLEPEKYRDLIVRVAGYSAYFVELCKEVQDEIISRTV
IEKF-----------
>gi++|51246879|ref|YP_066763.1| formate acetyltransferase [Desulfotalea psychrophila 
LSv54]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------MSVECC---RSPHEQMIMDKAAGKV
NKFRATHERVF-------------------------------------------------
------------------------------------------------------------
---------------------------KIL---------DKI-ET-AKPQ-IDIERALYF
TQGMQET-EGQ-HLN------LR----WAKSLMKCAENMTVYIDDD-QLLAGRIGYQ-GR
```

```
YGVLYPELD--GDFLDTAVVD---LPTRDNS--P--------------------------
---FSISQADADIVV-KEIAPYW-----KGKTYHETLAKT---LPA--------------
-DVHALT---------YDDPDGMVSRFIVNET--ASFRSS--------------------
------NQWVHDFDKVL--KRGFGGLRDEFTVQLEALDPL------SPGDNV---DKKPF
LQAAILVCEAVIVWAKRHAALAMELAEKC-ADPVRKAELLKMAEVCNHVPEHPARTFYEA
CQSQWFTQMFSRLEQKTGTI-ISNGRMDQYLYPFYKQDIE-A--GILTDDQ-----AIEY
VELMYVGMAQ-YIDLYISPTGGAFNEGYAHWEAVT---IGGQ-TP-DGL--DATNELTYL
FLRSKREF-PHHYPDLAARIH-ARAPERFLAEVAETIK-EGSGFPKLIN-DEEVIPLHLA
--------K------G---AKFEEIYDYSVS-GCAE------------------IRMPNR
-DTY-T----AGGCYINF--VAALESVFFNGK---MLKFGDAQL----------SI-ETG
DVT--KMETWEEFWNAYKAQHINFLKIAFEQQYYVIKTRARHFAA--PMGSALHDLAMKH
CIDIHQPYIPEGI-------DLGYFE-FMGVGTLVDSMSAIKKFVFEEKKV-TMTEVL--
----------EAMKNNFE---------------------G-Q------------------
-------------------------EDLRA------------------------------
------------LMMT--APCFGNNDPYADSIARDLDQLCVGYA-EKYQ-REL-------
--GVFLDLRYVPFTS-HVPFGKVVCATPNGRYAGTSLSD-GSSASHGADKNGPTAVLLSN
YTSKNFN-HRERA-------------ARLVNIKFTPKCVQGEEG--TQKLVHFIRTFCD-
----LRLWHIQFNVVNAETLRLAQENPEAYRTLIVRIAGYSAYFCDLSKDLQNDLIRRTA
HENM-----------
>gi++|160879323|ref|YP_001558291.1| pyruvate formate-lyase [Clostridium
phytofermentans ISDg]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------------------------------MMAEP
KKGYEKSPRIQ-------------------------------------------------
------------------------------------------------------------
---------------------------KLM---------DAL-YE-KMPE-IESKRAVLI
TESYQQT-EGE-PII------SR----RSKAFEHIVKNLPVVIREN-ELIVGSATVA-ER
GCQTFPEFS--FDWLIAELDT---VATRTAD--P--------------------------
---FYISEEAKKELR--KVHSYW-----KGKTTSELADYY---MAP--------------
-ETKLAM----------------EHNVFTPGN--YFYNGV--------------------
------GHITVQYDKVI--AIGYEGIKDEVLSRKKELHL-------GDADYA---SRLTF
YDAVIRSCDSAILYAKRYAAEAKRLALSC-QDEKRRQELLMISSNCERVPAKGANTFYEA
CQAFWFVQLLLQIEASGHS--ISPGRFDQYLYSYYKADRE-A--GRITGEQ-----AQEI
IDCIFVKLND-INKC-RDAASAEGFAGYGMFQNMI---VGGQ-DS-NGR--DATNELSFM
ILEASIHT-MLPQPSLSIRVW-NGSPHDLLIKAAEVTR-TGIGLPAYYN-DEVIIPAMMN
--------K------G---ATLEEARNYNII-GCVE------------------PQVPGK
TDGW------HDAAFFNM--CRPLEMVFSSGY-----ENGK-LV----------GA-PTG
SVE--NFTTFEAFYDAYKTQMEYFISLLVNADNSIDIAHAKLCPL--PFESSMVEDCIGR
GLCVQE----GGAKY-----NFTGPQ-GFGIANMTDSLYAIKKLVYEEGKV-SITELK--
----------EALLHNFG---------------MTTKNAGLKESSHLSIDIILAQQITVQ
IVKELKERGKEPSEKEIEQILKTVLEAKKENTESPISTRVSENTSNHSRYQEILQ-----
------------MIEV--LPKYGNDILEIDEFAREIAYTYTKPL-QKY--KNP--R----
--GGVFQAGLYPVSA-NVPLGEQTGATPDGRLANTPIAD-GVGPAPGRDTKGPTAAANS-
-VARLDH-MDATN-------------GTLYNQKFHPSALQGRGG--LEKFVALIRAFFD-
----QKGMHVQFNVVSRETLLDAQKHPENYKHLVVRVAGYSALFTTLSRSLQDDIINRTT
QGF------------
>gi|28901422|ref|NP_801077.1| putative pyruvate formate lyase [Vibrio
parahaemolyticus RIMD 2210633]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
MDLHTLPERIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------SAL-VNIVTPP-ICTERAEAY
TRAYQAN-EDK-PVI------VQ----RALALQEHLRTRTIWIKHD-ELIVGNQASK-VR
AAPIFPEYT--VRWIEAEIDE---LADRPGA--G--------------------------
```

```
---FSVSEEDKQSIH--AITPYW-----RGKTVQDRCYGL---FTD--------------
-EQQEIL----------------ASTIIKAEG--NMTSGD--------------------
------AHLAVDNEKIL--KIGMNGLLNEVRQHRANNDV-------STYEGL---KKEQF
YKAVEIVLLAIQEHMVSYADLALEMAQNE-TRPERKAELETIAENCRHVAFHAPTNFWQA
LQLSYFVQLMLQIESNGHS--VSFGRMDQFLNDYYVRGLE-S--GAMNKAF-----ALEL
LQSCWLKLLE-VNKI-RSGAHSKASAGSPLYQNVC---IGGQKLNENGEPEDAVNPLSWA
ILESCGQL-RSTQPNLSVRYH-EGLNQEFLMGCIEVIK-CGFGMPAFNN-DEIVIPEFIK
--------L------G---VEKADAYNYASI-GCIE------------------TAVPGK
-----WGYRCTGMSFINF--ARILLAALNEGV---DATTGK-AF----------LS-HDK
SLAKGNFESFEQVTASWAEQIRYYTRKSIEIDTVVDSVLEQQAQD--IFCSSLVDDCLAR
GKTVKE----GGAKY-----DWVSGL-QVGIANLGNSLAAIKHLVFEEAQI-SQTELA--
----------KALEEDFD---------------------GIE------------------
------------------------NEQLRQR-----------------------------
------------LINF--APKYGNDDDYVDQLLADAYQVYIDEL-AQF--VNT--RHGRG
PIGGGYYAGTSSISA-NVPFGASTMATPDGRKAKTPLAE-GASPASGSDRLGPTAVYNS-
-VGKIQA-NKILG-------------GVLLNQKLSPAAVASEGD--KLKLSMLIRTFFNH
----HKGWHVQYNIVSRETLLAAKKNPEQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HEL------------
>gi|206576877|ref|YP_002239528.1| formate C-acetyltransferase 3 [Klebsiella
pneumoniae 342]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MTT
LKLNTLSARIQ-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------MAL-VHIVKPP-VCTERARHY
TEMYQQH-LDK-PIP------VR----RALALAHHLAERTIWIKHD-ELIVGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FSVSEENKRVLH--EVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKALL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNYPLLL--EKGLDGMRAKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLEAVSDHSKRFAALAREMATAE-SRESRRHELLTIAENCDIIAHEPPKTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELQ--QSLDREQ-----AIEL
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLVDGQPQDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLATLEGGR---DATSGQ-VF----------LP-QEH
ALSKGNFANFDQVLADWDNQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFDQGAI-GQQELA--
----------KALAEDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDSVDELLARAYQTYIDEL-KQY--HNP--RYGRG
PIGGNYYAGTSSISA-NVPFGAQTMATPDGRKAHTPLAE-GASPASGTDHLGPTAVISS-
-VGKLPT-GAILG-------------GVLLNQKLNPSTLENESD--KQKLMVLLRTFFEV
----HKGWHIQYNIVSRDTLLEAKKHPDQYRDLVVRVAGYSAFFTALSPDTQDDIIARTE
HTL------------
>gi|215485909|ref|YP_002328340.1| predicted pyruvate formate lyase [Escherichia coli
O127:H6 str. E2348/69]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MTT
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------NAL-VNIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLANRTIWIKHD-ELIIGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FAVSEENKRVLH--EVCPWW-----RGQTVQDRCYGM---FTD--------------
```

```
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLREKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLVAVSEHIERFAALAREMAATE-TRESRRDELRAIAENCDLIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEM
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLVDGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGLSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEVMDAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGAI-GQQQLA--
----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDTVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAQTMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-AAILG-------------GVLLNQKLNPATLENESD--KQKLMILLRTFFEV
----HKGWHIQYNIVSRETLLEAKKHPNQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|161614901|ref|YP_001588866.1| hypothetical protein SPAB_02655 [Salmonella
enterica subsp. enterica serovar Paratyphi B str. SPB7]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MTQ
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------TAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLAERTIWIKHD-ELIVGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FSVSEENKRILH--DVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLRDKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLDAVSQHITRFAALARQMAGEE-SRESRRKELLTIAENCEVIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEL
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLINGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEVMAAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGVI-GQQQLA--
----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDSVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAATMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-GSILG-------------GVLLNQKLNPTTLENESD--KQKLMVLLRTFFEV
----HKGWHIQYNIVSRETLLDAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|15804975|ref|NP_286587.1| pyruvate-formate lyase [Escherichia coli O157:H7
EDL933]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MTT
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------NAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLANRTIWIKHD-ELIIGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FAVSEENKRVLH--EVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
```

```
------AHLAVNFPLLL--EKGLDGLREKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLVAVSEHIERFAALARAMAATE-TRESRRDELLAMAENCDLIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEL
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLVDGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYNYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEVMDAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGAI-SQQQLA--
----------AALANDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDTVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAQTMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-AAILG-------------GVLLNQKLNPATLENESD--KQKLMILLRTFFEV
----HKGWHIQYNIVSRETLLEAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|110641026|ref|YP_668754.1| putative formate acetyltransferase 3 [Escherichia
coli 536]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MTT
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------NAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLANRTIWIKHD-ELIIGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FAVSEENKRVLH--EVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLREKVAERRSHINL-------TVLEDL---HGEQF
LKAIDIVLVAVSEHIERFAALAREMAATE-TRESRRDELLTIAENCDLIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEM
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLVDGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QAK
ALSAGNFNNFDEVMDAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGAI-GQQQLA--
----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDTVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PIGGNYYAGTSSISA-NVPFGAQTMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-AAILG-------------GVLLNQKLNPATLENESD--KQKLMILLRTFFEV
----HKGWHIQYNIVSRETLLEAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|224582655|ref|YP_002636453.1| putative formate acetyltransferase 3 [Salmonella
enterica subsp. enterica serovar Paratyphi C strain RKS4594]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MTQ
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------TAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLAERTIWIKHD-ELIVGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FSVSEENKRILH--DVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLRDKVAERRSRINL-------TVLEDL---HGEQF
```

```
LKAIDIVLDAVSQHITRFAALARQMAGEE-SRESRRKELLTIAENCEVIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEL
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLINGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEVMAAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGVI-GQQQLA--
----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDTVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAATMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-GSILG-------------GVLLNQKLNPTTLENESD--KQKLMVLLRTFFEV
----HKGWHIQYNIVSRETLLDAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|218688606|ref|YP_002396818.1| putative glycyl radical cofactor protein
[Escherichia coli ED1a]
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------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MTT
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------NAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLANRTIWIKHD-ELIIGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FAVSEENKRVLH--EVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLREKVAERRSHINL-------TVLEDL---HGEQF
LKAIDIVLVAVSEHIERFAALAREMAATE-TRESRRDELLTIAENCDLIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEM
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLVDGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEVMDAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGAI-GQQQLA--
----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDTVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PIGGNYYAGTSSISA-NVPFGAQTMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-AAILG-------------GVLLNQKLNPATLENESD--KQKLMILLRTFFEV
----HKGWHIQYNIVSRETLLEAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|194443020|ref|YP_002040082.1| formate C-acetyltransferase 3 [Salmonella enterica
subsp. enterica serovar Newport str. SL254]
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---------------------------------------------------------MTQ
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------TAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLAERTIWIKHD-ELIVGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FSVSEENKRILH--DVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLRDKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLDAVSQHIMRFAALARQMAGEE-SRESRRKELLTIAENCEVIAHEPPQTFWQA
```

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LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----VIEL
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLINGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEVMAAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGVI-GQQQLA--
----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDSVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAATMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-GSILG-------------GVLLNQKLNPTTLENESD--KQKLMVLLRTFFEV
----HKGWHIQYNIVSRETLLDAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|152969414|ref|YP_001334523.1| putative formate acetyltransferase 3 [Klebsiella
pneumoniae subsp. pneumoniae MGH 78578]
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---------------------------------------------------------MTT
LKLNTLSARIQ-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------MAL-VHIVKPP-VCTERARHY
TEMYQRH-LDK-PIP------VR----RALALAHHLAERTIWIKHD-ELIVGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FSVSEENKRVLH--EVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKALL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNYPLLL--EKGLDGMRAKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLEAVSDHSKRFAALAREMATAE-SRESRRHELLTIAENCDVIAHEPPKTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELQ--QSLDREQ-----AIEL
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLVDGKPQDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLATLEGGR---DATSGQ-VF----------LP-QEH
ALSKGNFANFDQVLADWDRQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFDQGAI-GQQELA--
----------KALAEDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDSVDQLLARAYQTYIDEL-KQY--HNP--RYGRG
PIGGNYYAGTSSISA-NVPFGAQTMATPDGRKAHTPLAE-GASPASGTDHLGPTAVISS-
-VGKLPT-GAILG-------------GVLLNQKLNPSTLENESD--KQKLMVLLRTFFEV
----HKGWHIQYNIVSRDTLLEAKKHPDQYRDLVVRVAGYSAFFTALSPDTQDDIIARTE
HTL------------
>gi|91209857|ref|YP_539843.1| putative formate acetyltransferase 3 [Escherichia coli
UTI89]
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---------------------------------------------------------MTT
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------NAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLANRTIWIKHD-ELIIGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FAVSEENKRVLH--EVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLREKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLVAVSEHIERFAALAREMAATE-TRESRRDELLTIAENCDLIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEM
```

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LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLVDGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEVMDAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGAI-GQQQLA--
----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDTVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PIGGNYYAGTSSISA-NVPFGAQTMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-AAILG-------------GVLLNQKLNPATLENESD--KQKLMILLRTFFEV
----HKGWHIQYNIVSRETLLEAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|62179408|ref|YP_215825.1| putative pyruvate formate lyase [Salmonella enterica
subsp. enterica serovar Choleraesuis str. SC-B67]
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------------------------------------------------------------
---------------------------------------------------------MTQ
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------TAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PTP------VR----RALALAHHLAERTIWIKHD-ELIVGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FSVSEENKRILH--DVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLRDKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLDAVSQHITRFAALARQMAGEE-SRESRRKELLTIAENCEVIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEL
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLINGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEVMAAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGVI-GQQQLA--
----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDTVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAATMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-GSILG-------------GVLLNQKLNPTTLENESD--KQKLMVLLRTFFEV
----HKGWHIQYNIVSRETLLDAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|198242330|ref|YP_002214808.1| formate C-acetyltransferase 3 [Salmonella enterica
subsp. enterica serovar Dublin str. CT_02021853]
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------------------------------------------------------------
---------------------------------------------------------MTQ
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------TAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLAERTIWIKHD-ELIVGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FSVSEENKRILH--DVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLRDKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLDAVSQHITRFAALARQMAGEE-SRESRRKELLTIAENCEVIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEL
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLINGQPMDAVNPLSYA
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ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--IRVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEVMAAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGVI-GQQQLA--
----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDSVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAATMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-GSILG-------------GVLLNQKLNPTTLENESD--KQKLMVLLRTFFEV
----HKGWHIQYNIVSRETLLDAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|16764205|ref|NP_459820.1| putative pyruvate formate lyase [Salmonella
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---------------------------------------------------------MTQ
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------TAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLAERTIWIKHD-ELIVGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FSVSEENKRILH--DVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLYGLRDKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLDAVSQHITRFAALARQMAGEE-SRESRRKELLTIAENCEVIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEL
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-KLINGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEVMAAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGVI-GQQQLA--
----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDTVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAATMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-GSILG-------------GVLLNQKLNPTTLENESD--KQKLMVLLRTFFEV
----HKGWHIQYNIVSRETLLDAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|157155776|ref|YP_001462019.1| formate C-acetyltransferas [Escherichia coli
E24377A]
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LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------NAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLANRTIWIKHD-ELIIGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FAVSEENKRVLH--EMCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLREKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLVAVSEHIERFAALAREMAATE-TRESRRDELLTMAENCDLIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEM
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLVDGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
```

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--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEIMDAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGAI-GQQQLA--
----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDTVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAQTMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-AAILG-------------GVLLNQKLNPATLENESD--KQKLMILLRTFFEV
----HKGWHIQYNIVSRETLLEAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|218699196|ref|YP_002406825.1| putative glycyl radical cofactor protein
[Escherichia coli IAI39]
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LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------VHK---------NAL-VHIVKPP-VCTERAQHY
TGMYQQH-LDK-PIP------VR----RALALAHHLANRTIWIKHD-ELIIGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FAVSEENKRVLH--EVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLREKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLVAVSEHIERFAALAREMAATE-TRESRRDELLTIAENCDLIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEM
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLVDGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEVMDAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGAI-GQQQLA--
----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDTVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAQTMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-AAILG-------------GVLLNQKLNPATLENESD--KQKLMILLRTFFEV
----HKGWHIQYNIVSRETLLEAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
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Ss046]
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------------------------------------------------------------
---------------------------AHK---------NAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLANRTIWIKHD-ELIIGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FAVSEENKRVLH--EVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLREKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLVAVSEHIERFAALAREMAATE-TRESRRDELLAIAENCDLIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEL
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-TLVDGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
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-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEVMDAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGAI-GQQQLA--
----------AALADDFD---------------------GLT------------------
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------------LING--APKYGNDDDTVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAQTMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-AAILG-------------GVLLNQKLNPATLENESD--KQKLMILLRTFFEV
----HKGWHIQYNIVSRETLLEAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|218548343|ref|YP_002382134.1| putative glycyl radical cofactor protein
[Escherichia fergusonii ATCC 35469]
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LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------NAL-VNIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLANRTIWIKHD-ELIIGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FAVSEENKRVLH--EVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLREKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLVAVSEHIERFAALAREMAATE-PRESRRDELLAMAENCDLIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEM
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLVDGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEVMDAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGAI-GQQQLA--
----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDTVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PIGGNYYAGTSSISA-NVPFGAQTMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-AAILG-------------GVLLNQKLNPATLENESD--KQKLMILLRTFFEV
----HKGWHIQYNIVSRETLLEAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|82543268|ref|YP_407215.1| putative formate acetyltransferase [Shigella boydii
Sb227]
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------------------------------------------------------------
---------------------------------------------------------MTT
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------NAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLANRTIWIKHD-ELIIGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FAVSEENKRVLH--EVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLREKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLVAVSEHIERFAALAREMAATE-TRESRRDELLAIAENCDLIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEL
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-TLVDGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGN-VF----------LP-QEK
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ALSAGNFNNFDEVMDAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGAI-GQQQLA--
----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDTVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAQTMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-AAILG-------------GVLLNQKLNPATLENESD--KQKLMILLRTFFEV
----HKGWHIQYNIVSRETLLEAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|26246798|ref|NP_752838.1| putative formate acetyltransferase 3 [Escherichia coli
CFT073]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MTT
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------NAL-VHIVKPP-VCTERAQHY
TEMYHQH-LDK-PIP------VR----RALALAHHLANRTIWIKHD-ELIIGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FAVSEENKRVLH--EVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLREKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLVAVSEHIERFAALAREMAATE-TRESRRDELLTIAENCDLIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEM
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLVDGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEVMDAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGAI-GQQQLA--
----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDTVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PIGGNYYAGTSSISA-NVPFGAQTMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-AAILG-------------GVLLNQKLNPATLENESD--KQKLMILLRTFFEV
----HKGWHIQYNIVSRETLLEAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|16759760|ref|NP_455377.1| putative formate acetyltransferase 3 [Salmonella
enterica subsp. enterica serovar Typhi str. CT18]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MTQ
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------TAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLAERTIWIKHD-ELIVGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FSVSEENKRILH--DVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDDLRDKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLDAVSQHITRFAALARQMAGEE-SRESRRKELLTIAENCEVIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEL
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLINGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEVMAAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
```

```
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGVI-GQQQLA--
----------AALADDFD---------------------GLP------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDSVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAATMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-GSILG-------------GVLLNQKLNPTTLENESD--KQKLMVLLRTFFEV
----HKGWHIQYNIVSRETLLDAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|16128791|ref|NP_415344.1| predicted pyruvate formate lyase [Escherichia coli
str. K-12 substr. MG1655]
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MTT
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------NAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLANRTIWIKHD-ELIIGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FAVSEENKRVLH--EVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLREEVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLVAVSEHIERFAALAREMAATE-TRESRRDELLAMAENCDLIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEM
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLVDGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGH---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEVMDAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGAI-GQQQLA--
----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDTVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAQTMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-AAILG-------------GVLLNQKLNPATLENESD--KQKLMILLRTFFEV
----HKGWHIQYNIVSRETLLDAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|187733614|ref|YP_001880989.1| formate C-acetyltransferase 3 [Shigella boydii CDC
3083-94]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MTT
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------NAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLANRTIWIKHD-ELIIGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FAVSEENKRVLH--EVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLREKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLVAVSEHIERFAALAREMAATE-TRESRRDELLAIAENCDLIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEL
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-TLVDGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGN-VF----------LP-QEK
ALSAGNFNNFDEVMDAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGTI-GQQQLA--
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----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDTVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAQTMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-AAILG-------------GVLLNQKLNPATLENESD--KQKLMILLRTFFEV
----HKGWHIQYNIVSRETLLEAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|170020822|ref|YP_001725776.1| pyruvate formate-lyase [Escherichia coli ATCC
8739]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MTT
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------NAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLANRTIWIKHD-ELIIGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FAVSEENKRVLH--EVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLREKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLVAVSEHIERFAALAREMAATE-TRESRRDELLAIAENCDLIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELK--QTLDREH-----AIEL
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLVDGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEVMDAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGAI-GQQQLA--
----------AALADDFE---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDTVDMLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAQTMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-AAILG-------------GVLLNQKLNPATLENESD--KQKLMILLRTFFEV
----HKGWHIQYNIVSRETLLEAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|110804822|ref|YP_688342.1| putative formate acetyltransferase [Shigella flexneri
5 str. 8401]
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------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MTT
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------NAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLANRTIWIKHD-ELIIGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FAVSEENKRVLH--EVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLREKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLVAVSEHIERFAALARAMAATE-TRESRRDELLAMAENCDLIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEL
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLVDGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVHVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEVMDAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGAI-GQQQLA--
----------AALADDFD---------------------GLT------------------
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------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDTVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAQTMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-AAILG-------------GVLLNQKLNPATLENESD--KQKLMILLRTFFEV
----HKGWHIQYNIVSRETLLEAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|170680406|ref|YP_001742928.1| formate C-acetyltransferase 3 [Escherichia coli
SMS-3-5]
------------------------------------------------------------
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------------------------------------------------------------
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------------------------------------------------------------
---------------------------------------------------------MTT
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------NAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLANRTIWIKHD-ELIIGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FAVSEENKRVLH--EVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLREKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLVAVSEHIERFAALAREMAATE-TRESRRDELLTIAENCDLIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEM
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLVDGQPMDAVNPLSYA
LLESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGSFNNFDEVMDAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGAI-GQQQLA--
----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDTVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAQTMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-AAILG-------------GVLLNQKLNPATLENESD--KQKLMILLRTFFEV
----HKGWHIQYNIVSRETLLEAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|218704245|ref|YP_002411764.1| putative glycyl radical cofactor protein
[Escherichia coli UMN026]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MTT
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------NAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLANRTIWIKHD-ELIIGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FAVSEENKRVLH--EVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLREKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLVAVSEHIERFAALAREMAATE-TRESRRDELLAMAENCDLIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEM
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLVDGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEVMDAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGAI-GQQQLA--
----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
```

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------------LING--APKYGNDDDTVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAQTMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-AAILG-------------GVLLNQKLNPATLENESD--KQKLMILLRTFFEV
----HKGWHIQYNIVSRETLLEAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|24112190|ref|NP_706700.1| putative formate acetyltransferase [Shigella flexneri
2a str. 301]
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---------------------------------------------------------MTT
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------NAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLANRTIWIKHD-ELIIGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FAVSEENKRVLH--EVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLREKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIMLVAVSEHIERFAALARAMAATE-TRESRRDELLAMAENCDLIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEL
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLVDGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVHVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEVMDAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGAI-GQQQLA--
----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDTVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAQTMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-AAILG-------------GVLLNQKLNPATLENESD--KQKLMILLRTFFEV
----HKGWHIQYNIVSRETLLEAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|56414060|ref|YP_151135.1| putative formate acetyltransferase 3 [Salmonella
enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]
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---------------------------------------------------------MTQ
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------TAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLAERTIWIKHD-ELIVGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FSVSEENKRILH--DVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLRDKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLDAVSQHITRFAALARQMAGEK-SRESRRKELLTIAENCEVIAHEPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEL
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLINGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEVMAAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGVI-GQQQLA--
----------AALANDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDSVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
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PVGGNYYAGTSSISA-NVPFGAATMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-GSILG-------------GVLLNQKLNPTTLENESD--KQKLMVLLRTFFEV
----HKGWHIQYNIVSRETLLDAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
NML------------
>gi|157160302|ref|YP_001457620.1| formate C-acetyltransferas [Escherichia coli HS]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MTT
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------NAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLANRTIWIKHD-ELIIGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FAVSEENKRVLH--EVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLREKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLVAVSEHIERFAALAREMAATE-TRESRRDELLAIAENCDLIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QMLEREH-----AIEL
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLIDGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LA-QEK
ALSAGNFNNFDEVMDAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGAI-GQQQLA--
----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDTVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAQTMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-AAILG-------------GVLLNQKLNPATLENESD--KQKLMILLRTFFEV
----HKGWHIQYNIVSRETLLEAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|161503987|ref|YP_001571099.1| hypothetical protein SARI_02080 [Salmonella
enterica subsp. arizonae serovar 62:z4,z23:--]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MTQ
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------TAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLAERTIWIKHD-ELIVGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FSVSEENKRILH--DVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLRDKVAERRSRINL-------TVLEDL---HGGQF
LKAIDIVLDAVSQHITRFAALARQMAGEE-TRESRRKELLTIAENCEVIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELN--QTLDREH-----AIEL
LHCCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLINGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDDVMAAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGVI-GQQQLA--
----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDSVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAATMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-GSILG-------------GVLLNQKLNPTTLENESD--KQKLMVLLRTFFEV
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----HKGWHIQYNIVSRETLLDAKKHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HML------------
>gi|82776090|ref|YP_402437.1| putative formate acetyltransferase [Shigella
dysenteriae Sd197]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MTT
LKLDTLSDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------NAL-VHIVKPP-VCTERAQHY
TEMYQQH-LDK-PIP------VR----RALALAHHLANRTIWIKHD-ELIIGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FAVSEENKRVLH--EVCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL-----------------ATGIIKAEG--NMTSGD-------------------
------AHLAVNFPLLL--EKGLDGLREKVAERRSRINL-------TVLEDL---HGEQF
LKAIDIVLVAVSEHIERFAALAREMAATE-TRESRRDELLAMAENCDLIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPYYRRDVELK--QTLDREH-----AIEL
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-NLVDGQPMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---IEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEGGR---DATSGK-VF----------LP-QEK
ALSAGNFNNFDEVMDAWDTQIRYYTRKSIEIEYVVDTMLEENVHD--ILCSALVDDCIER
AKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGVI-GQQQLA--
----------AALADDFD---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDTVDTLLARAYQTYIDEL-KQY--HNP--RYGRG
PVGGNYYAGTSSISA-NVPFGAQTMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-AAILG-------------GVLLNQKLNPATLENESD--KQKLMILLRTFFEV
----HKGWHIQYNIVSRETLLEAKKHPDQYRDLVVRVAGYSAFFTALSPEAQNDIIARTE
HML------------
>gi|123441008|ref|YP_001004997.1| putative formate acetyltransferase [Yersinia
enterocolitica subsp. enterocolitica 8081]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MTT
LDLVTLSERTK-------------------------------------------------
------------------------------------------------------------
---------------------------QHK---------NAL-IHIVKPP-VCTERAVHY
TEVYQQH-QDK-PLS------VR----RALALAHHLQQRTIWIKND-ELIIGNQASQ-LR
AAPIFPEYT--VSWIESEIDE---LADRPGA--G--------------------------
---FSVSEEDKAVLH--QLCPWW-----RGQTVQDRCYGM---FTD--------------
-EQKALL-----------------ATGIIKAEG--NMTSGD-------------------
------AHLAVNFPLLL--EKGLDGLRSKVTSRRSRLQL-------TDWSDL---HKEQF
LKAIDISLAALSEHIERYAAVARQMAQEE-TRDWRRVELQKIAENCELIAHQPPQTFWQA
LQLCYFIQLILQIESNGHS--VSFGRLDQYLYPWYRRDVELE--NTLSREQ-----AIEM
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-KLVQGKSIDAVNPLSYA
VLESCGRL-RSTQPNLSVRYH-AGISDDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---VEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAALEQGR---DATSGQ-VF----------LP-QEQ
GLSKGNFSDFSQVMAQWDAQIRYYTRKSIEIECVVDTVLEENAHD--IVCSALVDDCIER
GKSIKQ----GGARY-----DWVSGL-QVGIANLGNSLAAVRKLVFEQQLI-SQQQLA--
----------TALANDFA---------------------GLN------------------
------------------------GEQLRQH-----------------------------
------------LINS--APKYGNDVDDVDQLLVRAYQTYIDEL-KQY--HNT--RFGRG
PIGGTYYAGTSSISA-NVPFGAATMATPDGRKAHSPLAE-GASPASGTDHLGPTAVFNS-
-LSKLPT-ASILG-------------GVLLNQKLNPSTLDNPRD--REKLMMMLRTFFEE
----YLGWHVQYNIVSRETLLEAKQHPDRYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
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HTL------------
>gi|146310975|ref|YP_001176049.1| pyruvate formate-lyase [Enterobacter sp. 638]
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------------------------------------------------------------
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------------------------------------------------------------
---------------------------------------------------------MTQ
LNLNTLTDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------TAL-VHIVKPP-VCTERAQHY
TEMYQQH-MDK-PIP------VR----RALALAHHLAKRTLWIKHD-ELIIGNQASE-VR
AAPIFPEYT--VSWIEKEIDD---LADRPGA--G--------------------------
---FAVSEENKRVLH--DICPWW-----RGQTVQDRCYGM---FTD--------------
-EQKGLL----------------ETGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGMRAKVAERRTRINL-------TVLDDL---HGDQF
LKAIDIVLDAVSLHIQRFASLAREMASNE-IRESRRDELLAMAENCDVIAHQPPKTFWQA
LQLCYFIQLILQIESNGHS--VSFARMDQYLYPFYRRDVELD--QSLNREH-----AIEM
LHSCWLKLLE-VNKI-RSGSHSKASAGSPLYQNVT---IGGQ-KLVNGEAMDAVNPLSYA
ILESCGRL-RSTQPNLSVRYH-AGMSNDFLDACVQVIR-CGFGMPAFNN-DEIVISEFIK
--------L------G---VEKEDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVMLAAMEGGR---DATSGK-VF----------LP-QDK
ALSAGNFDNFEQVMESWDNQIRYYTRKSIEIEYVVDTMLEENVPD--ILCSSLVDDCIER
AKSIKE----GGAKY-----DWVSGL-QVGIANLGNSLAAVKKLVFEQGTI-GQQQLA--
----------AALADDYE---------------------GLT------------------
------------------------HEQLRQR-----------------------------
------------LING--APKYGNDDDSVDLLLARAYQTYIEEL-KQY--HNP--RYGRG
PIGGNYYAGTSSISA-NVPFGAATMATPDGRKAHTPLAE-GASPASGTDHLGPTAVIGS-
-VGKLPT-EAILG-------------GVLLNQKLNPATLENDSD--RQKLMILLRTFFEV
----HKGWHIQYNIVSRETLLEAKRHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HTL------------
>gi|157370882|ref|YP_001478871.1| pyruvate formate-lyase [Serratia proteamaculans
568]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MTT
LDLTTLTARTL-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------NAL-IHIVKPP-VCTERAQHY
TEAYQQH-LDK-PLP------VR----RALALANHLAKRTLRIDND-ELIIGNQASE-LR
AAPIFPEYT--VSWIEDEIDQ---LADRPGA--G--------------------------
---FSISEENKAILH--RICPWW-----RGQTVQDRCYGM---FTD--------------
-EQRALL----------------ATGIIKAEG--NMTSGD--------------------
------AHLAVNFPLLL--EKGLDGLRDKVDERRSRIHL-------TDWQEL---QQEQF
LKAIDLTLEALSAHILRFAELARSMAQAE-SRHWRSEELQAIAENCELIAHRPPQTFWQA
LQLCYFIQLTLQIESNGHS--VSFGRLDQYLYPWYRRDVELE--QTLPRER-----AIEM
LHSCWLKLLE-INKI-RSGSHSKASAGSPLYQNVT---IGGQ-QLVDGSPRDAVNPLSYT
ILESCGRL-RSTQPNLSVRYH-AGMSSDFLDACVQVIR-CGFGMPAFNN-DEIVIPEFIK
--------L------G---VEPQDAYDYAAI-GCIE------------------TAVGGK
-----WGYRCTGMSFINF--ARVLLAALEQGR---DATSGK-VF----------LP-QEL
ALSRGNFSHFDQVLGAWDSQIRYYTRKSIEIECVVDSVLEENAHD--ILCSALVDDCIER
GKSIKQ----GGAKY-----DWVSGL-QVGIANLGNSLAAVRKLVFEQGAI-GQQQLA--
----------AALANDFD---------------------GLS------------------
------------------------GEQLRQR-----------------------------
------------LLNA--APKYGNDVDEVDQLLVRAYQSYIDEL-AQY--HNT--RFGRG
PIGGTYYAGTSSISA-NVPFGAATLATPDGRKAHTPLAE-GASPASGTDHLGPTAVFNS-
-LSKLPT-AAILG-------------GVLLNQKLNPATLENPVD--REKLMLMLRTFFET
----YLGWHVQYNIVSRETLLEAKQHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HTI------------
>gi|117620999|ref|YP_857360.1| pyruvate formate-lyase [Aeromonas hydrophila subsp.
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hydrophila ATCC 7966]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------------MTQ
LDLTTLPPRIR-------------------------------------------------
------------------------------------------------------------
---------------------------AHK---------ESL-IHIVQPP-VCTERARHY
TQAYQAH-LAR-PLP------VR----RALALALHLKERTIWIKHD-ELIVGNQASQ-VR
AAPLFPEYT--VGWIEKEIDE---LADRPGA--G--------------------------
---FAVSEADKLAIH--ALTPFW-----NGQTVQDRCYGL---FTD--------------
-EQKGLL----------------ESGIIKAEG--NMTSGD--------------------
------AHLAVNYEQLL--ALGLDGLKAKVAERCGRLDL-------ADWADL---QREQF
LQAVAITFDAVSQHIERYAALARELAQQE-PRPERRCELETIALNCAHIAHRPPETFWQA
LQLCYFIQLILQIESNGHS--VSFGRMDQYLYPWYRREVELS--ESLPRTR-----AIEL
LQGCWLKLLE-VNKI-RSGTHSKASAGSPLYQNVT---IGGQ-NWRDGKAHDAVNGLSYA
ILESCGQL-RSTQPNLSVRYH-AGMSEDFLDACIQVIR-CGFGMPAFNN-DEVVIPEFIK
--------L------G---VSEEDAHHYAAI-GCIE------------------TAVPGK
-----WGYRCTGMSFINF--ARILLAALDGGR---DATTGK-VF----------LP-QPQ
SLRQGTFGHFDEVMARWDEQVRYFTRKSIEIDCVVDSVLEAQAHD--ILCSALVDDCIER
GKTIKQ----GGAVY-----DWVSGL-QVGIANLGNSLAALKKLVFEQGVV-DQRELA--
----------EALEQDFA---------------------GLE------------------
------------------------GEQLRQR-----------------------------
------------LTHA--APKYGNDLDEVDLLLVQAYQSYIDEL-KGL--HNT--RFGRG
PIGGTYYAGTSSISA-NVPFGAATMATPDGRHARTPLAE-GASPASGSDRLGPTAVFNS-
-LGKLPT-AAILG-------------GVLLNQKLSPASLENERD--KTKLMSLLRTFFEV
----HKGWHVQYNIVSRETLLAAKAHPDQYRDLVVRVAGYSAFFTALSPDAQDDIIARTE
HSL------------
>gi|150015591|ref|YP_001307845.1| pyruvate formate-lyase [Clostridium beijerinckii
NCIMB 8052]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------------------------M
NHFGELTDRMH-------------------------------------------------
------------------------------------------------------------
---------------------------NFR---------EEL-LN-AKSM-VSVERARLT
TESYKEH-ADK-PMV------LR----RALCLENILKNMTIFIEDN-SIIAGNQAES-NR
SAPIFPEYA--MDWVINELDE---FEKREGD--I--------------------------
---FYITEESKNVLR--EIAPFW-----EHKTLKDRGLAG---MPA--------------
-ESRIFY----------------DLGIIKAEG--NITSGD--------------------
------AHIAVNYETVL--NLGLINYKERTEKKLKELDL-------TDYRNL---NKSYF
YRAILIVLDAVAAFAKRYADLALELAEKE-SDVNRKEELLEMSRILNKVPYYPAETFHEA
VQSLWIIHLVLQIESNGHS--LSYGRMDQYLNPFYEKDLK-L--GKITEDS-----ATEL
LTNLWLKTFT-INKI-RSWSHTRFSAGSPLYQNVT---VGGQ-TV-DKK--DEVNPLSYL
ILKSVAQT-KLPQPNLTVRYH-KGLSDDFMKECIEVVR-LGFGMPAFNS-DEVIIPSFIE
--------K------G---VDEKDAYNYSAI-GCVE------------------VAVPGK
-----WGYRCTGMSFLNF--PKSLLIALNDGV---DPESGT-KL----------CE-GVG
HFK--DMTTFDEVMKAWDKIIREFTRHSVIIDSCADLAIEEVTAD--VLCSALTDDCIER
GLNLKE----GGAVY-----DFISDL-QVGIANLGDSLAAIKKCVFEDKSF-TQAQVW--
----------DALLNNFE---------------------GED------------------
------------------------GKRIQDI-----------------------------
------------LLND--APKYGNDDDYIDLLLREAYEIYIDEI-KKY--KNT--RYGRG
PIGGCYYAGTSSISA-NVPQGAGTLATPDGRKAGEPLAE-GCSPSHAMDKNGPTAVFKS-
-VSKLPT-HDITG-------------GVLLNQKVTPQMLSKESD--REKLILLIRTFFNR
----LEGFHVQYNVVSRDTLLDAQKHPEEHRDLIVRVAGYSAFFNVLSKQTQDDIIERTE
QVL------------
>gi|170759591|ref|YP_001786592.1| pyruvate formate-lyase [Clostridium botulinum A3
str. Loch Maree]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----------------------------------------------------------ME
NRFGLLTSRMH-------------------------------------------------
------------------------------------------------------------
---------------------------NFR---------EEL-LE-TKAS-IDATRAILT
TDAYKQH-ADK-PII------VK----RAYMLKNILEKMPIFIEKQ-TLIVGNQAKA-NR
AAPIFPEYA--IDWVIRELDE---FEKRDGD--V--------------------------
---FYIDEKTKEELR--DIAPYW-----EHNTTLDKGLAN---VPP--------------
-KSRVLY----------------DLGIIKAEG--NITSGD--------------------
------AHIAVDYGRIM--KKGLKEYEERTIALREALDL-------TDFHNI---KKYHF
YEAILIVLDAIKTFAKRYSDLAREMITKE-DDETRKMELMEIARIMDKVPYEPADNFYEA
IQSMWFVHLILQIESNGHS--LSYGRMDQYLYPYLKKDLE-S--GDITEDK-----AVEL
LTNLWLKTFT-INKV-RSWSHTQFSAGSPLYQNVT---VGGQ-TT-DKK--DAVNKLSYL
IIKSVAQT-RLPQPNLTVRYH-KGLDDKFMNEAIEVLK-LGTGMPAFNS-DEVIIPSFIE
--------K------G---VREEDAYNYSAI-GCVE------------------VAVPGK
-----WGYRCTGMSFINF--PKTLLISMNEGV---DPASKT-KL----------VE-GLT
HFD--NMTSYEDLKESWDVTIREFTKHSVIIENCCDLVLEYDVPD--VLCSALTEDCIGR
GKTLKE----GGAIY-----DFISGL-QVGIANLADSLAAIKKLVFEEKKI-STTELW--
----------NALMEDFA------------------SDKG--------------------
-------------------------KMIQRI-----------------------------
------------LIED--APKYGNDDDYVDKLVVDAYNTYIDEV-KKY--PNT--RYKRG
PIGGVRYAGTSSISA-NVGQGKGTLATPDGRNAGTPLAE-GGSPSHAMDQNGPTAVFKT-
-VSKLPT-HEITG-------------GVLLNQKVTPAMLSTEEN--KIKLAMLIRTFFNR
----LEGFHVQYNVVSRDVLLDAQANPEKHRDLIVRVAGYSAFFNMLSKQTQDDIIERTE
QTL------------
>gi|28379125|ref|NP_786017.1| formate C-acetyltransferase [Lactobacillus plantarum
WCFS1]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----------------------------------------------MIMSETLTKTTTTI
NHFGKLTPMMD-------------------------------------------------
------------------------------------------------------------
---------------------------RLR---------DSI-ID-AKPY-VDPERAILT
TETYRQHQDEQVDIL------------RAKMLEHVLDKMSIFIEDD-TLIVGNQARQ-NR
WAPVFPEYS--MNWVIDELDT---FEKRPGD--V--------------------------
---FYITEKSKEELR--AIAPFW-----KHNTLEDRGYAS---FPE--------------
-ASRIFY----------------DLGIIGADG--NITSGD--------------------
------GHIAVDYKNVV--NKGLKWYEDRIKTALANLDL-------TDFNQQ---KQYYF
YKAGLIVIDAIHNFAKRYAQLASKQAQNT-TSATRKAQLEKIAQILNKVPYEPANSFYEA
IQAVWLVHLTLQIESNGHS--VSYGRLDQYLAPFYEHDLK-T--GAIDANG-----ATEL
LTNLCLKTLT-INKV-RSWQHTEFSAGSPLYQNIT---IGGQ-TP-DGK--DAVNPTSYL
ILRAIAQA-HLPQPNLTVRYH-HGLSDKFMRECVEVIK-QGLGMPAFNN-DEIIIPSFIR
--------R------G---VKKEDAYNYSAI-GCVE------------------TAIPGK
-----WGYRCTGMSFINF--PRVLLLIMNGGI---DPESGK-RL----------LP-DYG
KFT--DMTSFDQLMTAWDKALREMTRQSVIIENSCDLALEQNYPD--ILCSVLTDDCIGR
GKTIKE----GGAVY-----DFISGL-QVGIANLADSLAAIKKLVFEEKKL-TTTQLW--
----------HALTTDFA------------------DEDG--------------------
-------------------------EKIRQM-----------------------------
------------LIND--APKYGNDDDYVDDLIVEAYKPYIDEI-AKY--KNT--RYGRG
PIGGLRYAGTSSISA-NVGQGHSTLATPDGRHARTPLAE-GCSPEHAMDTDGPTAVFKS-
-VSKLST-KDITG-------------GVLLNQKMSPQILRSDES--CMKLVALLRTFFNR
----LHGYHVQYNIVSRDTLIDAQNHPDKHRDLIVRVAGYSAFFVGLSKETQDDIIERTE
QSL------------
>gi|195978904|ref|YP_002124148.1| pyruvate formate-lyase [Streptococcus equi subsp.
zooepidemicus MGCS10565]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------MTEAKN
PYFGTLTERMH-------------------------------------------------
------------------------------------------------------------
---------------------------RYR---------EAV-LD-KKPY-IDAERAILA
TEAYKKH-QNK-PSN------LK----RAYMLQNILENMTIYIEDE-SLIAGNQASS-NK
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKQQLR--ELAPFW-----ENNNLRARCGVL---LPE--------------
-EVQVYM----------------ETGFFGMEG--KMNSGD--------------------
------AHLAVNYQKLL--EVGLKGFEERTRAAKAALDL-------TIPESI---DKYHF
YDSVLIVIAAVKAYAERYAKLARELAKTA--DPERQTELLEIARICDKVPYQPAETFAEA
VQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYAKADLE-A--GRETEDS-----IVER
LTNLWIKTLT-INKV-RSQAHTFSSAGSPLYQNVT---IGGQ-TR-DKQ--DAVNPLSYL
VLRSVAQT-KLPQPNLTVRYH-KGLDNRFMNECIEVMK-LGFGMPAMNN-DEIIIPSFIK
--------K------G---VLEEDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYINF--PKILLITMNDGI---DPASGK-RF----------AT-GHG
HFK--DMTSYDELKAAWDATLREITRMSVIVENAIDLGLEREVPD--ILCSALTDDCIGR
GKTLKE----GGAVY-----DYISGL-QVGIANLSDSLAALKKLVFEEGRL-TTDELW--
----------HALETDFA---------------------GER------------------
------------------------GEEIRQM-----------------------------
------------LIND--APKYGNDDDYADSLVVEAYDTYIDEI-AKY--PNT--RYGRG
PIGGIRYSGTSSISA-NVGQGKGTLATPDGRHAGTPLAE-GCSPEHSMDKKGPTSVLKS-
-VAKLPT-DEIVG-------------GVLLNQKVNPQTLAKEED--KMKLMALLRTFFNR
----LHGYHIQYNVVSRETLIDAQKNPEKHRDLIVRVAGYSAFFNVLSKATQDDIIERTE
HTL------------
>gi|94993274|ref|YP_601373.1| formate acetyltransferase [Streptococcus pyogenes
MGAS2096]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------MTETKS
PYFGHLTDRMT-------------------------------------------------
------------------------------------------------------------
---------------------------HYR---------EAV-LD-KKPY-IDAERAILA
TEAYQKH-QNK-PAN------LK----RAYMLQTILENMTIYIEDE-SLIAGNQASS-NK
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKQQLR--DIAPFW-----ENNNLRARCGVL---LPE--------------
-EVQVYM----------------ETGFFGMEG--KMNSGD--------------------
------AHLAVNYQKLL--EHGLKGFEERARAAKAALDL-------TIPENI---DKYHF
YDSVFIVIDAVKTYAKRYAKLARELAKTA--KPERQAELLDIARICDKVPYEPAKTFAEA
VQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYVKADLE-A--GRETEAS-----IVER
LTNLWIKTLT-INKV-RSQAHTFSSAGSPLYQNVT---IGGQ-TR-DKK--DAVNPLSYL
VLRSVAQT-KLPQPNLTVRYH-KGLDNTFMNECIEVMK-LGFGMPAMNN-DEIIIPSFIK
--------K------G---VSEEDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYINF--PKILLITMNDGI---DPASGK-RF----------AK-GHG
HFK--DMTSYEELKAAWDATLREITRMSVIVENAIDLGLEREVPD--ILCSALTDDCIGR
GKTLKE----GGAVY-----DYISGL-QVGIANLSDSLAALKKLVFEEGQL-TPEELW--
----------QALESDFA---------------------GER------------------
------------------------GEEIRQM-----------------------------
------------LIND--APKYGNDDDYADSLVVEAYDTYIDEI-AKY--PNT--RYGRG
PIGGIRYSGTSSISA-NVGQGKGTLATPDGRHAGTPLAE-GCSPEHSMDKKGPTSVLKS-
-VAKLPT-DEIVG-------------GVLLNQKVNPQTLAKEED--KLKLMALLRTFFNR
----LHGYHIQYNVVSRETLIDAQKHPEKHRDLIVRVAGYSAFFNVLSKATQDDIIERTE
HTL------------
>gi|50915089|ref|YP_061061.1| formate acetyltransferase [Streptococcus pyogenes
MGAS10394]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------MTETKI
PYFGHLTDRMT-------------------------------------------------
------------------------------------------------------------
---------------------------HYR---------EAV-LD-KKPY-IDAERAILA
TEAYQKH-QNK-PAN------LK----RAYMLQTILENMTIYIEDE-SLIAGNQASS-NK
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKQQLR--DIAPFW-----ENNNLRARCGVL---LPE--------------
-EVQVYM----------------ETGFFGMEG--KMNSGD--------------------
------AHLAVNYQKLL--EHGLKGFEERARAAKAALDL-------TIPENI---DKYHF
YDSVFIVIDAVKTYAKRYAKLARELAETA--SPERQAELLDIACICDKVPYEPAATFAEA
VQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYVKADLE-A--GRETEDT-----IVER
LTNLWIKTLT-INKV-RSQAHTFSSAGSPLYQNVT---IGGQ-TR-DKK--DAVNPLSYL
VLRSVAQT-KLPQPNLTVRYH-KGLDNTFMNECIEVMK-LGFGMPAMNN-DEIIIPSFIK
--------K------G---VSEEDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYINF--PKILLITMNDGI---DPASGK-RF----------AK-GHG
HFK--DMTSYEELKAAWDATLREITRMSVIVENAIDLGLEREVPD--ILCSALTDDCIGR
GKTLKE----GGAVY-----DYISGL-QVGIANLSDSLAALKKLVFEEGQL-TPEELW--
----------HALESDFA---------------------GER------------------
------------------------GEEIRQM-----------------------------
------------LIND--APKYGNDDDYADSLVVEAYDTYIDEI-AKY--PNT--RYGRG
PIGGIRYSGTSSISA-NVGQGKGTLATPDGRHAGTPLAE-GCSPEHSMDKKGPTSVLKS-
-VAKLPT-DEIVG-------------GVLLNQKVNPQTLAKEED--KLKLMALLRTFFNR
----LHGYHIQYNVVSRETLIDAQKHPEKHRDLIVRVAGYSAFFNVLSKATQDDIIERTE
HTL------------
>gi|19746932|ref|NP_608068.1| putative pyruvate formate-lyase 2 [Streptococcus
pyogenes MGAS8232]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------MTETKS
PYFGHLTDRMT-------------------------------------------------
------------------------------------------------------------
---------------------------HYR---------EAV-LD-KKPY-IDAERAILA
TEAYQKH-QNK-PAN------LK----RAYMLQTILENMTIYIEDE-SLIAGNQASS-NK
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKQQLR--DIAPFW-----ENNNLRARCGVL---LPE--------------
-EVQVYM----------------ETGFFGMEG--KMNSGD--------------------
------AHLAVNYQKLL--EHGLKGFEERARAAKAALDL-------TIPENI---DKYHF
YDSVFIVIDAVKTYAKRYAQLARELAETA--SPERQAELLDIACICDKVPYEPAATFAEA
VQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYVKADLE-A--GRETEDT-----IVER
LTNLWIKTLT-INKV-RSQAHTFSSAGSPLYQNVT---IGGQ-TR-DKK--DAVNPLSYL
VLRSVAQT-KLPQPNLTVRYH-KGLDNTFMNECIEVMK-LGFGMPAMNN-DEIIIPSFIK
--------K------G---VSEEDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYINF--PKILLITMNDGI---DPASGK-RF----------AK-GHG
HFK--DMTSYEELKAAWDATLREITRMSVIVENAIDLGLEREVPD--ILCSALTDDCIGR
GKTLKE----GGAVY-----DYISGL-QVGIANLSDSLAALKKLVFEEGRL-TPEELW--
----------QALESDFA---------------------G--------------------
----------------------ERGEEIRQM-----------------------------
------------LIND--APKYGNDDDYADSLVVEAYDTYIDEI-AKY--PNT--RYGRG
PIGGIRYSGTSSISA-NVGQGKGTLATPDGRHAGTPLAE-GCSPEHSMDKKGPTSVLKS-
-VAKLPT-DEIVG-------------GVLLNQKVNPQTLAKEED--KLKLMALLRTFFNR
----LHGYHIQYNVVSRETLIDAQKHPEKHRDLIVRVAGYSAFFNVLSKATQDDIIERTE
HTL------------
>gi|21911285|ref|NP_665553.1| putative pyruvate formate-lyase [Streptococcus
pyogenes MGAS315]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------MTETKS
PYFGHLTDRMT-------------------------------------------------
------------------------------------------------------------
---------------------------HYR---------EAV-LD-KKPY-IDAERAILA
TEAYQKH-QNK-PAN------LK----RAYMLQTILENMTIYIEDE-SLIAGNQASS-NK
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKQQLR--DIAPFW-----ENNNLRARCGVL---LPE--------------
-EVQVYM----------------ETGFFGMEG--KMNSGD--------------------
------AHLAVNYQKLL--EHGLKGFEERARAAKAALDL-------TIPENI---DKYHF
YDSVFIVIDAVKTYAKRYAKLARELAKTA--KPERQAELLDIARICDKVPYEPAKTFAEA
VQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYVKADLE-A--GRETEDS-----IVER
LTNLWIKTLT-INKV-RSQAHTFSSAGSPLYQNVT---IGGQ-TR-DKK--DAVNPLSYL
VLRSVAQT-KLPQPNLTVRYH-KGLDNTFMNECIEVMK-LGFGMPAMNN-DEIIIPSFIK
--------K------G---VSEEDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYINF--PKILLITMNDGI---DPASGK-RF----------AK-GHG
HFK--DMTSYEELKAAWDATLREITRMSVIVENAIDLGLEREVPD--ILCSALTDDCIGR
GKTLKE----GGAVY-----DYISGL-QVGIANLSDSLAALKKLVFEEGQL-TPEELW--
----------QALESDFA---------------------G--------------------
----------------------ERGEEIRQM-----------------------------
------------LIND--APKYGNDDDYADSLVVEAYDTYIDEI-AKY--PNT--RYGRG
PIGGIRYSGTSSISA-NVGQGKGTLATPDGRHAGTPLAE-GCSPEHSMDKKGPTSVLKS-
-VAKLPT-DEIVG-------------GVLLNQKVNPQTLAKEED--KLKLMALLRTFFNR
----LHGYHIQYNVVSRETLIDAQKHPEKHRDLIVRVAGYSAFFNVLSKATQDDIIERTE
HTL------------
>gi|15675819|ref|NP_269993.1| putative pyruvate formate-lyase 2 [Streptococcus
pyogenes M1 GAS]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------MTETKS
PYFGHLTDRMT-------------------------------------------------
------------------------------------------------------------
---------------------------HYR---------EAV-LD-KKPY-IDAERAILA
TEAYQKH-QNK-PAN------LK----RAYMLQTILENMTIYIEDE-SLIAGNQASS-NK
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKQQLR--DIAPFW-----ENNNLRARCGVL---LPE--------------
-EVQVYM----------------ETGFFGMEG--KMNSGD--------------------
------AHLAVNYQKLL--EHGLKGFEERARAAKAALDL-------TIPENI---DKYHF
YDSVFIVIDAVKTYAKRYAKLARELAKTA--KPERQAELLDIARICDKVPYEPAKTFAEA
VQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYVKADLE-A--GRETEDT-----IVER
LTNLWIKTLT-INKV-RSQAHTFSSAGSPLYQNVT---IGGQ-TR-DKK--DAVNPLSYL
VLRSVAQT-KLPQPNLTVRYH-KGLDNTFMNECIEVMK-LGFGMPAMNN-DEIIIPSFIK
--------K------G---VSEEDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYINF--PKILLITMNDGI---DPASGK-RF----------AK-GHG
HFK--DMTSYEELKAAWDATLREITRMSVIVENAIDLGLEREVPD--ILCSALTDDCIGR
GKTLKE----GGAVY-----DYISGL-QVGIANLSDSLAALKKLVFEEGRL-TPEELW--
----------KALESDFA---------------------GER------------------
------------------------GEDIRQM-----------------------------
------------LIND--APKYGNDDDYADSLVVEAYDTYIDEI-AKY--PNT--RYGRG
PIGGIRYSGTSSISA-NVGQGKGTLATPDGRHAGTPLAE-GCSPEHSMDKKGPTSVLKS-
-VAKLPT-DEIVG-------------GVLLNQKVNPQTLAKEED--KLKLMALLRTFFNR
----LHGYHIQYNVVSRETLIDAQKHPEKHRDLIVRVAGYSAFFNVLSKATQDDIIERTE
HTL------------
>gi|225871371|ref|YP_002747318.1| formate acetyltransferase [Streptococcus equi
subsp. equi 4047]
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------------------------------------------------------------
------------------------------------------------------MTEAKN
PYFGTLTERMH-------------------------------------------------
------------------------------------------------------------
---------------------------RYR---------EAV-LD-KKPY-IDAERAILA
TEAYQKH-QNK-PSN------LK----RAYMLQNILENMTIYIEDE-SLIAGNQASS-NK
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKQQLR--ELAPFW-----ENNNLRARCGVL---LPK--------------
-EVQVYM----------------ETGFFGMEG--KMNSGD--------------------
------AHLAVNYQKLL--EVGLKGFEERTRAAKAALDL-------TIPESI---DKYHF
YDSVLIVIAAVKAYAERYAKLARELAKTA--NPERQAELLEIARICDKVPYQPAETFAEA
VQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYAKADLE-A--GRETEDS-----IVER
LINLWIKTLT-INKV-RSQAHTFSSAGSPLYQNVT---IGGQ-TR-DKQ--DAVNPLSYL
VLRSVAQT-KLPQPNLTVRYH-KGLDNRFMNECIEVMK-LGFGMPAMNN-DEIIIPSFIK
--------K------G---VLEEDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYINF--PKILLITMNDGI---DPASGK-RF----------AT-GHG
HFK--DMTSYDELKAAWDATLREITRMSVIVENAIDLGLEREVPD--ILCSALTDDCIGR
GKTLKE----GGAVY-----DYISGL-QVGIANLSDSLAALKKLVFEEGRL-TTDELW--
----------HALETDFA---------------------GER------------------
------------------------GEEIRQM-----------------------------
------------LIND--APKYGNDDDYADSLVVEAYDTYIDEI-AKY--PNT--RYGRG
PIGGIRYSGTSSISA-NVGQGKGTLATPDGRHAGTPLAE-GCSPEHSMDKKGPTSVLKS-
-VAKLPT-DEIVG-------------GVLLNQKVNPQTLAKEED--KMKLMALLRTFFNR
----LHGYHIQYNVVSRETLIDAQKNPEKHRDLIVRVAGYSAFFNVLSKATQDDIIERTE
HTL------------
>gi|94991321|ref|YP_599421.1| formate acetyltransferase [Streptococcus pyogenes
MGAS10270]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------MIETKS
PYFGHLTDRMA-------------------------------------------------
------------------------------------------------------------
---------------------------HYR---------EAV-LD-KKPY-IDAERAILA
TEAYQKH-QNK-PAN------LK----RAYMLQTILENMTIYIEDE-SLIAGNQASS-NK
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKQQLR--DIAPFW-----ENNNLRARCGVL---LPE--------------
-EVQVYM----------------ETGFFGMEG--KMNSGD--------------------
------AHLAVNYQKLL--EHGLKGFEERARAAKAALDL-------TIPENI---DKYHF
YDSVFIVIDAVKTYAKRYAKLARELAKTA--KPERQAELLDIARICDKVPYEPAKTFAEA
VQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYVKADLE-A--GRETEDT-----IVER
LTNLWIKTLT-INKV-RSQAHTFSSAGSPLYQNVT---IGGQ-TR-DKK--DAVNPLSYL
VLRSVAQT-KLPQPNLTVRYH-KGLDNTFMNECIEVMK-LGFGMPAMNN-DEIIIPSFIK
--------K------G---VSEEDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYINF--PKILLITMNDGI---DPASGK-RF----------AK-GHG
HFK--DMTSYEELKAAWDATLREITRMSVIVENAIDLGLEREVPD--ILCSALTDDCIGR
GKTLKE----GGAVY-----DYISGL-QVGIANLSDSLAALKKLVFEEGQL-TPEELW--
----------HALESDFA---------------------GER------------------
------------------------GEDIRQM-----------------------------
------------LIND--APKYGNDDDYADSLVVEAYDTYIDEI-AKY--PNT--RYGRG
PIGGIRYSGTSSISA-NVGQGKGTLATPDGRHAGTPLAE-GCSPEHSMDKKGPTSVLKS-
-VAKLPT-DEIVG-------------GVLLNQKVNPQTLAKEED--KLKLMALLRTFFNR
----LHGYHIQYNVVSRETLIDAQKHPEKHRDLIVRVAGYSAFFNVLSKATQDDIIERTE
HTL------------
>gi|209560173|ref|YP_002286645.1| Putative pyruvate formate lyase 3 [Streptococcus
pyogenes NZ131]
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------------------------------------------------------MTETKS
PYFGHLTDRMT-------------------------------------------------
------------------------------------------------------------
---------------------------HYR---------EAV-LD-KKPY-IDAERAILA
TEAYQKH-QNK-PAN------LK----RAYMLQTILENMTIYIEDE-SLIAGNQASS-NK
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKQQLR--DIAPFW-----ENNNLRARCGVL---LPE--------------
-EVQVYM----------------ETGFFGMEG--KMNSGD--------------------
------AHLAVNYQKLL--EHGLKGFEERARAAKAALDL-------TIPENI---DKYHF
YDSVFIVIDAVKTYAKRYAKLARELAETA--SPERQAELLEIARICDKVPYEPAATFAEA
VQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYVKADLE-A--GRETEAS-----IVER
LTNLWIKTLT-INKV-RSQAHTFSSAGSPLYQNVT---IGGQ-TR-DKK--DAVNPLSYL
VLRSVAQT-KLPQPNLTVRYH-KGLDNTFMNECIEVMK-LGFGMPAMNN-DEIIIPSFIK
--------K------G---VSEEDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYINF--PKILLITMNDGI---DPASGK-RF----------AK-GHG
HFK--DMTSYEELKAAWDATLREITRMSVIVENAIDLGLEREVPD--ILCSALTDDCIGR
GKTLKE----GGAVY-----DYISGL-QVGIANLSDSLAALKKLVFEEGRL-TPEELW--
----------HALESDFA---------------------GER------------------
------------------------GEEIRQM-----------------------------
------------LIND--APKYGNDDDYADSLVVEAYDTYIDEI-AKY--PNT--RYGRG
PIGGIRYSGTSSISA-NVGQGKGTLATPDGRHAGTPLAE-GCSPEHSMDKKGPTSVLKS-
-VAKLPT-DEIVG-------------GVLLNQKVNPQTLAKEED--KLKLMALLRTFFNR
----LHGYHIQYNVVSRETLIDAQNHPEKHRDLIVRVAGYSAFFNVLSKATQDDIIERTE
HTL------------
>gi|225869364|ref|YP_002745312.1| formate acetyltransferase [Streptococcus equi
subsp. zooepidemicus]
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------------------------------------------------------------
------------------------------------------------------MTEVKN
PYFGTLTERMH-------------------------------------------------
------------------------------------------------------------
---------------------------RYR---------EAV-LD-KKPY-IDAERAILA
TEAYKKH-QNK-PSN------LK----RAYMLQNILENMTIYIEDE-SLIAGNQASS-NK
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKQQLR--ELAPFW-----ENNNLRARCGVL---LPK--------------
-EVQVYM----------------ETGFFGMEG--KMNSGD--------------------
------AHLAVNYQKLL--ELGLKGFEERTRAAKAALDL-------TIPESI---DKYHF
YDSVLIVIAAVKAYAERYAKLARELAKTA--NPERQAELLEIACICDKVPYQPAETFAEA
VQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYAKADLE-A--GRETEDS-----IVER
LTNLWIKTLT-INKV-RSQAHTFSSAGSPLYQNVT---IGGQ-TR-DKQ--DAVNPLSYL
VLRSVAQT-KLPQPNLTVRYH-KGLDNRFMNECIEVMK-LGFGMPAMNN-DEIIIPSFIK
--------K------G---VLEEDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYINF--PKILLITMNDGI---DPASGK-RF----------AI-GHG
HFK--DMTSYDELKAAWDATLREITRMSVIVENAIDLGLEREVPD--ILCSALTDDCIGR
GKTLKE----GGAVY-----DYISGL-QVGIANLSDSLAALKKLVFEEGRL-TTDELW--
----------HALETDFA---------------------GER------------------
------------------------GEEIRQM-----------------------------
------------LIND--APKYGNDDDYADSLVVEAYDTYIDEI-AKY--PNT--RYGRG
PIGGIRYSGTSSISA-NVGQGKGTLATPDGRHAGTPLAE-GCSPEHSMDKKGPTSVLKS-
-VAKLPT-DEIVG-------------GVLLNQKVNPQTLAKEED--KMKLMALLRTFFNR
----LHGYHIQYNVVSRETLIDAQKNPEKHRDLIVRVAGYSAFFNVLSKATQDDIIERTE
HTL------------
>gi|71904392|ref|YP_281195.1| formate acetyltransferase [Streptococcus pyogenes
MGAS6180]
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------------------------------------------------------------
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------------------------------------------------------MIETKS
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PYFGHLTDRMA-------------------------------------------------
------------------------------------------------------------
---------------------------HYR---------EAV-LD-KKPY-IDAERAILA
TEAYQKH-QNK-PAN------LK----RAYMLQTILENMTIYIEDE-SLIAGNQASS-NK
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKQQLR--DIAPFW-----ENNNLRARCGVL---LPE--------------
-EVQVYM----------------ETGFFGMEG--KMNSGD--------------------
------AHLAVNYQKLL--EHGLKGFEERARAAKAALDL-------TIPENI---DKYHF
YDSVFIVIDAVKTYAKRYAKLARELAKTA--KPERQAELLDIARICDKVPYEPAKTFAEA
VQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYVKADLE-A--GRETEDT-----IVER
LTNLWIKTLT-INKV-RSQAHTFSSAGSPLYQNVT---IGGQ-TR-DKK--DAVNPLSYL
VLRSVAQT-KLPQPNLTVRYH-KGLDNTFMNECIEVMK-LGFGMPAMNN-DEIIIPSFIK
--------K------G---VSEEDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYINF--PKILLITMNDGI---DPASGK-RF----------AK-GHG
HFK--DMTSYEELKAAWDATLREITRMSVIVENAIDLGLEREVPD--ILCSALTDDCIGR
GKTLKE----GGAVY-----DYISGL-QVGIANLSDSLAALKKLVFEEGRL-TPEELW--
----------HALESDFA---------------------G--------------------
----------------------ERGEEIRQM-----------------------------
------------LIND--APKYGNDDDYADSLVVEAYDTYIDEI-AKY--PNT--RYGRG
PIGGIRYSGTSSISA-NVGQGKGTLATPDGRHAGTPLAE-GCSPEHSMDKKGPTSVLKS-
-VAKLPT-DEIVG-------------GVLLNQKVNPQTLAKEED--KLKLMALLRTFFNR
----LHGYHIQYNVVSRETLIDAQKHPEKHRDLIVRVAGYSAFFNVLSKATQDDIIERTE
HTL------------
>gi|71911556|ref|YP_283106.1| formate acetyltransferase [Streptococcus pyogenes
MGAS5005]
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------------------------------------------------------------
---------MT-------------------------------------------------
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---------------------------HYR---------EAV-LD-KKPY-IDAERAILA
TEAYQKH-QNK-PAN------LK----RAYMLQTILENMTIYIEDE-SLIAGNQASS-NK
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKQQLR--DIAPFW-----ENNNLRARCGVL---LPE--------------
-EVQVYM----------------ETGFFGMEG--KMNSGD--------------------
------AHLAVNYQKLL--EHGLKGFEERARAAKAALDL-------TIPENI---DKYHF
YDSVFIVIDAVKTYAKRYAKLARELAKTA--KPERQAELLDIARICDKVPYEPAKTFAEA
VQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYVKADLE-A--GRETEDT-----IVER
LTNLWIKTLT-INKV-RSQAHTFSSAGSPLYQNVT---IGGQ-TR-DKK--DAVNPLSYL
VLRSVAQT-KLPQPNLTVRYH-KGLDNTFMNECIEVMK-LGFGMPAMNN-DEIIIPSFIK
--------K------G---VSEEDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYINF--PKILLITMNDGI---DPASGK-RF----------AK-GHG
HFK--DMTSYEELKAAWDATLREITRMSVIVENAIDLGLEREVPD--ILCSALTDDCIGR
GKTLKE----GGAVY-----DYISGL-QVGIANLSDSLAALKKLVFEEGRL-TPEELW--
----------KALESDFA---------------------GER------------------
------------------------GEDIRQM-----------------------------
------------LIND--APKYGNDDDYADSLVVEAYDTYIDEI-AKY--PNT--RYGRG
PIGGIRYSGTSSISA-NVGQGKGTLATPDGRHAGTPLAE-GCSPEHSMDKKGPTSVLKS-
-VAKLPT-DEIVG-------------GVLLNQKVNPQTLAKEED--KLKLMALLRTFFNR
----LHGYHIQYNVVSRETLIDAQKHPEKHRDLIVRVAGYSAFFNVLSKATQDDIIERTE
HTL------------
>gi|157150032|ref|YP_001451057.1| pyruvate formate-lyase [Streptococcus gordonii
str. Challis substr. CH1]
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------------------------------------------------------------
------------------------------------------------------------
----------------------------------------------MIQVKEVERTTIKT
DYFGSLTERMN-------------------------------------------------
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------------------------------------------------------------
---------------------------KYR---------EDV-LN-KKPY-IDAERAVLA
TKAYDEH-KEK-PNV------LK----RAYMLQEILENMTLYIEDE-TMIVGNQASS-NK
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKEQLR--SIAPFW-----ENNNLRARAGAL---LPE--------------
-EVQVYM----------------ETGFFGMEG--KMNSGD--------------------
------AHLAVNYQKLL--AYGLKGFEEKARAAKEALDL-------TDPASI---DKYHF
YDSIFIVVNAVKAYAERFVALANQLAEKA--DPKRRQELLEIARICSKVPYEPASTFAEA
VQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYVKADLE-A--GRETEAS-----IVER
LTNLWIKTIT-INKV-RSQAHTFSSAGSPLYQNVT---IGGQ-TR-DKR--DAVNPLSYL
VLKSVAQT-HLPQPNLTVRYH-AGLDARFMNECIEVMK-LGFGMPAFNN-DEIIIPSFIA
--------K------G---VLEEDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYMNF--PKVLLITMNDGI---DPASGK-RF----------AP-SFG
HFK--DMKSFAELQTAWDKTLRHLTRMSVIVENSIDLSLEREVPD--ILCSALTDDCIGR
GKHLKE----GGAVY-----DYISGL-QVGIANLSDSLAAIKKLVFEEGRL-TPAELW--
----------HALETDYA---------------------GER------------------
------------------------GKEIQEM-----------------------------
------------LIHD--APKYGNDDDYADKLVTDAYDIYVDEI-AKY--PNT--RYGRG
PIGGIRYSGTSSISA-NVGQGRGTLATPDGRNAGTPLAE-GCSPSHNMDKNGPTSVLKS-
-VSKLPT-DEIVG-------------GVLLNQKVNPQTLSKEED--KLKLIALLRTFFNR
----LHGYHIQYNVVSRETLIDAQKHPEKHRDLIVRVAGYSAFFNVLSKATQDDIIGRTE
HTL------------
>gi|94995233|ref|YP_603331.1| Formate acetyltransferase [Streptococcus pyogenes
MGAS10750]
------------------------------------------------------------
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------------------------------------------------------MTETKS
PYFGHLTDRMT-------------------------------------------------
------------------------------------------------------------
---------------------------HYR---------EAV-LD-KKPY-IDAERAILA
TEAYQKH-QNK-PAN------LK----RAYMLQTILENMTIYIEDE-SLIAGNQASS-NK
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKQQLR--DIAPFW-----ENNNLRARCGVL---LPE--------------
-EVQVYM----------------ETGFFGMEG--KMNSGD--------------------
------AHLAVNYQKLL--EHGLKGFEERARAAKAALDL-------TIPENI---DKYHF
YDSVFIVIDAVKTYAKRYAKLARELAKTA--KPERQAELLDIARICDKVPYEPAKTFAEA
VQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYVKADLE-A--GRETEDS-----IVER
LTNLWIKTLT-INKV-RSQAHTFSSAGSPLYQNVT---IGGQ-TR-DKK--DAVNPLSYL
VLRSVAQT-KLPQPNLTVRYH-KGLDNTFMNECIEVMK-LGFGMPAMNN-DEIIIPSFIK
--------K------D---VSEEDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYINF--PKILLITMNDGI---DPASGK-RF----------AK-GYG
HFK--DMTSYEELKAAWDATLREITRMSVIVENAIDLGLEREVPD--ILCSALTDDCIGR
GKTLKE----GGAVY-----DYISGL-QVGIANLSDSLAALKKLVFEEGRL-TPEELW--
----------QSLESDFA---------------------GER------------------
------------------------GEEIRQM-----------------------------
------------LIND--APKYGNDDDYADSLVVEAYDTYIDEI-AKY--PNT--RYGRG
PIGGIRYSGTSSISA-NVGQGKGTLATPDGRHAGTPLAE-GCSPEHSMDKKGPTSVLKS-
-VAKLPT-DEIVG-------------GVLLNQKVNPQTLAKEED--KLKLMALLRTFFNR
----LHGYHIQYNVVSRETLIDAQKHPEKHRDLIVRVAGYSAFFNVLSKATQDDIIERTE
HTL------------
>gi|222152354|ref|YP_002561529.1| formate acetyltransferase [Streptococcus uberis
0140J]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------------------------------MTQTK
PYFGQLTDRMN-------------------------------------------------
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---------------------------KYR---------EAV-LT-KKPY-IDAERALLV
TETYKKH-MDK-PAN------LK----RAYMLQNILEHMTIYIEDD-SFIAGNQASS-NK
DAPIFPEYT--LEFVINELDL---FEKRDGD--V--------------------------
---FYITEETKEQLR--SIAPFW-----ENNNLRARAGAL---LPK--------------
-EVDVYM----------------ETGFFGMEG--KMNSGD--------------------
------AHLAVNYQKVL--EYGLKGFEERARVAKDALDL-------TVPENI---DKYHF
YDSIFIVIDAVKTYAHRYASLAREMAENA--SPERKAELLEIARICDKVPYQPAETFAEA
VQSVWFIQCVLQIESNGHS--LSYGRFDQYMYPYAKADIE-A--GRETEDS-----IVER
LTNLWIKTLT-INKV-RSQSHTFSSAGSPMYQNVT---IGGQ-TR-DKK--DAVNPMSYM
VLKSVAQT-KLPQPNLTVRYH-KGLDNHFLNECIEVMK-LGFGMPAMNN-DEIIIPSFIK
--------K------G---VLEEDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYINF--PKILLITMNDGI---DPSSGK-RF----------AK-GHG
HFT--EMTSYEELKAAWDETLREITRMSVIVENAIDLGLERECPD--ILCSALTDDCIGR
GKTLKE----GGAVY-----DYISGL-QVGIANLSDSLAALKKLVFEEKRL-TTSELW--
----------WALETDFA---------------------GDR------------------
------------------------GEEIRQM-----------------------------
------------LIND--APKYGNDDDYADQLVVDAYDTYIDEI-AKY--PNT--RYGRG
PIGGVRYSGTSSISA-NVGQGKGTLATPDGRHAGTPLAE-GCSPEHSMDKKGPTSVLKS-
-VSKLRT-DEIVG-------------GVLLNQKVNPQTLAKEED--KLKLMALLRTFFNR
----LHGYHIQYNVVSRETLIDAQKHPEKHRDLIVRVAGYSAFFNVLSKATQDDIIERTE
HTL------------
>gi|125717159|ref|YP_001034292.1| formate acetyltransferase 3, putative
[Streptococcus sanguinis SK36]
------------------------------------------------------------
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------------------------------------------------------------
----------------------------------------------MIQVKEVEKTTIKT
DYFGSLTERMD-------------------------------------------------
------------------------------------------------------------
---------------------------KYR---------EDV-LN-KKPY-IDAERAVLA
TKAYDKH-KEK-PNV------LK----RAYMLKEILENMTLYIEDE-TMIVGNQASS-NK
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKEQLR--SIAPFW-----ENNNLRARAGAL---LPE--------------
-EVQVYM----------------ETGFFGMEG--KMNSGD--------------------
------AHLAVNYQKLL--AYGLKGFEEKARAAKEALDL-------TDPASI---DKYHF
YDSIFIVVDAVKAYAERFVALANQMAEKA--DPKRRQELLEIARICSKVPYEPASTFAEA
VQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYVKADLE-A--GRETEAS-----IVER
LTNLWIKTIT-INKV-RSQAHTFSSAGSPLYQNVT---IGGQ-TR-DKR--DAVNPLSYL
VLKSVAQT-HLPQPNLTVRYH-AGLDARFMNECIEVMK-LGFGMPAFNN-DEIIIPSFIA
--------K------G---VLEEDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYMNF--PKVLLITMNDGI---DPASGK-RF----------AP-SFG
HFK--DMKSFAELQTAWDKTLRHLTRMSVIVENSIDLSLEREVPD--ILCSALTDDCIGR
GKHLKE----GGAVY-----DYISGL-QVGIANLSDSLAAIKKLVFEEGRL-TPAELW--
----------HALETDYA---------------------G--------------------
----------------------ERGKEIQEM-----------------------------
------------LIHD--APKYGNDDDYADKLVTDAYDIYVDEI-AKY--PNT--RYGRG
PIGGIRYSGTSSISA-NVGQGRGTLATPDGRNAGTPLAE-GCSPSHNMDKNGPTSVLKS-
-VSKLPT-DEIVG-------------GVLLNQKVNPQTLSKEED--KVKLIALLRTFFNR
----LHGYHIQYNVVSRETLIDAQKHPEKHRDLIVRVAGYSAFFNVLSKATQDDIIGRTE
HTL------------
>gi|22536514|ref|NP_687365.1| formate acetyltransferase [Streptococcus agalactiae
2603V/R]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------MTKQLLTQKYTNDVQQNSQ
KHFGYLTERMY-------------------------------------------------
------------------------------------------------------------
---------------------------SYR---------DKV-LD-KKPF-IDAERAILV
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TEAYQKH-QEK-PNV------LK----RAYMLQNILEKMTIYIDDE-TMIVGNQASS-DK
DAPIFPEYT--LEFVVNELDL---FEKRDGD--V--------------------------
---FYITEETKEQIR--NIAPFW-----ENNNLRARAGVM---LPE--------------
-EVQVYM----------------ETGFFGMEG--KMNSGD---------------------
------AHLAVNYQKLL--EEGLIGFEKKARKAKADLDL-------TKPESI---DKYHF
YDSILITIEAVKTYAERFAILAKKQAKTA--NAKRRQELLDIASICERVPYYPAETFAEA
VQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYVKSDLE-A--GRETEDS-----IVER
LTNLWIKTIT-INKV-RSQAHTFSSAGSPLYQNVT---IGGQ-TR-HKE--DAVNPLSFL
VLKSVAQT-HLPQPNLTVRYH-ANLDKSFMNEAIEVMK-LGFGMPAFNN-DEIIIPSFIK
--------K------G---VSEEDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYINF--PKVLLITMNDGI---DPASGK-RF----------AP-SYG
HFT--QMTSYKELKEAWDKTLRYLTRMSVIVENAIDISLEREVPD--ILCSALTDDCIGR
GKHLKE----GGAVY-----DYISGL-QVGIANLSDSLAALKKLVFEEKRL-TTLEVW--
----------QALQSDYA---------------------GPR------------------
------------------------GEEIRQM-----------------------------
------------LINE--APKYGNDDDYADSLVRECYDVYVEEI-AKY--PNT--RYGRG
PIGGIRYSGTSSISA-NVGQGRGTLATPDGRHAGTPLAE-GCSPSHNMDKKGPTSVLKS-
-VSKLPT-DEIVG-------------GVLLNQKVNPQTLAKEED--KQKLIALLRTFFNR
----LHGYHIQYNVVSRETLIDAQKHPEKHRDLIVRVAGYSAFFNVLSKATQDDIIARTE
HAL------------
>gi|15900186|ref|NP_344790.1| formate acetyltransferase, putative [Streptococcus
pneumoniae TIGR4]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------------MVNTEVARTTIKT
EYFGSLTERMN-------------------------------------------------
------------------------------------------------------------
---------------------------KYR---------EDV-LN-KKPY-IDAERAVLA
TRAYERY-KEQ-PNV------LK----RAYMLKEILENMTIYIEEE-SMIAGNQASS-NK
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKEQLR--SIAPFW-----ENNNLRARAGAL---LPE--------------
-EVSVYM----------------ETGFFGMEG--KMNSGD---------------------
------AHLAVNYQKLL--QFGLRGFEERARKAKVALDL-------TDPASI---DKYHF
YDSIFIVIDAIKVYAKRFVALAKSLAENA--NPKRKKELLEIADICSRVPYEPATTFAEA
IQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYMKADLE-S--GKETEDS-----IVER
LTNLWIKTIT-INKV-RSQSHTFSSAGSPLYQNVT---IGGQ-TR-DKK--DAVNPLSYL
VLKSVAQT-HLPQPNLTVRYH-AGLDARFMNECIEVMK-LGFGMPAFNN-DEIIIPSFIA
--------K------G---VLEDDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYMNF--PKVLLITMNDGI---DPASGK-RF----------AP-SFG
RFK--DMKNFSELENAWDKTLRYLTRMSVIVENSIDLSLEREVPD--ILCSALTDDCIGR
GKHLKE----GGAVY-----DYISGL-QVGIANLSDSLAAIKKLVFEEERI-SPSQLW--
----------HALETDYA---------------------GEE------------------
------------------------GKVIQEM-----------------------------
------------LIHD--APKYGNDDDYADKLVTAAYDIYVDEI-AKY--PNT--RYGRG
PIGGIRYSGTSSISA-NVGQGRGTLATPDGRNAGTPLAE-GCSPSHNMDQHGPTSVLKS-
-VSKLPT-DEIVG-------------GVLLNQKVNPQTLAKEED--KLKLIALLRTFFNR
----LHGYHIQYNVVSRETLIDAQKHPEKHRDLIVRVAGYSAFFNVLSKATQDDIIGRTE
HTL------------
>gi|225858103|ref|YP_002739613.1| pyruvate formate-lyase [Streptococcus pneumoniae
70585]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------------MVNTEVARTTIKT
EYFGSLTERMN-------------------------------------------------
------------------------------------------------------------
---------------------------KYR---------EDV-LN-KKPY-IDAERAVLA
TRAYERY-KEQ-PNV------LK----RAYMLKEILENMFIYIEEE-SMIAGNQASS-NK
```

```
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKEQLR--SIAPFW-----ENNNLRARAGAL---LPE--------------
-EVSVYM----------------ETGFFGMEG--KMNSGD--------------------
------AHLAVNYQKLL--QFGLRGFEERARKAKVDLDL-------TDPASI---DKYHF
YDSIFIVIDAIKVYAKRFVALAKSLAENA--NPKRKKELLEIADICSRVPYEPATTFAEA
IQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYMKADLE-S--GKETEDS-----IVER
LTNLWIKTIT-INKV-RSQSHTFSSAGSPLYQNVT---IGGQ-TR-DKK--DAVNPLSYL
VLKSVAQT-HLPQPNLTVRYH-AGLDARFMNECIEVMK-LGFGMPAFNN-DEIIIPSFIA
--------K------G---VLEDDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYMNF--PKVLLITMNDGI---DPASGK-RF----------AP-SFG
HFK--DMKNFSELENAWDKTLRYLTRMSVIVENSIDLSLEREVPD--ILCSALTDDCIGR
GKHLKE----GGAVY-----DYISGL-QVGIANLSDSLAAIKKLVFEEERI-SPSQLW--
----------HALETDYA---------------------GEE------------------
------------------------GKVIQEM-----------------------------
------------LIHD--APKYGNDDDYADKLVTAAYDIYVDEI-AKY--PNT--RYGRG
PIGGIRYSGTSSISA-NVGQGRGTLATPDGRNAGTPLAE-GCSPSHNMDQHGPTSVLKS-
-VSKLPT-DEIVG-------------GVLLNQKVNPQTLAKEED--KLKLIALLRTFFNR
----LHGYHIQYNVVSRETLIDAQKHPEKHRDLIVRVAGYSAFFNVLSKATQDDIIGRTE
HTL------------
>gi|146318368|ref|YP_001198080.1| pyruvate-formate lyase [Streptococcus suis
05ZYH33]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----------------------------------------------MKTVTEVAGTSIKT
EYFGSLTDRMN-------------------------------------------------
------------------------------------------------------------
---------------------------KYR---------EDV-LD-KKPY-IDAERAVLA
TKAYQEH-REK-PNV------LK----RAYMLKEILENMTLYIEEE-SLIAGNQASS-NK
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKEQLR--SIAPFW-----EKNNLRSRAGVL---LPE--------------
-EVQVYM----------------ETGFFGMEG--KMNSGD--------------------
------AHLAVNYQKVL--EQGLRGFEERVRVAKANLDL-------TDPASI---DKYHF
YDSIFIIIDAVKAYADRFVALATELAEKA-PTAQRRQELLEIARICAKVPYEPAETFAEA
VQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYVKADLE-A--GRETEDS-----IVER
LTNLWIKTIT-INKV-RSQSHTFSSAGSPLYQNVT---IGGQ-TR-DKK--DAVNPLSYL
VLKSVAQT-HLPQPNLTVRYH-AGLDARFMNECIEVMK-LGFGMPAFNN-DEIIIPSFIE
--------K------G---VLEEDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYMNF--PKVLLITMNDGI---DPASGK-RF----------AP-AFG
HFK--DMKSFEVLETAWEKTLRHLTRMSVIVENAIDIALEREVPD--ILCSALTDDCIGR
GKHLKE----GGAIY-----DYISGL-QVGIANLSDSLAAIKKLVFEEGRL-TPEELW--
----------HALETDYA---------------------GER------------------
------------------------GKEIQEM-----------------------------
------------LIED--APKYGNDDDYADQLVTAAYDIYINEI-AKY--PNT--RFGRG
PIGGIRYSGTSSISA-NVGQGRGTLATPDGRNAGTPLAE-GCSPSHNMDKNGPTSVLKS-
-VAKLPT-HEIVG-------------GVLLNQKVNPQTLAKEED--KQKLIALLRTFFNR
----LHGYHIQYNVVSRETLIDAQLHPEKHRDLIVRVAGYSAFFNVLSRATQDDIIGRTE
HTL------------
>gi|116515577|ref|YP_815753.1| pyruvate formate-lyase [Streptococcus pneumoniae D39]
------------------------------------------------------------
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------------------------------------------------------------
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------------------------------------------------------------
-----------------------------------------------MVNTEVARTTIKT
EYFGSLTERMN-------------------------------------------------
------------------------------------------------------------
---------------------------KYR---------EDV-LN-KKPY-IDAERAVLA
TRAYERY-KEQ-PNV------LK----RAYMLKEILENMSIYIEEE-SMIAGNQASS-NK
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKEQLR--SIAPFW-----ENNNLRARAGAL---LPE--------------
```

```
-EVSVYM----------------ETGFFGMEG--KMNSGD--------------------
------AHLAVNYQKLL--QFGLRGFEERARKAKVALDL-------TDPASI---DKYHF
YDSIFIVIDAIKVYAKRFVALAKSLAENA--NPKRKKELLEIADICSRVPYEPATTFAEA
IQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYMKADLE-S--GKETEDS-----IVER
LTNLWIKTIT-INKV-RSQSHTFSSAGSPLYQNVT---IGGQ-TR-DKK--DAVNPLSYL
VLKSVAQT-HLPQPNLTVRYH-AGLDARFMNECIEVMK-LGFGMPAFNN-DEIIIPSFIA
--------K------G---VLEDDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYMNF--PKVLLITMNDGI---DPASGK-RF----------AP-SFG
HFK--DMKNFSELENAWDKTLRYLTRMSVIVENSIDLSLEREVPD--ILCSALTDDCIGR
GKHLKE----GGAVY-----DYISGL-QVGIANLSDSLAAIKKLVFEEERI-SPSQLW--
----------HALETDYA---------------------GEE------------------
------------------------GKVIQEM-----------------------------
------------LIHD--APKYGNDDDYADKLVTAAYDIYVDEI-AKY--PNT--RYGRG
PIGGIRYSGTSSISA-NVGQGRGTLATPDGRNAGTPLAE-GCSPSHNMDQHGPTSVLKS-
-VSKLPT-DEIVG-------------GVLLNQKVNPQTLAKEED--KLKLIALLRTFFNR
----LHGYHIQYNVVSRETLIDAQKHPEKHRDLIVRVAGYSAFFNVLSKATQDDIIGRTE
HTL------------
>gi|15902276|ref|NP_357826.1| formate acetyltransferase 3 [Streptococcus pneumoniae 
R6]
------------------------------------------------------------
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------------------------------------------------------------
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------------------------------------------------------------
--------------------------------------------MLTMVNTEVARTTIKT
EYFGSLTERMN-------------------------------------------------
------------------------------------------------------------
---------------------------KYR---------EDV-LN-KKPY-IDAERAVLA
TRAYERY-KEQ-PNV------LK----RAYMLKEILENMSIYIEEE-SMIAGNQASS-NK
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKEQLR--SIAPFW-----ENNNLRARAGAL---LPE--------------
-EVSVYM----------------ETGFFGMEG--KMNSGD--------------------
------AHLAVNYQKLL--QFGLRGFEERARKAKVALDL-------TDPASI---DKYHF
YDSIFIVIDAIKVYAKRFVALAKSLAENA--NPKRKKELLEIADICSRVPYEPATTFAEA
IQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYMKADLE-S--GKETEDS-----IVER
LTNLWIKTIT-INKV-RSQSHTFSSAGSPLYQNVT---IGGQ-TR-DKK--DAVNPLSYL
VLKSVAQT-HLPQPNLTVRYH-AGLDARFMNECIEVMK-LGFGMPAFNN-DEIIIPSFIA
--------K------G---VLEDDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYMNF--PKVLLITMNDGI---DPASGK-RF----------AP-SFG
HFK--DMKNFSELENAWDKTLRYLTRMSVIVENSIDLSLEREVPD--ILCSALTDDCIGR
GKHLKE----GGAVY-----DYISGL-QVGIANLSDSLAAIKKLVFEEERI-SPSQLW--
----------HALETDYA---------------------GEE------------------
------------------------GKVIQEM-----------------------------
------------LIHD--APKYGNDDDYADKLVTAAYDIYVDEI-AKY--PNT--RYGRG
PIGGIRYSGTSSISA-NVGQGRGTLATPDGRNAGTPLAE-GCSPSHNMDQHGPTSVLKS-
-VSKLPT-DEIVG-------------GVLLNQKVNPQTLAKEED--KLKLIALLRTFFNR
----LHGYHIQYNVVSRETLIDAQKHPEKHRDLIVRVAGYSAFFNVLSKATQDDIIGRTE
HTL------------
>gi|194398478|ref|YP_002036953.1| pyruvate formate-lyase [Streptococcus pneumoniae 
G54]
------------------------------------------------------------
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------------------------------------------------------------
-----------------------------------------------MVNTEVARTTIKT
EYFGSLTERMN-------------------------------------------------
------------------------------------------------------------
---------------------------KYR---------EDV-LN-KKPY-IDAERAVLA
TRAYERY-KEQ-PNV------LK----RAYMLKEILENMTIYIEEE-SMIAGNQASS-NK
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKEQLR--SIAPFW-----ENNNLRARAGAL---LPE--------------
-EVSVYM----------------ETGFFGMEG--KMNSGD--------------------
```

```
------AHLAVNYQKLL--QFGLRGFEERARKAKVALDL-------TDPASI---DKYHF
YDSIFIVIDAIKVYAKRFVALAKSLAENA--NPKRKKELLEIADICSRVPYEPATTFAEA
IQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYMKADLE-S--GKETEDS-----IVER
LTNLWIKTIT-INKV-RSQSHTFSSAGSPLYQNVT---IGGQ-TR-DKK--DAVNPLSYL
VLKSVAQT-HLPQPNLTVRYH-AGLDARFMNECIEVMK-LGFGMPAFNN-DEIIIPSFIA
--------K------G---VLEDDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYMNF--PKVLLITMNDGI---DPASGK-RF----------AP-SFG
HFK--DMKNFSELENAWDKTLRYLTRMSVIVENSIDLSLEREVPD--ILCSALTDDCIGR
GKHLKE----GGAVY-----DYISGL-QVGIANLSDSLAAIKKLVFEEERI-SPSQLW--
----------HALETDYA---------------------GEE------------------
------------------------GKVIQEM-----------------------------
------------LIHD--APKYGNDDDYADKLVTAAYDIYVDEI-AKY--PNT--RYGRG
PIGGIRYSGTSXISA-NVGQGRGTLATPDGRNAGTPLAE-GCSPSHNMDQHGPTSVLKS-
-VSKLPT-DEIVG-------------GVLLNQKVNPQTLAKEED--KLKLIALLRTFFNR
----LHGYHIQYNVVSRETLIDAQKHPEKHRDLIVRVAGYSAFFNVLSKATQDDIIGRTE
HTL------------
>gi|24378977|ref|NP_720932.1| formate acetyltransferase (pyruvate formate-lyase 2)
[Streptococcus mutans UA159]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------MVIPLLTQKYTNDVQKNSQ
KHFGYLTERMY-------------------------------------------------
------------------------------------------------------------
---------------------------SYR---------DKV-LD-KKPY-IDAERAILA
TEAYKEH-QEK-PNV------LK----RAYMLKNILEKMSLYIDDE-TMIVGNQASS-DK
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKKQIR--DIAPFW-----ENNNLRARAGAM---LPD--------------
-EVQVYM----------------ETGFFGMEG--KMNSGD--------------------
------AHLAVNYQKLL--ELGLVGFEERTREAKADLDL-------TDPASI---DKYHF
YDSILVTIDAVKTYAQRFVTLAKEMAETA--AAKRRRELLEIAAICERVPYYPARTFAEA
VQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYVKADLE-A--GRETEDS-----IVER
LTNLWIKTLT-INKV-RSQAHTFSSAGSPLYQNVT---VGGQ-TR-AKK--DAVNPLSFL
VLKSVAQT-HLPQPNLTVRYH-AGLNPDFMNEAIEVMK-LGFGMPAFNN-DEIIIPSFIA
--------K------G---VAEEDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYMNF--PKILLITMNNGI---DPASGK-RF----------AP-EFG
HFV--DMTSYEDLKSAWDKTIRYLTRMSVIVENAIDLSLEREVPD--ILCSALTDDCIGR
GKHLKE----GGAVY-----DYISGL-QVGIANLSDSLAAVKKLVFEEKRL-TTAELW--
----------EALQSDYA---------------------GEH------------------
------------------------GGEIRQM-----------------------------
------------LIND--APKYGNDNDYADQLVCDCYDVYVDEI-AKY--PNT--RYGRG
PIGGIRYSGTSSISA-NVGQGRGTLATPDGRHAGAPLAE-GCSPSHNMDKNGPTSVLKS-
-VSKLPT-AEIVG-------------GVLLNQKVNPQTLSKEED--KQKLIALLRAFFNR
----LHGYHIQYNVVSRETLIDAQKHPEKHRDLIVRVAGYSAFFNVLSKATQDDIIARTE
HAL------------
>gi|187932732|ref|YP_001885707.1| pyruvate formate-lyase [Clostridium botulinum B
str. Eklund 17B]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------------------------M
MDYIIKSERIK-------------------------------------------------
------------------------------------------------------------
---------------------------KLR---------ECI-LN-KTPS-VCIERARYF
TKAYKEN-EDK-PIY------IK----RAKAVEKTLENMSIYIKDG-ELIVGNQSFD-ER
TAPIFPEYA--VQWIEDELKEYGNFNKREGD--N--------------------------
---FYINEKNIDELL--EIVQYW-----KGKTLKDKCYGI---MPE--------------
-EIKKAI----------------NVKVIHGEG--NMTSGD--------------------
------GHIVPDFEKAL--NLGLSGIIKEAEEALEKVDI-------SENDGF---KKKSF
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LESVIIINKAIINFGLRYSELAKKLALAE-KDINRKNELLLISDICLRIPKEAPKNFYEA
VQMIWFVHLVIQIESNGHS--ASLGRVDQYLYPYYKEGIE-N--GTLTEDF-----AKEL
LQCLWIKLFS-ILKI-RPTSHAGYGAGYPTYQNVT---IGGC-NE-LGE--DCTNSLSYL
ILQSVGEM-KLTQPNLSARLF-SNSSARFIRECANVIK-TGFGMPALHT-DEIIVQSLLN
--------K------G---VNYKDAYNYTMV-GCVE------------------VAVPGK
-----WGYRCTGMSFLNM--IKAVELTLNDGY---DERTGE-TL-------------LTG
NRDLLSFNNFEELWAAWEKNIAYYTKLTVALDKIADTNLEEF-PD--IFCSSLVDDCIGR
GKSIKE----GGSIY-----DIVAGL-QVGLANATNSLFALKDVIFDKNIL-SKEEVV--
----------NALKNNFE---------------------G-L------------------
-------------------------EGIKVKK----------------------------
------------ILFS--SPKYGNDIDCVDNMARNVYQTYINEI-SKY--KTT--RYGRG
PIGGIYGLSTSGISS-NVPMGCVTGATPDGRFAWTPAAE-GASPVQGSDIEGPTSVLKS-
-ITKLPT-ILMTG-------------GQLLNMKFSPNLLVGDDQ--FTKFINLIKSFVS-
----MKGWHIQFNVIDTKTLREAQKDPEKYRDVIVRVAGYCAQFVTLDQTTQEDIISRTE
EAF------------
>gi|118443080|ref|YP_877303.1| pyruvate formate-lyase [Clostridium novyi NT]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----------------------------------------------------------MS
RGFSAPTERVK-------------------------------------------------
------------------------------------------------------------
---------------------------KLR---------AQI-LD-VVPC-VETERALLI
TESYKET-EEK-PMI------LR----RALALKKILNNLPIVIREG-ELIVGSLTKR-PR
SSQVFPEFS--NKWLQDELDR---LDKRKGD--V--------------------------
---FEIAEEDKKKLK--EVFEYW-----DGKTTHELATSY---MSK--------------
-ETIDAM----------------NSDIFTVGN--YYFNGV--------------------
------GHISVNYGKVL--AVGFNGIIEEAKKSLESSDK-------TSPSYI---KKEQF
LNSVIISCEAAIDYAKRYSDEAKKLADKT-SDPIRKSELNEIARICSKVPKEGASSFYEA
CQAFWFVHAIINVESNGHS--ISPTRFDQYMYPYYKKDMD-E--GKITQDF-----AQEL
VDCIWIKLND-INKV-RDEISTKYFGGYPMYQNLI---VGGQ-NF-EGK--DVTNELSYM
ALEASAHV-RLPQPSLSVRIW-NKTPDEFLLRACELTR-EGLGLPAYYN-DEVIIPALVA
--------R------G---VTLEDARSYGVI-GCVE------------------PQCPGK
-TEG-W----HDSAFFNL--ARIVELAIHSGK---DKGV---QI----------GP-KTK
EFT--EMKSFDEFMEAYKAQMEYFVKHMCVADNCIDIAHAERAPL--PFLSSMVENCISV
GKSLQE----GGAHY-----NFSGPQ-GVGVANVGDSLMAIKKLVFEDEKI-TKEQLK--
----------EALDSNFE---------------------K-Y------------------
-------------------------PEVKQI-----------------------------
------------LSKQ--APKYGNDIDEVDELARVGALVYSKEV-NKY--TNP--R----
--GGQFQPGLYPSSI-NVYFGSLTGATPDGRSAEEPLAD-GVSPSRGKDVSGPTAAGNS-
-VAKLDH-FIASN-------------GTLFNQKFHPAALKGDKG--LQNLAAVVRSYFD-
----QKGMHVQYNVIDRDTLIKAQQKPEDYRDLIVRVAGYSAQFISLDKTIQDDIIKRTE
HVM------------
>gi|77918998|ref|YP_356813.1| glycerol dehydratase [Pelobacter carbinolicus DSM
2380]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------------MSIQVKVNPA
VASQGPTERVE-------------------------------------------------
------------------------------------------------------------
---------------------------KIK---------ARF-LA-TTPE-ICAERAKLI
TESYKET-EGQ-PMS------IR----RAKALEKILLEMSVYIDDD-ELIVGNQCSM-PR
SAPIYPEFS--CEWVEDELDR---LAKRSAD--V--------------------------
---FLISEDVKKTLR-EDVFPYW-----KGKTNHEIATAL---MKQ--------------
-EAIDAG----------------NAVVYTVGN--YYFNGV--------------------
------GHISANYGKVM--NQGLNSVIAKAEAAKEKFDF-------ADAHQM---KSLHF
LESTIIANKAVIAFANRFADEAESLAAAE-KNAARKAELLEIARICRKVPAEPAETFQEA
VQAFWFIHLVIQIESNGHS--ISPMRFDQYCYPFYAAS---K--NSLSDEK-----AQEM
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LDLLWLKFNG-LNKV-RDENSTMAFAGYPMFMNII---VGGV-DR-EGK--DATNELSLM
LLQCAANT-KLYAPSLSIRVH-EGTPDVLYMKAAEVSR-MGLGVPAYFN-DRTIIPALLS
--------R------G---LTLEDARDYGII-GCVE------------------PQVGGK
-TEG-W----HDAAFFNM--AKVVELTLNNGY---DKRTEM-QV----------GP-KTG
DVT--EMKSFDDVMAAYAKQMEYFVGLMCHADNMVDLAHGQNVPL--PFLSSLVEDCIGR
GKSLQE----GGAIY-----NFSGPQ-GVGVANAGDSLTAIKKLCFDDKVI-SLPELK--
----------EVLDKDFA---------------------G-A------------------
-------------------------EEIRQM-----------------------------
------------VINR--APKYGNDDDYADEIAVESANIYCAEV-NKY--RNP--R----
--GGQFQPGLYPASA-NVPFGGVVEATPDGRKKGTPLAD-GVSPIGGADISGPTATVNS-
-VAKLDH-EVTSN-------------GTLLNQKFHPNAVKGEEG--LRNLIAVTETYFK-
----NGGFHVQYNVIDRNTLLDAQKKPEDFKGLVVRVAGYSAFFTALDKSLQDDIISRTE
QVF------------
>gi|94989383|ref|YP_597484.1| formate acetyltransferase [Streptococcus pyogenes
MGAS9429]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------MTETKS
PYFGHLTDRMT-------------------------------------------------
------------------------------------------------------------
---------------------------HYR---------EAV-LD-KKPY-IDAERAILA
TEAYQKH-QNK-PAN------LK----RAYMLQTILENMTIYIEDE-SLIAGNQASS-NK
DAPIFPEYT--LEFVLNELDL---FEKRDGD--V--------------------------
---FYITEETKQQLR--DIAPFW-----ENNNLRARCGVL---LPE--------------
-EVQVYM----------------ETGFFGMEG--KMNSGD--------------------
------AHLAVNYQKLL--EHGLKGFEERARAAKAALDL-------TIPENI---DKYHF
YDSVFIVIDAVKTYAKRYAKLARELAKTA--KPERQAELLDIARICDKVPYEPAKTFAEA
VQSVWFIQCILQIESNGHS--LSYGRFDQYMYPYVKADLE-A--GRETEAS-----IVER
LTNLWIKTLT-INKV-RSQAHTFSSAGSPLYQNVT---IGGQ-TR-DKK--DAVNPLSYL
VLRSVAQT-KLPQPNLTVRYH-KGLDNTFMNECIEVMK-LGFGMPAMNN-DEIIIPSFIK
--------K------G---VSEEDAYDYSAI-GCVE------------------TAVPGK
-----WGYRCTGMSYINF--PKILLITMNDGI---DPASGK-RF----------AK-GHG
HFK--DMTSYEELKAAWDATLREITRMSVIVENAIDLGLEREVPD--ILCSALTDDCIGR
GKTLKE----GGAVY-----DYISGL-QVGIANLSDSLAALKKLVFEEGQL-TPEELW--
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------------------------------------------------------------
--------------------------------------------------QAP-------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
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>gi|118444929|ref|YP_878877.1| pyruvate formate-lyase [Clostridium novyi NT]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------------------------------MDVLA
RGFSIPTKRVE-------------------------------------------------
------------------------------------------------------------
---------------------------KLK---------EQI-LS-ATPC-IEVERARLL
TESFKET-ENQ-PII------IR----KAKALEKILNEMPIVIREG-ELIVGSLTKN-SR
SAQVFPEFS--NKWLVEEFEK---LPKRTSD--S--------------------------
---FQISEEVKSELI--DIFKYW-----EGKTVSELATSY---MPK--------------
-ETLEAM----------------GAKVFTVAN--YYFNGL--------------------
------GHISVDYKKVL--ELGFKGIIEEIKAKMDSADK-------SDPEYI---KKRTF
WEAVIISCEAAIDYARRYAKLAKELSENT-EDCKRKEELLKIAEICSKVPENPATTFYEA
CQSFWFVQAIISLESNGHA--ISPARFDQYMYPYFKSDVD-N--NVVTKEE-----NREI
LQCLWVKFND-LTKV-RDETTTKAFSGYSMFQNLI---VGGQ-TE-EGK--DATNELSYM
CLDATGSL-KLPQPSLSVRIW-SKTPEEFLIRTCELTR-LGTGLPAFYN-DEVIIPMLVN
```

```
--------N------G---MTLEDARDYAIV-GCVE------------------PQKPGK
-TDG-W----YDAAFFNL--AQILKLTIDNGK-----MDGK-QV----------GP-KTG
EFE--EFKDIDEVIEAYKKQMEYFVAQMVSADNCVDIAHRERAPL--PFLSAMLDDCIAK
GKSIQE----GGGHY-----RFSGPL-GVGIANVGDSFMAIKKLVFDDEKI-TLDKLK--
----------QALDGNFG---------------KDEKDEGKK------------------
----------------------NELQGIKQM-----------------------------
------------LLHR--APKFGNDIDEVDEFTREGALIYCNEV-LKH--FNQ--R----
--GGKFLPGLYPVSN-NVHLGSLVGATPDGREAYQPIAD-GVSPTRGADVNGPTAAANS-
-VAKLEH-YAAPS-------------GTLFNQKFNPSSLKGDNG--LRNLGTLIRSYFD-
----HKGMHIQFNVVDKNVLLDAQKHPEKYRDLIVRVAGYSAQFICLNKEIQDDIIKRTE
QEL------------
>gi|188588000|ref|YP_001921047.1| pyruvate formate-lyase [Clostridium botulinum E3
str. Alaska E43]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------------------------------MDILA
KGFIRPTKRVE-------------------------------------------------
------------------------------------------------------------
---------------------------KLK---------EEI-FS-ATPY-IEADRAIIL
TESFKET-ENE-PII------IR----KAKSLEKILNEIPIVIRDN-ELIVGSLTKN-PR
SCQVFPEFS--NQWLVDEFDK---FEKRTSD--L--------------------------
---FKIPEETKSKLK--EVFKYW-----QGKTVSELATSY---MTN--------------
-ETKDAM---------------NTKVFTVAN--YHFNGL---------------------
------GHISVDYPKVL--EKGFLGIIKETENAIINADK-------SNPEYV---KKKVF
WDSIIISCKAAIKYANRYSELAKKLAGET-LDINRKNELLKIAEICSKVPANPAETFYEA
CQSFWFVQAIISLESNGHA--ISPARFDQYMYPYYKNDID-N--KFATKEV-----NTEI
LHCLWVKFND-LTKV-RDETTTKAFSGYSMFQNLI---VGGQ-TP-DGK--DATNELSYM
CLEATGSL-KLPQPSLCVRIW-SKTPDEFLIRTCELTR-LGTGLPAFYN-DEVVIPTLIN
--------Q------G---LTIEDARDYAIV-GCVE------------------PQKPGK
-TDG-W----YDAAFFNL--AKILELSMNNGR-----LNGK-QV----------GP-ETG
EFT--SFKNIDDFINAYKKQIEYFVFHMVAADNCVDIAHAKRAPL--PFLSSMLDDCIGT
GKSIQE----GGGHY-----RFSGPL-GVGIANVGDSFMAIKKLIFDENKI-TLLKLK--
----------AAVDSNFG------------ENEDDPIKKAEY------------------
-------------------------EDIKQL-----------------------------
------------ILNR--VPKFGNDIDEVDEFTRDGALIYCKEV-LKY--TNQ--R----
--GGKFIPGLYPVSN-NVYLGSLVGATPDGRNAFKPLAD-GVSPTRGADVNGPTAAANS-
-VSKLEH-FAAPS-------------GTLFNQKFNPNSLQGDNG--LKNLGSLIRSYFD-
----RKGMHIQFNVIDKKVLLEAQKHPEQYRDLIVRVAGYSAQFICLDKGVQDDIIKRTE
QNL------------
>gi|187932402|ref|YP_001886034.1| pyruvate formate-lyase [Clostridium botulinum B
str. Eklund 17B]
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------------------------------------------------------------
------------------------------------------------------------
-------------------------------------------------------MDILA
KGFINPTKRVE-------------------------------------------------
------------------------------------------------------------
---------------------------KLK---------EEI-FS-AIPC-IEADRAIIL
TESFKET-ENE-PII------IR----KAKSLEKILSEIPVVIRDN-ELIVGSLTKN-PR
SCQVFPEFS--NQWLVDEFDK---FEKRTSD--L--------------------------
---FKIPEETKSKLK--EVFKYW-----QGKTVSELATSY---MSN--------------
-ETKDAM---------------NTKVFTVAN--YHFNGL---------------------
------GHISVDYPKVL--EKGFLGIIKETENAIINADK-------SNPEYV---KKKVF
WDSIIISCKAAIKYANRYSELAKKLAGET-LDINRKNELLKIAEICSKVPANPAETFYEA
CQSFWFVQAIISLESNGHA--ISPARFDQYMYPYYKNDID-N--KFATKEV-----NTEI
LHCLWVKFND-LTKV-RDETTTKAFSGYSMFQNLI---VGGQ-TP-DGK--DATNELSYM
CLEATGSL-KLPQPSLCVRIW-SKTPDEFLIRTCELTR-LGTGLPAFYN-DEVVIPTLIN
--------Q------G---LTIEDARDYAIV-GCVE------------------PQKPGK
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-TDG-W----YDAAFFNL--AKILELSMNNGR-----LNGR-QV----------GP-ETG
EFT--SFKNIDDFINAYKKQIEYFVFHMVAADNCVDIAHAERAPL--PFLSSMLDDCIGT
GKSIQE----GGGHY-----RFSGPL-GVGIANVGDSFMAIKKLIFDENKI-TLLKLK--
----------SAVDSNFG------------ENEDDPIKKAEY------------------
-------------------------EDIKQL-----------------------------
------------ILNR--VPKFGNDIDEVDEFTRDGALIYCKEV-LKY--TNQ--R----
--GGKFIPGLYPVSN-NVYLGSLVGATPDGRSAFKPLAD-GVSPTRGADVNGPTAAANS-
-VSKLEH-FAAPS-------------GTLFNQKFNPNSLQGDNG--LKNLGSLIRSYFD-
----RKGMHIQFNVIDKKVLVEAQKHPEQYRDLIVRVAGYSAQFICLDKGVQDDIIKRTE
QNL------------
>gi|28210647|ref|NP_781591.1| formate acetyltransferase 2 [Clostridium tetani E88]
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------------------------------------------------------------
-------------------------------------------------------MSFLE
KGFSESTDRVK-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------EQI-FS-AVPC-VEADRAILL
TESFKET-EDQ-PII------IR----KAKALEKILNEIPIVIRDG-ELIVGSLTKN-PR
SAQVFPEFS--NKWLVEEFDK---LNKRTSD--A--------------------------
---FEISDEAKSQLI--EVFKYW-----EGKTVSELATSY---MTD--------------
-DTIDAM----------------NAKVFTVAN--YHFNGL--------------------
------GHISVDYEKVL--KKGFSGIIKEVNETINNADK-------NNPEYI---KQRRF
WDAIIISCEAAISYAKRYSQLAKELAQKE-TNATRKDELLNISKICEKVPEKPATTFQEA
CQSFWFVQAIISLESNGHA--ISPARFDQYMYPYFKHDID-L--HPKNRES-----AREI
LHCLWVKFND-LTKV-RDETTTKAFSGYSMFQNLI---VGGQ-TP-EGK--DATNELSYM
CMDATGTL-MLPQPSLSVRIW-SKAPEEFLIRSCELTR-LGTGLPAFYN-DEVIIPMLVN
--------H------G---LTLEDARDYAIV-GCVE------------------PQKPGK
-TDG-W----YDAAFFNM--AKVLEMTINNGK-----VDGK-QI----------GP-KTG
EFT--SFSNIDEFIEAYKKQTEYFVSYMVSADNCVDIAHAERAPL--PFLSCMLDDCISK
GKSIQE----GGGHY-----RFSGPL-GVGIANIGDSFMAIKKLVFDEKKL-TLNEIK--
----------EAIDTNYG------------------------------------------
-------------EFEENPEKKIKYKDIQQM-----------------------------
------------LLNR--APKFGNDIDEVDEYTRLGALIYCKEV-EKH--TNQ--R----
--GGQFIPGLYPVSN-NVHLGTLVSATPDGRGAKKPLAD-GVSPTRGVDVNGPTAAANS-
-VAKLEH-FCAPS-------------GTLFNQKFSPSSLQGDNG--LKNLASLIRSYFD-
----QKGMHMQFNVVDKNVLIDAQKRPEQYRDLIVRVAGYSAQFICLDNAIQDDIIKRTE
QSF------------
>gi|219667304|ref|YP_002457739.1| pyruvate formate-lyase [Desulfitobacterium
hafniense DCB-2]
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------------------------------------------------------------
-------------------------------------------------MYNVVFMKDKG
KKQEQVSERIR-------------------------------------------------
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---------------------------ALR---------EEI-VA-TVPE-IFMDRALLV
TESYEET-FGS-SYI------YR----RAKALEKVLLNMDICINDK-ELIVGSYAGK-PR
GCQVFPEYD--MKFLVDEMDE---FALRQAD--K--------------------------
---FTISEDNKAIAR--QIYEKW-----KGNTITDQALNL---FPE--------------
-EAAKAS----------------QQLIFLLTC---LGSGI--------------------
------GHMLVNYEKVI--QKGLAGFMLEIEELENGLDI-------CDPEYN---DKKTY
YQSLTIVCQAVCKFAGRFSLLALAQAEKT-ADPQRKEELLQIAENCRRVPAQPAQNFWQA
LQALWFVQLVLHLESNGHS--VSPGRFDQYMYPYYAAETD--------KDA-----CEEL
LHCLWLKFFE-LNKI-RNKVSSVVFGGYPMFQNIV---VGGQ-NA-NGE--SAVNELSHL
CLEATAKV-HLPQPSLSVRWF-YGCPEEFIRHALEVVS-YGTGMPALFN-DEVIIPNMLQ
--------L------G---YTIEEARDYAII-GCTE------------------MNVPHK
TEPF------LTGGFLNI--LKILELTIFDGF---DPVSQT-QQ----------AF-QSG
CVE--SFTTFEEFQKAYYEQLSYYLRQHVTCDNILDALHGKICPT--PFESMLLSDCLEN
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GKSNLE----GGARY-----NTTTLQ-LVGMANVADSLATIKKLIYVEKSL-TWNQLK--
----------AALQNNYE------------------------------------------
-----------------------DDELLRQR-----------------------------
------------IINH--VPKYGNDHDFVDRLGRDVVYHCCREA-AKY--RSP--R----
--NGTYNIAVYTLAT-NVLWASKVGATPDGRKMGSVLADGGVSCSHGMDKNGLTALFNS-
-VRKIDP-YKPLG-------------SALLNIRLSPSSFNETD---FQKTVDVVKSFFM-
----NKGQHVQFNVFDVNALRDAQKNPEKYPLLMVRVAGFSVLFTTIETILQEDIINRTL
HSSH-----------
>gi|82778873|ref|YP_405222.1| putative formate acetyltransferase 2 [Shigella
dysenteriae Sd197]
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------------------------------------------------------------
-----MTNRIS-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------TAL---FANTREISLERARLY
TASHRQT-EGE-PVI------LR----RAKATAYILEHVEISIRDE-ELIAGNRTVK-LR
AGIMSPEMD--PYWLLKELDQ---FPTRPQD--R--------------------------
---FAISEEDKRIYR-EELFPYW-----EKRSMKDFINGQ---MTD--------------
-EVKAAT----------------STQIFSINQ---TDKGQ--------------------
------GHIIIDYPRLL--NHGLGELVAQMQQHCQQQ------------------PENHF
YQAALLLLEASQKHILRYAELAETMAASC-TDAQRREELLTIAEISRHNAEHKPQTFWQA
CQLFWYMNIILQYESNASS--LSLGRFDQYMLPFYQASLT----QGEDPAF-----LKEL
LESLWVKCND-IVLL-RSTSSARYFAGFPTGYTAL---LGGL-TE-NGR--SAVNVLSFL
CLDAYQSV-QLPQPNLGVRTN-ALIDTPFLMKTAETIR-LGTGIPQIFN-DEVVVPAFLN
--------R------G---VSLEDARDYSVV-GCVE------------------LSIPGR
-TYGL-----HDIAMFNL--LKVMEICLHENE----------------------GN----
-----AALTYEGLLEQIRAKISHYITLMVEGSNICDIGHRDWAPV--PLLSSFISDCLEK
GRDITD----GGARY-----NFSGVQ-GIGIANLSDSLHALKGMVFDQQRL-SFDELL--
----------SVLKANFA------------------TLEG--------------------
-------------------------EKVRAR-----------------------------
------------LINR--FEKYGNDIDEVDNISAELLRHYCKEV-EKY--QNP--R----
--GGYFTPGSYTVSA-HVPLGSVVGATPDGRFAGEQLADGGLSPMLGQDTQGPTAVLKS-
-VSKLDN-TLLSN-------------GTLLNVKFTPATLEGEAG--LRKLADFLRAFTQ-
----LKLQHIQFNVVNADTLREAQQRPQDYAGLVVRVAGYSAFFVELSKEIQDDIIRRTA
HQL------------
>gi|91213499|ref|YP_543485.1| putative formate acetyltransferase 2 [Escherichia coli
UTI89]
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------------------------------------------------------------
-----MTNRIS-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------TAL---FANTREISLERALLY
TASHRQT-EGE-PVI------MR----RAKATAYILEHVEISIRDE-ELIAGNRTVK-PR
AGIMSPEMD--PYWLLKELDQ---FPTRPQD--R--------------------------
---FAISEEDKRIYR-EELFPYW-----EKRSMKDFINGQ---MTD--------------
-EVKAAT----------------STQIFSINQ---TDKGQ--------------------
------GHIIIDYPRLL--NHGLGELVAQMQQHCQQQ------------------PENHF
YQAALLLLEASQKHILRYAELAETMAASC-TDGQRREELLTIAEISRHNAEHKPQTFWQA
CQLFWYMNIILQYESNASS--LSLGRFDQYMLPFYQTSLT----QGEDPAF-----LKEL
LESLWVKCND-IVLL-RSTSSARYFAGFPTGYTAL---LGGL-TE-NGR--SAVNVLSFL
CLDAYQSV-QLPQPNLGVRTN-ALIDTPFLMKTAETIR-LGTGIPQIFN-DEVVVPAFLN
--------R------G---VSLEDARDYSVV-GCVE------------------LSIPGR
-TYGL-----HDIAMFNL--LKVMEICLHENE----------------------GN----
-----AALTYEGLLEQIRAKISHYITLMVEGSNICDIGHRDWAPV--PLLSSFISDCLEK
GRDITD----GGARY-----NFSGVQ-GIGIANLSDSLHALKGMIFDQQRL-SFDELL--
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----------SVLKANFA------------------TPEG--------------------
-------------------------EKVRAR-----------------------------
------------LINR--FEKYGNDIDEVDNISAELLRHYCKEV-EKY--QNP--R----
--GGYFTPGSYTVSA-HVPLGSVVGATPDGRFAGEQLADGGLSPMLGQDAQGPTAVLKS-
-VSKLDN-TLLSN-------------GTLLNVKFTPATLEGEAG--LRKLADFLRAFTQ-
----LKLQHIQFNVVNADTLREAQQRPQDYAGLVVRVAGYSAFFVELSKEIQDDIIRRTA
HQL------------
>gi|218551058|ref|YP_002384849.1| putative formate acetyltransferase 2 [Escherichia fergusonii ATCC 35469]
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------------------------------------------------------------
-----MTNRIS-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------TAL---FANTREISLERALLY
TASHRQT-EGE-PVI------LR----RAKATAYILEHVEISIRDE-ELIAGNRTVK-PR
AGIMSPEMD--PYWLLKELDQ---FPTRPQD--R--------------------------
---FAISEEDKRIYR-EELFPYW-----EKRSMKDFINGQ---MTD--------------
-EVKAAT----------------STQIFSINQ---TDKGQ--------------------
------GHIIIDYPRLL--NHGLGELVAQMQQHCQQQ------------------PENHF
YQAALLLLEASQKHILRYAELAETMAANC-TDAQRREELLTIAEISRHNAEHKPQTFWQA
CQLFWYMNIILQYESNASS--LSLGRFDQYMLPFYQASLT----QGEDPAF-----LKEL
LESLWVKCND-IVLL-RSTSSARYFAGFPTGYTAL---LGGL-TE-NGR--SAVNVLSFL
CLDAYQSV-QLPQPNLGVRTN-ALIDTPFLMKTAETIR-LGTGIPQIFN-DEVVVPAFLN
--------R------G---VSLEDARDYSVV-GCVE------------------LSIPGR
-TYGL-----HDIAMFNL--LKVMEICLHENE----------------------GN----
-----AALSYEGLLGQIRAKISHYITLMVEGSNICDIGHRDWAPV--PLLSSFISDCLEK
GRDITD----GGARY-----NFSGVQ-GIGIANLSDSLHALKGMVFEQQRL-SFDELL--
----------SVLKANFA------------------TPEG--------------------
-------------------------EKVRAR-----------------------------
------------LINR--FEKYGNDIDEVDNISAELLRHYCKEV-EKY--QNP--R----
--GGYFTPGSYTVSA-HVPLGAVVGATPDGRFAGEQLADGGLSPMLGQDAQGPTAVLKS-
-VSKLDN-TLLSN-------------GTLLNVKFTPATLEGEAG--LRKLADFLRAFTQ-
----LKLQHIQFNVVNADTLREAQQRPQDYAGLVVRVAGYSAFFVELSKEIQDDIIRRTA
HQL------------
>gi|209921435|ref|YP_002295519.1| putative formate acetyltransferase 2 [Escherichia coli SE11]
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------------------------------------------------------------
-----MTNRIS-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------TAL---FANTREISLERALLY
TASHRQT-EGE-PVI------LR----RAKATAYILEHVEISIRDE-ELIAGNRTVK-PR
AGIMSPEMD--PYWLLKELDQ---FPTRPQD--R--------------------------
---FAISEEDKRIYR-EELFPYW-----EKRSMKDFINGQ---MTD--------------
-EVKAAT----------------STQIFSINQ---TDKGQ--------------------
------GHIIIDYPRLL--NHGLGELVAQMQQHCQQQ------------------PENHF
YQAALLLLEASQKHILRYAELAETMAANC-TDAQRREELLTIAEISRHNAEHKPQTFWQA
CQLFWYMNIILQYESNASS--LSLGRFDQYMLPFYQASLT----QGEDPAF-----LKEL
LESLWVKCND-IVLL-RSTSSARYFAGFPTGYTAL---LGGL-TE-NGR--SAVNVLSFL
CLDAYQSV-QLPQPNLGVRTN-ALIDTPFLMKTAETIR-LGTGIPQIFN-DEVVVPAFLN
--------R------G---VSLEDARDYSVV-GCVE------------------LSIPGR
-TYGL-----HDIAMFNL--LKVMEICLHENE----------------------GN----
-----ATLTYEGLLEQIRAKISHYITLMVEGSNICDIGHRDWAPV--PLLSSFISDCLEK
GRDITD----GGARY-----NFSGVQ-GIGIANLSDSLHALKGMVFDQQRL-SFDELL--
----------SVLKANFA------------------TPEG--------------------
```

```
-------------------------EKVRAR-----------------------------
------------LINR--FEKYGNDIDEVDNISAELLRHYCKEV-EKY--QNP--R----
--GGYFTPGSYTVSA-HVPLGSVVGATPDGRFAGEQLADGGLSPMLGQDAQGPTAVLKS-
-VSKLDN-TLLSN-------------GTLLNVKFTPATLEGEAG--LRKLADFLRAFTQ-
----LKLQHIQFNVVNADTLREAQQRPQDYAGLVVRVAGYSAFFVELSKEIQDDIIRRTA
HQL------------
>gi|150388343|ref|YP_001318392.1| pyruvate formate-lyase [Alkaliphilus
metalliredigens QYMF]
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--------------------------------------------------MKNVVTYNEK
ELRRSMTPRIE-------------------------------------------------
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---------------------------AMR---------KEI-VH-SKPI-LCSERALLV
TEAYAET-EAL-PSV------TR----RAFALKKILGNMTQNIFEG-ELIVGSHGSNGRR
SAPVFPEFS--TKWLEEELDE--ILETRTQD--T--------------------------
---FIVPKNVKEDLK--DIFPYW-----RGKTIHDRYRAM---LPD--------------
-ETKRAR----------------DAYMFTRGL--FEQNGY--------------------
------GHTAYDIPKLL--KVGLVGIKSEVNEKMQTLDL-------TTSEGL---EKKLF
YEGLIVCCDSVIAYAKRYAQRALELADQE-KNPVRKKELEKIADVCQWVPENPARDTWDA
IQVVAFMQLIIQTETNGDS--VCPGRLDQYLYSYYKNDMA-E--GRYTIDE-----IQEL
LDCLWIKLNE-IIKI-QASESVRIHPGFPMTPTVT---IGGQ-TP-EGE--DATNELSYL
MLNSQEHI-RLTNPQFTVRFH-KDTPEDFKLRVVEVVK-LGTGMPAMFG-DEACIAALKR
---------------GCPDMPMERIRDYRIV-GCVELAP---------------RGFQGR
----------VNGGFLNV--ARVVDLALNNGV---DRLTNE-QI----------GP-QTG
APE--DLKDFDDVLTAVRTQTAYFVKHQVINAAVVDMVQREHTPH--LFLSSLVEGCIEN
GKDMTQ----GGSLW-----GGTPIL-HVGEATAADSLIGVKKAVFDDQLI-SMKELK--
----------EILDSNFA---------------------GAQ------------------
------------------------GEKIYQ------------------------------
------------ALLA--MPKYGNDDDYADEVMQKMINIFFDEI-EKH--KDI--D----
--GRFYTSTILTLGA-TVPHGWTTGATANGRKATMPVAD-SMSASNGADKEGPTAMLLS-
-ASKIDQ-TRTIE-------------GNVVNLKFTKMALEEKKN--LQQLVNLVSVYFDD
----LKGQEIQVNVVDESTLKDAQEYPEKHQDLIIRVAGYSARFTELAKELQDDIIRRTE
YNTL-----------
>gi|218701339|ref|YP_002408968.1| putative formate acetyltransferase 2 [Escherichia
coli IAI39]
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------------------------------------------------------------
-----MTNRIS-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------TAL---FANTREISLERALLY
TASHRQT-EGE-PVI------LR----RAKATAYILEHVEISIRDE-ELIAGNRTVK-PR
AGIMSPEMD--PYWLLKELDQ---FPTRPQD--R--------------------------
---FAISEEDKRIYR-EELFPYW-----EKRSMKDFINGQ---MTD--------------
-EVKAAT----------------STQIFSINQ---TDKGQ--------------------
------GHIIIDYPRLL--NHGLGELVAQMQQHCQQQ------------------PENHF
YQAALLLLEASQKHILRYAELAETMAANC-TDAQRRKELLTIAEISRHNAQHKPQTFWQA
CQLFWYMNIILQYESNASS--LSLGRFDQYMLPFYQASLT----QGEDPAF-----LKEL
LESLWVKCND-IVLL-RSTSSARYFAGFPTGYTAL---LGGL-TE-NGR--SAVNVLSFL
CLDAYQSV-QLPQPNLGVRTN-ALIDTPFLMKTAETIR-LGTGIPQIFN-DEVVVPAFLN
--------R------G---VSLEDARDYSVV-GCVE------------------LSIPGR
-TYGL-----HDIAMFNL--LKVMEICLHENE----------------------GN----
-----AALTYEGLLEQIRAKISHYITLMVEGSNICDIGHRDWAPV--PLLSSFISDCLEK
GRDITD----GGARY-----NFSGVQ-GIGIANLSDSLHALKGMVFEQQRL-SFDELL--
----------SVLKANFA------------------TPEG--------------------
-------------------------EKVRAR-----------------------------
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------------LINR--FEKYGNDIDEVDNISAELLRHYCKEV-EKY--QNP--R----
--GGYFTPGSYTVSA-HVPLGSVVGATPDGRFAGEQLADGGLSPMLGQDAQGPTAVLKS-
-VSKLDN-TLLSN-------------GTLLNVKFTPATLEGEAG--LRKLADFLRAFTQ-
----LKLQHIQFNVVNADTLREAQQRPQDYAGLVVRVAGYSAFFVELSKEIQDDIIRRTA
HQL------------
>gi|157163428|ref|YP_001460746.1| putative formate acetyltransferase 2 [Escherichia
coli HS]
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------------------------------------------------------------
-----MTNRIS-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------TAL---FANTREISLERALLY
TASHRQT-EGE-PVI------LR----RAKATAYILEHVEISIRDE-ELIAGNRTVK-PR
AGIMSPEMD--PYWLLKELDQ---FPTRPQD--R--------------------------
---FAISEEDKRIYR-EELFPYW-----EKRSMKDFINGQ---MTD--------------
-EVKAAT----------------STQIFSINQ---TDKGQ--------------------
------GHIIIDYPRLL--NHGLGELVAQMQQHCQQQ------------------PENHF
YQAALLLLEASQKHILRYAELAETMAANC-TDAQRREELLTIAEISRHNAQHKPQTFWQA
CQLFWYMNIILQYESNASS--LSLGRFDQYMLPFYQTSLT----QGEDAAF-----LKEL
LESLWVKCND-IVLL-RSTSSARYFAGFPTGYTAL---LGGL-TE-NGR--SAVNVLSFL
CLDAYQSV-QLPQPNLGVRTN-ALIDTPFLMKTAETIR-LGTGIPQIFN-DEVVVPAFLN
--------R------G---VSLEDARDYSVV-GCVE------------------LSIPGR
-TYGL-----HDIAMFNL--LKVMEICLHENE----------------------GN----
-----AALTYEGLLEQIRAKISHYITLMVEGSNICDIGHRDWAPV--PLLSSFISDCLEK
GRDITD----GGARY-----NFSGVQ-GIGIANLSDSLHALKGMVFDQQRL-SFDELL--
----------SVLKANFA------------------TPEG--------------------
-------------------------EKVRAR-----------------------------
------------LINR--FEKYGNDIDEVDNISAELLRHYCKEV-EKY--QNP--R----
--GGYFTPGSYTVSA-HVPLGSVVGATPDGRFAGEQLADGGLSPMLGQDAQGPTAVLKS-
-VSKLDN-TLLSN-------------GTLLNVKFTPATLEGEAG--LRKLADFLRAFTQ-
----LKLQHIQFNVVNADTLREAQQRPQDYAGLVVRVAGYSAFFVELSKEIQDDIIRRTA
HQL------------
>gi|218707578|ref|YP_002415097.1| putative formate acetyltransferase 2 [Escherichia
coli UMN026]
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------------------------------------------------------------
-----MTNRIS-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------TAL---FANTREISLERALLY
TASHRQT-EGE-PVI------LR----RAKATAYILEHVEISIRDE-ELIAGNRTVK-PR
AGIMSPEMD--PYWLLKELDQ---FPTRPQD--R--------------------------
---FAISEEDKRIYR-EELFPYW-----EKRSMKDFINGQ---MTD--------------
-EVKAAT----------------STQIFSINQ---TDKGQ--------------------
------GHIIIDYPRLL--NHGLGELVAQMQQHCQQQ------------------PENHF
YQAALLLLEASQKHILRYAELAETMAANC-TDAQRREELLTIAEISRHNAQHKPQTFWQA
CQLFWYMNIILQYESNASS--LSLGRFDQYMLPFYQASLT----QGEDPAF-----LKEL
LESLWVKCND-IVLL-RSTSSARYFAGFPTGYTAL---LGGL-TE-NGR--SAVNVLSFL
CLDAYQSV-QLPQPNLGVRTN-ALIDTPFLMKTAETIR-LGTGIPQIFN-DEVVVPAFLN
--------R------G---VSLEDARDYSVV-GCVE------------------LSIPGR
TYGL------HDIAMFNL--LKVMEICLHENE----------------------GN----
-----AALTYEGLLEQIRAKISHYITLMVEGSNICDIGHRDWAPV--PLLSSFISDCLEK
GRDITD----GGARY-----NFSGVQ-GIGIANLSDSLHALKGMVFEQQRL-SFDELL--
----------SVLKANFA------------------TPEG--------------------
-------------------------EKVRAR-----------------------------
------------LINR--FEKYGNDIDEVDNISAELLRHYCKEV-EKY--QNP--R----
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--GGYFTPGSYTVSA-HVPLGSVVGATPDGRFAGEQLADGGLSPMLGQDAQGPTAVLKS-
-VSKLDN-TLLSN-------------GTLLNVKFTPATLEGEAG--LRKLADFLRAFTQ-
----LKLQHIQFNVVNADTLREAQQRPQDYAGLVVRVAGYSAFFVELSKEIQDDIIRRTA
HQL------------
>gi|110644291|ref|YP_672021.1| putative formate acetyltransferase 2 [Escherichia
coli 536]
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------------------------------------------------------------
-----MTNRIS-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------TAL---FANTREISLERALLY
TASHRQT-EGE-PVI------MR----RAKATAYILEHVEISIRDE-ELIAGNRTVK-PR
AGIMSPEMD--PYWLLKELDQ---FPTRPQD--R--------------------------
---FAISEEDKRIYR-EELFPYW-----EKRSMKDFINGQ---MTD--------------
-EVKAAT----------------STQIFSINQ---TDKGQ--------------------
------GHIIIDYPRLL--NHGLGELVAQMQQHCQQQ------------------PENHF
YQAALLLLEASQKHILRYAELAETMAASC-TDGPRREELLTIAEISRHNAEHKPQTFWQA
CQLFWYMNIILQYESNASS--LSLGRFDQYMLPFYQTSLT----QGEDPAF-----LKEL
LESLWVKCND-IVLL-RSTSSARYFAGFPTGYTAL---LGGL-TE-NGR--SAVNVLSFL
CLDAYQSV-QLPQPNLGVRTN-ALIDTPFLMKTAETIR-LGTGIPQIFN-DEVVVPAFLN
--------R------G---VSLEDARDYSVV-GCVE------------------LSIPGR
TYGL------HDIAMFNL--LKVMEICLHENE----------------------GN----
-----AALTYEGLLEQIRAKISHYITLMVEGSNICDIGHRDWAPV--PLLSSFISDCLEK
GRDITD----GGARY-----NFSGVQ-GIGIANLSDSLHALKGMIFDQQRL-SFDELL--
----------SVLKANFA------------------TPEG--------------------
-------------------------EKVRAR-----------------------------
------------LINR--FEKYGNDIDEVDNISAELLRHYCKEV-EKY--QNP--R----
--GGYFTPGSYTVSA-HVPLGSVVGATPDGRFAGEQLADGGLSPMLGQDAQGPTAVLKS-
-VSKLDN-TLLSN-------------GTLLNVKFTPATLEGEAG--LRKLADFLRAFTQ-
----LKLQHIQFNVVNADTLREAQQRPQDYAGLVVRVAGYSAFFVELSKEIQDDIIRRTA
HQL------------
>gi|206577165|ref|YP_002239374.1| formate C-acetyltransferase 2 [Klebsiella
pneumoniae 342]
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------------------------------------------------------------
-----MTNRTQ-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------ASL---FAQPREISLERALLY
TASHRQT-EGE-PVI------IR----RAKATAWILDKVMISIRED-ELIAGNRTVK-PR
AGIMSPEMD--PYWLLNELDA---FPTRPQD--R--------------------------
---FAISEEDKQIYR-EALYPYW-----EKRSMKDFINGQ---MTE--------------
-EVKAAV----------------NTQIFSVNQ---TDKGQ--------------------
------GHIIIDYPRLL--NHGLGALVAELKTHCARQ------------------PENPF
YQAVLILLEASQRHILRYAALAEEMAGHF-QDPQRQQELLTIAAISRHNAQHRPTDFPQA
CQLFWYMNIILQYESNASS--ISLGRFDQYMLPFYQASLN----QGQDPAY-----LKEL
LESLWVKCND-IVLL-RSSSSARYFAGFPTGYTAL---LGGL-TD-TGR--SAVNELSFL
CLDAYQNV-QLPQPNLGVRVN-ELIDRPFLRKTAETIR-LGTGIPQIFN-DEVVVPAFLN
--------R------G---VSLEDARDYAVV-GCVE------------------LSIPGR
-TYGL-----HDIAMFNL--LKVMEIVLQENE-------------------------HQP
DVT------WDGLICQIRDKIRHYIKLMVEGSNICDIGHRDWAPV--PLLSSFIEDCVQH
GKDITA----GGARY-----NFSGVQ-GIGIANLSDSLYALKGMVFDQQRL-SFDQLM--
----------AVLKANFQ------------------TPEG--------------------
-------------------------EKIRAR-----------------------------
------------LINH--FDKYGNDIDDVDNISADLLRFYCKEV-EQY--LNP--R----
--GGHFTPGSYTVSA-HVPLGSVVGATPDGRLAGEQLADGGLSPMVGQDSQGPTAVLKS-
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-VSKLDN-YLLSN-------------GTLLNVKFTPATLAGDGG--LNKLADFLQAFCK-
----LKLQHIQFNVVNADTLREAQQRPQDFAGLVVRVAGYSAFFVELSKEIQDDIIRRTA
HQL------------
>gi|170680527|ref|YP_001746343.1| formate C-acetyltransferase 2 [Escherichia coli
SMS-3-5]
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------------------------------------------------------------
------------------------------------------------------------
-----MTNRIS-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------TAL---FANTREISLERALLY
TASHRQT-EGE-PVI------LR----RAKATAYILEHVEISIRDE-ELIAGNRTVK-PR
AGIMSPEMD--PYWLLKELDQ---FPTRPQD--R--------------------------
---FAISEEDKRIYR-EELFPYW-----EKRSMKDFINGQ---MTD--------------
-EVKAAT----------------STQIFSINQ---TDKGQ--------------------
------GHIIIDYPRLL--NHGLGELVAQMQQHCQQQ------------------PENHF
YQAALLLLEASQKHILRYAELAETMAASC-TDGQRREELLTIAEISRHNAEHKPQTFWQA
CQLFWYMNIILQYESNASS--LSLGRFDQYMLPFYQASLT----QGEDPAF-----LKEL
LESLWVKCND-IVLL-RSTSSARYFAGFPTGYTAL---LGGL-TE-NGR--SAVNVLSFL
CLDAYQSV-QLPQPNLGVRTN-ALIDTPFLMKTAETIR-LGTGIPQIFN-DEVVVPAFLN
--------R------G---VSLEDARDYSVV-GCVE------------------LSIPGR
-TYGL-----HDIAMFNL--LKVMEICLHENE----------------------GN----
-----AALTYEGLLEQIRAKISHYITLMVEGSNICDIGHRDWAPV--PLLSSFISDCLEK
GRDITD----GGARY-----NFSGVQ-GIGIANLSDSLHALKGMVFEQQRL-SFDELL--
----------SVLKANFA------------------TPEG--------------------
-------------------------EKVRAR-----------------------------
------------LINR--FEKYGNDIDEVDNISAELLRHYCKEV-EKY--QNP--R----
--GGYFTPGSYTVSA-HVPLGSVVGATPDGRFAGEQLADGGLSPMLGQDAQGPTAVLKS-
-VSKLDN-TLLSN-------------GTLLNVKFTPATLEGEAG--LRKLADFLRAFTQ-
----LKLQHIQFNVVNADTLREAQQRPQDYAGLVVRVAGYSAFFVELSKEIQDDIIRRTA
HQL------------
>gi|24115241|ref|NP_709751.1| putative formate acetyltransferase 2 [Shigella
flexneri 2a str. 301]
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------------------------------------------------------------
-----MTNRIS-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------TAL---FANTREISLERALLY
TASHRQT-EGE-PVI------LR----RAKATAYILEHVEISIRDE-ELIAGNRTVK-PR
AGIMSPEMD--PYWLLKELDQ---FPTRPQD--R--------------------------
---FAISEEDKRIYR-EELFPYW-----EKRSMKDFINGQ---MTD--------------
-EVKAAT----------------NTQIFSINQ---TDKGQ--------------------
------GHIIIDYPRLL--NHGLGELVAQMQQHCQQQ------------------PENHF
YQAALLLLEASQKHILRYAELAETMAANC-TDAQRREELLTIAEISRHNAQHKPQTFWQA
CQLFWYMNIILQYESNASS--LSLGRFDQYMLPFYQASLT----QGEDPAF-----LKEL
LESLWVKCND-IVLL-RSTSSARYFAGFPTGYTAL---LGGL-TE-NGR--SAVNVLSFL
CLDAYQSV-QLPQPNLGVRTN-ALIDTPFLMKTAETIR-LGTGIPQIFN-DEVVVPAFLN
--------R------G---VSLEDARDYSVV-GCVE------------------LSIPGR
-TYGL-----HDIAMFNL--LKVMEICLHENE----------------------GN----
-----AALTYEGLLEQIRAKISHYITLMVEGSNICDIGHRDWAPV--PLLSSFISDCLEK
GRDITD----GGARY-----NFSGVQ-GIGIANLSDSLHALKGMVFEQQRL-SFDELL--
----------SVLKANFA------------------TPEG--------------------
-------------------------EKVRAR-----------------------------
------------LINR--FEKYGNDIDEVDNISAELLRHYCKEV-EKY--QNP--R----
--GGYFTPGSYTVSA-HVPLGSVVGATPDGRFAGEQLADGGLSPMLGQDAQGPTAVLKS-
-VSKLDN-TLLSN-------------GTLLNVKFTPATLEGEAG--LRKLADFLRVFTQ-
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----LKLQHIQFNVVNADTLREAQQRPQDYAGLVVRVAGYSAFFVELSKEIQDDIIRRTA
HQL------------
>gi|26250724|ref|NP_756764.1| putative formate acetyltransferase 2 [Escherichia coli
CFT073]
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------------------------------------------------------------
-----MTNRIS-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------TAL---FANTREISLERALLY
TASHRQT-EGE-PVI------MR----RAKATAYILEHVEISIRDE-ELIAGNRTVK-PR
AGIMSPEMD--PYWLLKELDQ---FPTRPQD--R--------------------------
---FAISEEDKRIYR-EELFPYW-----EKRSMKDFINGQ---MTD--------------
-EVKAAT----------------STQIFSINQ---TDKGQ--------------------
------GHIIIDYPRLL--NHGLGELVAQMQQHCQQQ------------------PENHF
YQAALLLLEASQKHILRYAELAETMAASC-TDGPRREELLTIAEISRHNAEHKPQTFWQA
CQLFWYMNIILQYESNASS--LSLGRFDQYMLPFYQASLT----QGEDPAF-----LKEL
LESLWVKCND-IVLL-RSTSSARYFAGFPTGYTAL---LGGL-TE-NGR--SAVNVLSFL
CLDAYQSV-QLPQPNLGVRTN-ALIDTPFLMKTAETIR-LGTGIPQIFN-DEVVVPAFLN
--------R------G---VSLEDARDYSVV-GCVE------------------LSIPGR
-TYGL-----HDIAMFNL--LKVMEICLHENE----------------------GN----
-----AALTYEGLLEQIRAKISHYITLMVEGSNICDIGHRDWAPV--PLLSSFISDCLEK
GRDITD----GGARY-----NFSGVQ-GIGIANLSDSLHALKGMIFDQQRL-SFDELL--
----------SVLKANFA------------------TPEG--------------------
-------------------------EKVRAR-----------------------------
------------LINR--FEKYGNDIDEVDNISAELLRHYCKEV-EKY--QNP--R----
--GGYFTPGSYTVSA-HVPLGSVVGATPDGRFAGEQLADGGLSPMLGQDAQGPTAVLKS-
-VSKLDN-TLLSN-------------GTLLNVKFTPATLEGEAG--LRKLADFLRAFTQ-
----LKLQHIQFNVVNADTLREAQQRPQDYAGLVVRVAGYSAFFVELSKEIQDDIIRRTA
HQL------------
>gi|16767379|ref|NP_462994.1| putative formate acetyltransferase 2 [Salmonella
typhimurium LT2]
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------------------------------------------------------------
-----MTHRIQ-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------AAL-FQ-NHRE-ISLERALLY
TASHQQT-EGE-PVI------LR----RAKATAYILEHVEISIRDE-ELIAGNRTVK-PR
AGIMSPEMD--PYWLLNELDR---FPTRPQD--R--------------------------
---FDISEEDKRLYR-EVLFPYW-----EKRSMKDFINGQ---MTD--------------
-EVKAAV----------------STQIFSINQ---TDKGQ--------------------
------GHIIIDYPRLL--NNGLGELAAQMRARCEQQ------------------PENDF
YQAALLLLEASQRHILRYAVLAEQQAERC-PDARRRQELLTIAANSRHNAQHKPQTFWQA
CQLFWYMNIILQYESNASS--LSLGRFDQYMLPFYQTSLT----QGDDPAF-----LKEL
LESLWVKCND-IVLL-RSTSSARYFAGFPTGYTAL---LGGL-TE-SGR--SAVNVLSFL
CLDAYQSV-QLPQPNLGVRTN-ALIDTPFLLKTAETIR-LGTGIPQIFN-DEVVVPAFLN
--------R------G---VSLEDARDYAVV-GCVE------------------LSIPGR
-TYGL-----HDIAMFNL--LKVMEISLYENE----------------------GN----
-----DTLTYEALLAHIRAKISHYITLMVEGSNICDIGHRDWAPV--PLLSSFISDCLEK
GRDITD----GGARY-----NFSGVQ-GIGIANLSDSLHALNGLVFDQQRL-SFDALL--
----------SILKNNFA------------------TPEG--------------------
-------------------------EKIRAR-----------------------------
------------LINR--FEKYGNDIDNVDNISAELLRYYCKEV-EKY--QNP--R----
--GGQFTPGSYTVSA-HVPLGAVVGATPDGRFAGEQLADGGLSPMLGQDMQGPTAVLKS-
-VSKLDN-TLLSN-------------GTLLNVKFTPATLEGEAG--LRKLADFLRAFTQ-
----LKLQHIQFNVVNADTLREAQLRPQDFAGLVVRVAGYSAFFVELSKEIQDDIIRRTA
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HQL------------
>gi|157158917|ref|YP_001465448.1| putative formate acetyltransferase 2 [Escherichia coli E24377A]
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------------------------------------------------------------
-----MTNRIS-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------TAL---FANTREISLERALLY
TASHRQT-EGE-PVI------LR----RAKATAYILEHVEISIRDE-ELIAGNRTVK-PR
AGIMSPEMD--PYWLLKELDQ---FPTRPQD--R--------------------------
---FAISEEDKRIYR-EELFPYW-----EKRSMKDFINGQ---MTD--------------
-EVKAAT----------------STQIFSIN---QTDKGQ--------------------
------GHIIIDYPRLL--NHGLGELVAQMQQHCQQQ-------------------PENHF
YQAALLLLEASQKHILRYAELAETMAANC-TDAQRREELLTIAEISRHNAQHKPQTFWQA
CQLFWYMNIILQYESNASS--LSLGRFDQYMLPFYQTSLT----QGEDAAF-----LKEL
LESLWVKCND-IVLL-RSTSSARYFAGFPTGYTAL---LGGL-TE-NGR--SAVNVLSFL
CLDAYQSV-QLPQPNLGVRTN-ALIDTPFLMKTAETIR-LGTGIPQIFN-DEVVVPAFLN
--------R------G---VSLEDARDYSVV-GCVE-------------------LSIPGR
-TYG-L----HDIAMFNL--LKVMEICLYENE----------------------GN----
-----AALTYEGLLEQIRAKISHYITLMVEGSNICDIGHRDWAPV--PLLSSFISDCLEK
GRDITD----GGARY-----NFSGVQ-GIGIANLSDSLHALKGMVFEQQRL-SFDELL--
----------SVLKANFA------------------TPEG--------------------
-------------------------EKVRAR-----------------------------
------------LINR--FEKYGNDIDEVDNISAELLRHYCKEV-EKY--QNP--R----
--GGYFTPGSYTVSA-HVPLGSVVGATPDGRFAGEQLADGGLSPMLGQDAQGPTAVLKS-
-VSKLDN-TLLSN-------------GTLLNVKFTPATLEGEAG--LRKLADFLRAFTQ-
----LKLQHIQFNVVNADTLREAQQRPQDYAGLVVRVAGYSAFFVELSKEIQDDIIRRTA
HQL------------
>gi|198242547|ref|YP_002218043.1| formate C-acetyltransferase 2 [Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853]
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------------------------------------------------------------
-----MTHRIQ-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------AAL-FQ-NHRE-ISLERALLY
TASHQQT-EGE-PVI------LR----RAKATAYILEHVEISIRDE-ELIAGNRTVK-PR
AGIMSPEMD--PYWLLNELDR---FPTRPQD--R--------------------------
---FDISEEDKRLYR-EVLFPYW-----EKRSMKDFINGQ---MTD--------------
-EVKAAV----------------STQIFSIN---QTDKGQ--------------------
------GHIIIDYPRLL--NNGLGELAAQMRARCEQQ-------------------PENDF
YQAALLLLEASQRHILRYAVLAEHQAERC-PDARRRQELLTIAANSRHNAQHKPQTFWQA
CQLFWYMNIILQYESNASS--LSLGRFDQYMLPFYQTSLT----QGDDPAF-----LKEL
LESLWVKCND-IVLL-RSTSSARYFAGFPTGYTAL---LGGL-TE-SGR--SAVNVLSFL
CLDAYQSV-QLPQPNLGVRTN-ALIDTPFLLKTAETIR-LGTGIPQIFN-DEVVVPAFLN
--------R------G---VSLEDARDYAVV-GCVE-------------------LSIPGR
-TYG-L----HDIAMFNL--LKVMEISLYENE----------------------GN----
-----DTLTYEALLAHIRAKISHYITLMVEGSNICDIGHRDWAPV--PLLSSFISDCLEK
GRDITD----GGARY-----NFSGVQ-GIGIANLSDSLHALNGLVFDQQRL-SFDALL--
----------SILKNNFA------------------TPEG--------------------
-------------------------EKIRAR-----------------------------
------------LINR--FEKYGNDIDNVDNISAELLRYYCKEV-EKY--QNP--R----
--GGQFTPGSYTVSA-HVPLGAVVGATPDGRFAGEQLADGGLSPMLGQDMQGPTAVLKS-
-VSKLDN-TLLSN-------------GTLLNVKFTPATLEGEAG--LRKLADFLRAFTQ-
----LKLQHIQFNVVNADTLREAQLRPQDFAGLVVRVAGYSAFFVELSKEIQDDIIRRTA
HQL------------
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>gi|16131789|ref|NP_418386.1| predicted formate acetyltransferase 2 (pyruvate
formate lyase II) [Escherichia coli str. K-12 substr. MG1655]
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------------------------------------------------------------
-----MTNRIS-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------TAL---FANTREISLERALLY
TASHRQT-EGE-PVI------LR----RAKATAYILEHVEISIRDE-ELIAGNRTVK-PR
AGIMSPEMD--PYWLLKELDQ---FPTRPQD--R--------------------------
---FAISEEDKRIYR-EELFPYW-----EKRSMKDFINGQ---MTD--------------
-EVKAAT----------------NTQIFSIN---QTDKGQ--------------------
------GHIIIDYPRLL--NHGLGELVAQMQQHCQQQ------------------PENHF
YQAALLLLEASQKHILRYAELAETMAANC-TDAQRREELLTIAEISRHNAQHKPQTFWQA
CQLFWYMNIILQYESNASS--LSLGRFDQYMLPFYQTSLT----QGEDAAF-----LKEL
LESLWVKCND-IVLL-RSTSSARYFAGFPTGYTAL---LGGL-TE-NGR--SAVNVLSFL
CLDAYQSV-QLPQPNLGVRTN-ALIDTPFLMKTAETIR-FGTGIPQIFN-DEVVVPAFLN
--------R------G---VSLEDARDYSVV-GCVE------------------LSIPGR
-TYG-L----HDIAMFNL--LKVMEICLHENE----------------------GN----
-----AALTYEGLLEQIRAKISHYITLMVEGSNICDIGHRDWAPV--PLLSSFISDCLEK
GRDITD----GGARY-----NFSGVQ-GIGIANLSDSLHALKGMVFEQQRL-SFDELL--
----------SVLKANFA------------------TPEG--------------------
-------------------------EKVRAR-----------------------------
------------LINR--FEKYGNDIDEVDNISAELLRHYCKEV-EKY--QNP--R----
--GGYFTPGSYTVSA-HVPLGSVVGATPDGRFAGEQLADGGLSPMLGQDAQGPTAVLKS-
-VSKLDN-TLLSN-------------GTLLNVKFTPATLEGEAG--LRKLADFLRAFTQ-
----LKLQHIQFNVVNADTLREAQQRPQDYAGLVVRVAGYSAFFVELSKEIQDDIIRRTA
HQL------------
>gi|82546302|ref|YP_410249.1| putative formate acetyltransferase 2 [Shigella boydii
Sb227]
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------------------------------------------------------------
-----MTNRIS-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------TAL---FANTREISLERALLY
TASHRQT-EGE-PVI------LR----RAKATAYILEHVEISIRDE-ELIAGNRTVK-PR
AGIMSPEMD--PYWLLKELDQ---FPTRPQD--R--------------------------
---FAISEEDKRIYR-EELFPYW-----EKRSMKDFINGQ---MTD--------------
-EVKAAT----------------STQIFSINQ---TDKGQ--------------------
------GHIIIDYPRLL--NHGLGELVAQMQQHCQQQ------------------PENHF
YQAALLLLEASQKHILRYAVLAETMAANC-TDAQRREELLTIAEISRHNAEHKPQTFWQA
CQLFWYMNIILQYESNASS--LSLGRFDQYMLPFYQASLT----QGEDPAF-----LKEL
LESLWVKCND-IVLL-RSTSSARYFAGFPTGYTAL---LGGL-TE-NGR--SAVNVLSFL
CLDAYQSV-QLPQPNLGVRTN-ALIDTPFLMKTAETIR-LGTGIPQIFN-DEVVVPAFLN
--------R------G---VSLEDARDYSVV-GCVE------------------LSIPGR
-TYGL-----HDIAMFNL--LKVMEICLHENE----------------------GN----
-----AALTYEGLLEQIRAKISHYITLMVEGSNICDIGHRDWAPV--PLLSSFISDCLEK
GRDITD----GGARY-----NFSGVQ-GIGIANLSDSLHALKGMVFEQQRL-SFDELL--
----------SVLKANFA------------------TPEG--------------------
-------------------------EKVRAR-----------------------------
------------LINR--FEKYGNDIDEVDNISAELLRHYCKEV-EKY--QNP--R----
--GGYFTPGSYTVSA-HVPLGSVVGATPDGRFAGEQLADGGLSPMLGQDEQGPTAVLKS-
-VSKLDN-TLLSN-------------GTLLNVKFTPATLEGEAG--LRKLADFLRAFTQ-
----LKLQHIQFNVVNADTLWEAQQRPQDYAGLVVRVAGYSAFFVELSKEIQDDIIRRTA
HQL------------
>gi|161617256|ref|YP_001591221.1| putative formate acetyltransferase 2 [Salmonella
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enterica subsp. enterica serovar Paratyphi B str. SPB7]
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-----MTHRIQ-------------------------------------------------
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---------------------------RLK---------AAL-FQ-NHRE-ISLERALLY
TASHQQT-EGE-PVI------LR----RAKATAYILEHVEISIRDE-ELIAGNRTVK-PR
AGIMSPEMD--PYWLLNELDR---FPTRPQD--R--------------------------
---FDISEEDKRLYR-EVLFPYW-----EKRSMKDFINGQ---MTD--------------
-EVKAAV----------------STQIFSINQ---TDKGQ--------------------
------GHIIIDYPRLL--NNGLGELAAQMRARCEQQ------------------PENDF
YQAALLLLEASQRHILRYAVLAEQQAERC-PDARRRQELLTIAANSRHNAQHKPQTFWQA
CQLFWYMNIILQYESNASS--LSLGRFDQYMLPFYQTSFT----QGDDPAF-----LKEL
LESLWVKCND-IVLL-RSTSSARYFAGFPTGYTAL---LGGL-TE-SGR--SAVNVLSFL
CLDAYQSV-QLPQPNLGVRTN-ALIDTPFLLKTAETIR-LGTGIPQIFN-DEVVVPAFLN
--------R------G---VSLEDARDYAVV-GCVE------------------LSIPGR
-TYGL-----HDIAMFNL--LKVMEISLYENE----------------------GN----
-----DTLTYEALLAHIRAKISHYITLMVEGSNICDIGHRDWAPV--PLLSSFISDCLEK
GRDITD----GGARY-----NFSGVQ-GIGIANLSDSLHALNGLVFDQQRL-SFDALL--
----------SILKNNFA------------------TPEG--------------------
-------------------------EKIRAR-----------------------------
------------LINR--FEKYGNDIDNVDNISAELLRYYCKEV-EKY--QNP--R----
--GGQFTPGSYTVSA-HVPLGAVVGATPDGRFAGEQLADGGLSPMLGQDMQGPTAVLKS-
-VSKLDN-TLLSN-------------GTLLNVKFTPATLEGEAG--LRKLADFLRAFTQ-
----LKLQHIQFNVVNADTLREAQLRPQDFAGLVVRVAGYSAFFVELSKEIQDDIIRRTA
HQL------------
>gi|215489288|ref|YP_002331719.1| putative formate acetyltransferase 2 [Escherichia
coli O127:H6 str. E2348/69]
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------------------------------------------------------------
-----MTNRIS-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------TAL---FANTREISLERALLY
TASHRQT-EGE-PVI------MR----RAKATAYILEHVEISIRDE-ELIAGNRTVK-PR
AGIMSPEMD--PYWLLKELDQ---FPTRPQD--R--------------------------
---FAISEEDKRIYR-EELFPYW-----EKRSMKDFINGQ---MTD--------------
-EVKAAT----------------STQIFSIN---QTDKGQ--------------------
------GHIIIDYPRLL--NHGLGELVAQMQQHCQQQ------------------PENHF
YQAALLLLEASQKHILRYAELAETMAASC-TDGPRREELLTIAEISRHNAEHKPQTFWQA
CQLFWYMNIILQYESNASS--LSLGRFDQYMLPFYQASLT----QGEDPAF-----LKEL
LESLWVKCND-IVLL-RSTSSARYFAGFPTGYTAL---LGGL-TE-NGR--SAVNVLSFL
CLDAYQSV-QLPQPNLGVRTN-ALIDTPFLMKTAETIR-LGTGIPQIFN-DEVVVPAFLN
--------R------G---VSLEDARDYSVV-GCVE------------------LSIPGR
-TYG-L----HDIAMFNL--LKVMEICLHENE----------------------GN----
-----AALTYEGLLEQIRAKISHYITLMVEGSNICDIGHRDWAPV--PLLSSFISDCLEK
GRDITD----GGARY-----NFSGVQ-GIGIANLSDSLHALKGMVFEQQRL-SFDELL--
----------SVLKANFA------------------TPEG--------------------
-------------------------EKVRAR-----------------------------
------------LINR--FEKYGNDIDEVDNISAELLRHYCKEV-EKY--QNP--R----
--GGYFTPGSYTVSA-HVPLGSVVGATPDGRFAGEQLADGGLSPMLGQDAQGPTAVLKS-
-VSKLDN-TLLSN-------------GTLLNVKFTPATLEGEAG--LRKLADFLRAFTQ-
----LKLQHIQFNVVNADTLREAQQRPQDYAGLVVRVAGYSAFFVELSKEIQDDIIRRTA
HQL------------
>gi|15804547|ref|NP_290588.1| putative formate acetyltransferase 2 [Escherichia coli
O157:H7 EDL933]
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------------------------------------------------------------
-----MTNRIS-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------TAL---FANTREISLERALLY
TASHRQT-EGE-PVI------LR----RAKATAYILEHVEISIRDE-ELIAGNRTVK-PR
AGIMSPEMD--PYWLLKELGQ---FPTRPQD--R--------------------------
---FAISEEDKRIYR-EELFPYW-----EKRSMKDFINGQ---MTD--------------
-EVKAAT----------------STQIFSINQ---TDKGQ--------------------
------GHIIIDYPRLL--NHGLGELVAQMQQHCQQQ------------------PENHF
YQAALLLLEASQKHILRYAELAETMAASC-TDAQRREELLTIAEISRHNAEHKPQTFWQA
CQLFWYMNIILQYESNASS--LSLGRFDQYMLPFYQASLT----QGEDPAF-----LKEL
LESLWVKCND-IVLL-RSTSSARYFAGFPTGYTAL---LGGL-TE-NGR--SAVNVLSFL
CLDAYQSV-QLPQPNLGVRTN-ALIDTPFLMKTAETIR-LGTGIPQIFN-DEVVVPAFLN
--------R------G---VSLEDARDYSVV-GCVE------------------LSIPGR
-TYGL-----HDIAMFNL--LKVMEICLHENE----------------------GN----
-----AALTYEGLLEQIRAKISHYITLMVEGSNICDIGHRDWAPV--PLLSSFISDCLEK
GRDITD----GGARY-----NFSGVQ-GIGIANLSDSLHALKGMVFDQQRL-SFDELL--
----------SVLKANFA------------------TPEG--------------------
-------------------------EKVRAR-----------------------------
------------LINR--FEKYGNDIDEVGNISAELLRHYCKEV-EKY--QNP--R----
--GGYFTPGSYTVSA-HVPLGSVVGATPDGRFAGEQLADGGLSPMLGQDAQGPTAVLKS-
-VSKLDN-TLLSN-------------GTLLNVKFTPATLEGEAG--LRKLADFLRAFTQ-
----LKLQHIQFNVVNADTLREAQQRPQDYAGLVVRVAGYSAFFVELSKEIQDDIIRRTA
HQL------------
>gi|205354308|ref|YP_002228109.1| putative formate acetyltransferase 2 [Salmonella
enterica subsp. enterica serovar Gallinarum str. 287/91]
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------------------------------------------------------------
-----MTHRIQ-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------AAL-FQ-NHRE-ISLERALLY
TASHQQT-EGE-PVI------LR----RAKATAYILEHVEISIRDE-ELIAGNRTVK-PR
AGIMSPEMD--PYWLLNELDR---FPTRPQD--R--------------------------
---FDISEEDKRLYR-EVLFPYW-----EKRSMKDFINGQ---MTD--------------
-EVKAAV----------------STQIFSINQ---TDKGQ--------------------
------GHIIIDYPRLL--NNGLGELAAQMRARCEQQ------------------PENDF
YQAALLLLEASQRHILRYAVLAEHQAERC-PDARRRQELLTIAANSRHNAQHKPQTFWQA
CQLFWYMNIILQYESNASS--LSLGRFDQYMLPFYQTSLT----QGDDPAF-----LKEL
LESLWVKCND-IVLL-RSTSSARYFAGFPTGYTAL---LGGL-TE-SGR--SAVNVLSFL
CLDAYQSV-QLPQPNLGVRTN-ALIDTPFLLKTAETIR-LGTGIPQIFN-DEVVVPAFLN
--------R------G---VSLEDERDYAVV-GCVE------------------LSIPGR
-TYGL-----HDIAMFNL--LKVMEISLYENE----------------------GN----
-----DTLTYEALLAHIRAKISHYITLMVEGSNICDIGHRDWAPV--PLLSSFISDCLEK
GRDITD----GGARY-----NFSGVQ-GIGIANLSDSLHALNGLVFDQQRL-SFDALL--
----------SILKNNFA------------------TPEG--------------------
-------------------------EKIRAR-----------------------------
------------LINR--FEKYGNDIDNVDNISAELLRYYCKEV-EKY--QNP--R----
--GGQFTPGSYTVSA-HVPLGAVVGATPDGRFAGEQLADGGLSPMLGQDMQGPTAVLKS-
-VSKLDN-TLLSN-------------GTLLNVKFTPATLEGEAG--LRKLADFLRAFTQ-
----LKLQHIQFNVVNADTLREAQLRPQDFAGLVVRVAGYSAFFVELSKEIQDDIIRRTA
HQL------------
>gi|150015205|ref|YP_001307459.1| pyruvate formate-lyase [Clostridium beijerinckii
NCIMB 8052]
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------------------------------------------------------------
MDELIMSQRIK-------------------------------------------------
------------------------------------------------------------
---------------------------NLK---------QKM-LS-EKRY-ASIEQALII
TETYKEN-EDK-PVI------IK----RALALKNSLSKLEIGVDDE-ELIVGNRTKG-VR
YGVVFPESG--SSWIDKEFES---LPTRPQD--K--------------------------
---FNVNLNDIETFR-KVIKPYW-----DGHSLEDVIRQR---YGK--------------
-EIDEIA----------------KVVKINQKD--HAQ-----------------------
------GHICPNCREWL--ALGPEGIKQRAIEKMKNSTK----------------ESKEF
YESVIIVMEGAQEFMMRYHDLMKEKAESI-CEEELVADMLQVAEICKNISRRPAQTFHEA
VQAIWFLFVILHMESNASS--FSPGRMDEFLYPYYKRDIH-L--GNIDDKK-----ALEI
IECLWLKFNE-IVYL-RNSHSAKFFAGFPIGFNIA---IGGQ-DE-KSN--DFSNELSFL
FLKAQEHL-GLPQPNLSVRLH-KNTSEKLLKESIKVVA-KGSGMPQFFN-DESVVPSMID
--------L------G---IKEKDARDYAIV-GCVE------------------LTTQGN
-NLG-W----SDAAMFNL--NKVLEITLNGGK---CLISGD-SL----------SQ-DLG
NLT--TYEKYEDLEEAFAKQIDYFIDRMILACEQVEKAHIDVLPS--PFLSSVIDDCIEK
GVDVTA----GGAVY-----NLSGIQ-MIQVANLADSLAAIKLLVYDEKRI-SKEELL--
----------KALQNNFE---------------------G-Y------------------
-------------------------EVIRAM-----------------------------
------------LLNR--APKYGNDIQWVDEIGAKWARYFNGKL-KSY--TNY--R----
--GGKYHTGMYTVSA-HVPMGENVGASADGRYAKAPLADGGMSPVYGRDIAGPTAVLKS-
-VSKLDN-VLTTN-------------GGLLNMKFLPEFFKHEIG--RDKFARFLRTFVD-
----LEIPHIQFNVLRKEDLLAAQKDPENYRSLTVRVAGYTAYFTELAGELQNEIIARTS
YGDI-----------
>gi|126698712|ref|YP_001087609.1| glycerol dehydratase [Clostridium difficile 630]
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---MSQTNRIE-------------------------------------------------
------------------------------------------------------------
---------------------------AFR---------QEY-IN-SKPM-ICCERARIF
TESHKKT-EGE-AIC------IR----RAKAFLETCKELPIKIFEN-ELIVGTAGKF-RR
TGILTPEFS--WQWVDKEMDT---FDKRTQD--P--------------------------
---YVISKEQIEFIR-KEIFPYW-----KGKSLEEVFLAR---IPE--------------
-DTAKIL--------------V-DTGIIDNDS--KWRQAV--------------------
------GEVTPDYQDILF-VKGYKGIKEDADKKIKELDI-------SVSENI---EKIDF
YKSVSIVAQGIMTLAQRYSNLAKEMSKQE-TDEKRKLELIKISEICMNVPANPPTNFYEA
IQFVWFVQLGGILSENPLA--LNLGRFDQYMYPYYENDAR-E--GKITESE-----AQEL
IEALWIKLSE-WVWT-ISANTANYFAGYNQFQNLT---VGGK-KR-NGT--DGTNDISYM
CLKATESV-KTHQPGLSVRVS-QGAPDNFVMAVAKLVK-QGTGFPAIHS-DSAGAQMLLQ
--------D------G---YDAEDARDWSNC-GCVV------------------PHFRKT
--GQ-W----TSAVNINF--AAALEYAMNEGK---SRLTGE-KM----------GL-DTK
NIT--EFTSFEELKDEFLKQLAYLVKSSVIGTTVAQQIHKEMVPR--PFLSTCVDGCLDK
GVDLSK----GGAKY-----NIGPVLTGIGLGVVSNSLAAIKKLVFEDKVT-TLEELT--
----------KALNNDWE---------------------G-Y------------------
-------------------------EELRK------------------------------
------------LALD--VPKYGNDNDYVDSLAIEVSDFYYTET-RKY--KDI--F----
--GSKFNSAFMGISN-YVPTGKIVGATPCGRKATKPLTE-GVSPFVGTDTTSPLAAMKS-
-ASKINH-DVHTG-------------GTLLNLRLNQDLVETERG--LRNLTSMIKSYFA-
----LGGFHVQFNTISNDTLLKAQENPEEYKDLLVRVAGYSTQFVNLSREMQDAIIARNS
HSNF-----------
>gi|158321708|ref|YP_001514215.1| pyruvate formate-lyase [Alkaliphilus oremlandii
OhILAs]
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----MSTERIA-------------------------------------------------
------------------------------------------------------------
---------------------------QLK---------KSY-IN-TKPS-ICVERAIAF
TNSHKKT-EGE-AMI------LR----RAKAFKEVCKAVPVTIFDQ-ELIVGTPGIY-KR
SGFICPEFS--WQWVEKEMDD---FQNRSQD--A--------------------------
---YLIGEEQKEILK-NDIFPYW-----VGKSLEEAFLSR---IPE------------E-
-TRKIAV----------------DTGIVDNDS--KWRSAV--------------------
------GEITPDYQDIIF-VKGFGGIRAEAMEKLRKLEP-------LSAEAL---EKINF
YQAIIESCDGIINLAKRYSKKALEMAEAE-KDVKRKEELIRIHQVCKNIPENPPRSFYEA
IQMVWFVQLGSILSENSLA--LNLGRFDQYMYPFYEKDLK-D--GKIKEEE-----AQEL
IEALWLKLSE-WVWA-ISKNTAQYFAGYNSFQNLT---VGGR-KR-DGS--DATNTISYM
ALKASKNV-KTHQPGLSVRIH-PDSPQEFLIAVCDLIR-EGTGFPAVHN-DRIGSQMLLA
--------A------G---LSPEDARDWSNC-GCVV------------------PHFR-K
-VGE-W----TSAVNINL--AAALEYALNSGK---SRITKE-QM----------GL-KEE
NHL--GMNSFKDIKDHFYRQLSNLIKHGVISSVIAQQIHTEMVPR--PFLSTLVDGCMDK
GVDLSK----GGAFY-----NIGPVLTGIGIADVANSLMAIKKLVYEDKKI-TLNQLN--
----------SALNNNWE---------------------D-Q------------------
-------------------------EDLRK------------------------------
------------EALN--CPKYGNDIDEVDQIAVEISDFYNKEI-KKY--KDY--F----
--GVPFNSAFMGISN-YIPAGSVIGATPDGRRSGDPLTE-GVSPHAGTDLTSPTAAMRS-
-AAKINH-DIHTG-------------GTLLNVKLSPELLKTDKS--LVNLASLIRAYFE-
----LGAFHVQFNVISVDTLRKAQENPEAYRDLLVRVAGYSTQFVNLSKEVQDAIIQRTT
YANM-----------
>gi|153940314|ref|YP_001392534.1| formate acetyltransferase [Clostridium botulinum F
str. Langeland]
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------------------------------------------------------------
----MMTDRVK-------------------------------------------------
------------------------------------------------------------
---------------------------KLR---------EES-LK-AVPR-ISMERTRIV
TDVYKKY-EGTVSIP------VL----RALVLKELMERKELCIYDG-ELIVGERGEA-AA
ATPTYPELC---CHTVEDFDI---MDKREKI--S--------------------------
---FKTTDEDKEIQE-ELIIPFW-----EKRSMRHKILEK---MTP--------------
-EWKACY----------------EAGIFTEFM---EQRGP--------------------
------GHTAGG-DKYY--KMGFLDIKEQIKEAISKLDYL------NDDEAL---DKKEQ
LDAMDIACDAIMIYGKRYSEYAAQLAQKE-ADTVRKKELMEISEVCSWVPAHAPRTFREA
IQMYWFVHLCVISELNPWDA-FNPGRLDQHLYPFYKKQIE-E--GTLDREL-----AREL
LQCFWVKFNN-QPAPPKVGITLKESGTYTDFANIN---SGGM-KA-DGS--DGVNDVSYL
VLEVIDEM-KLLQPSSNVQIS-KKTPQRFLKKACEVIR-KGWGQPSIFN-ADSVVQELVR
--------A------G---KSIEDARCGGTS-GCVE------------------AGAFGK
-EAY------ILTGYFNL--PKILEITLLNGV---DSQTGK-QL----------GI-KTG
DIS--TLKTYEDLLDAFKKQLKYFIDIKVNGNRVIERLYATLMPA--PFLSVVTDDCIAK
GKDYNA----GGARY-----NTSYIQ-GVGIGTITDSLSAIKYQVFDEKNI-TMEELM--
----------EALRSNFE---------------------G-H------------------
-------------------------EDIYNL-----------------------------
------------VKNK--TPKYGNDDDYADEIMKEVFDAYYNEV-NGR--PNG--R----
--GGCYRIDMLPTTC-HVYFGAVINATPDGRKAHIPVSE-GISPSKGADVNGPTGVIKS-
-AAKMDH--LRTG-------------GTLLNQKFVPSVVQGEEG--IDNMANLVRAYFT-
----MDGHHIQFNIVSKETLLKAQQNPDEYKDLIVRVAGYSDYFNNLDKVLQNEIIERTE
QEFN-----------
>gi|170754495|ref|YP_001782822.1| formate acetyltransferase [Clostridium botulinum
B1 str. Okra]
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------------------------------------------------------------
----MMTDRVK-------------------------------------------------
------------------------------------------------------------
---------------------------KLR---------EES-LK-AVPR-ISMERTRIV
TDVYKKY-EGIVSIP------VL----RALVLKELMERKELCIYDG-ELIVGERGEA-AA
ATPTYPELC---CHTVEDFDI---MDKREKI--S--------------------------
---FKTTDEDKEIQE-ELIIPFW-----EKRSMRHKILEK---MTP--------------
-EWKACY----------------EAGIFTEFM---EQRGP--------------------
------GHTAGG-DKYY--KMGFLDIKEQIKEAISKLDYL------NDDEAL---DKKEQ
LDAMDIACDAIMIYGKRYSEYAAKLAQKE-ADPVRKKELMEISEVCSWVPAHAPRTFREA
IQMYWFVHLCVISELNPWDA-FNPGRLDQHLYPFYKKQIE-E--GTLDREQ-----AREL
LQCFWVKFNN-QPAPPKVGITLKESGTYTDFANIN---SGGM-KA-DGS--DGVNDVSYL
VLEVIDEM-KLLQPSSNVQIS-KKTPQRFLKKACEVIR-KGWGQPSIFN-ADSVVQELVR
--------A------G---KSIEDARCGGTS-GCVE------------------AGAFGK
-EAY------ILTGYFNL--PKILEITLLNGV---DSQTGK-QL----------GI-KTG
DIS--TLKTYEDLLDAFKKQLKYFIDIKVNGNRVIERLYATLMPA--PFLSVVTDDCIAK
GKDYNA----GGARY-----NTSYIQ-GVGIGTITDSLSAIKYQVFDEKNI-TMEELM--
----------EALRSNFE---------------------G-H------------------
-------------------------EDIYNL-----------------------------
------------VKNK--TPKYGNDDDYADEIMKEVFDAYYNEV-NGR--PNG--R----
--GGCYRIDMLPTTC-HVYFGSVINATPDGRKAHIPVSE-GISPSKGADVNGPTGVIKS-
-AAKMDH--LRTG-------------GTLLNQKFVPSVVQGEEG--IDNMANLVRAYFT-
----MDGHHIQFNIVSKETLLKAQQNPDEYKDLIVRVAGYSDYFNNLDKVLQNEIIERTE
QEFN-----------
>gi|148381131|ref|YP_001255672.1| formate acetyltransferase [Clostridium botulinum A
str. ATCC 3502]
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------------------------------------------------------------
----MMTDRVK-------------------------------------------------
------------------------------------------------------------
---------------------------KLR---------EES-LK-AVPR-ISMERTRIV
TDVYKKY-EGTVSIP------VL----RALVLKELMERKELCIYDG-ELIVGERGEA-AA
ATPTYPELC---CHTVEDFDI---MDKREKI--S--------------------------
---FKTTDEDKEIQQ-ELIIPFW-----EKRSMRHKILEK---MTP--------------
-EWKACY----------------EAGIFTEFM---EQRGP--------------------
------GHTAGG-DKYY--KMGFLDIKEQIKEAISKLDYL------NDDEAL---DKKEQ
LDAMDIACDAIMIYGKRYSEYAAKLAQKE-ADPVRKKELMEISEVCSWVPAHAPRTFREA
IQMYWFVHLCVISELNPWDA-FNPGRLDQHLYPFYKKQIE-E--GTLDREQ-----AREL
LQCFWVKFNN-QPAPPKVGITLKESGTYTDFANIN---SGGM-KA-DGS--DGVNDVSYL
VLEVIDEM-KLLQPSSNVQIS-KKTPQRFLKKACEVIR-KGWGQPSIFN-ADSVVQELVR
--------A------G---KSIEDARCGGTS-GCVE------------------AGAFGK
-EAY------ILTGYFNL--PKILEITLLNGV---DSQTGK-QL----------GI-KTG
DIS--TLKTYEDLLDAFKKQLKYFVDIKVNGNRVIERLYATLMPA--PFLSVVTDDCIAK
GKDYNA----GGARY-----NTSYIQ-GVGIGTITDSLSAIKYQVFDEKNI-TMEELM--
----------EALRFNFE---------------------G-H------------------
-------------------------EDIYNL-----------------------------
------------VKNK--TPKYGNDDDYADEIMKEVFDAYYNEV-NGR--PNG--R----
--EGCYRIDMLPTTC-HVYFGSVINATPDGRKAHIPVSE-GISPSKGADVNGPTGVIKS-
-AAKMDH--LRTG-------------GTLLNQKFVPSVVQGEEG--IDNMANLVRGYFT-
----MDGHHIQFNIVSKETLLKAQQNPDEYKDLIVRVAGYSDYFNNLDKVLQNEIIERTE
QEFN-----------
>gi|150388421|ref|YP_001318470.1| formate C-acetyltransferase [Alkaliphilus
metalliredigens QYMF]
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-----------------------------------------------------------M
EELRGINARTK-------------------------------------------------
------------------------------------------------------------
---------------------------KLR---------KQS--ETIHPS-ISIERAVLM
TQAYEKY-SGKVSEP------ML----RALSFKHLMENKTICINDD-ELIVGERGPT-PQ
SAPTYPELC---CHTIEDLEM---MNDREKI--S--------------------------
---FTVTAEDKKIQR-EKIIPYW-----QGKSIRDFIFNE---MTE--------------
-EWKDCY----------------HGGIFTEFM---EQRAP--------------------
------GHTVGD-DKIY--KRGFLDFKLEIMEQLESLDYY------NDIEAY---EKQEQ
LKAMEICADAIIIFAHRHAEKAKELAENE-ENPQKKRELEKIAEVCLRVPALPPGNFWEA
LQSYWFVHLGVITELNTWDA-FCPGRLDQHLHPFYQKGIE-G--GTLTPQG-----AKEL
LECFWVKFNN-QPAPPKVGITLQESGTYTDFANIN---IGGL-KI-DGS--DGVNEVSYL
LLEVIDEM-KLLQPSSNIQVS-KKNPDYFIKKAAEVIR-KGWGQPSVFN-ADAVVEELLR
--------Q------G---KSIEDARCGGTS-GCVE------------------TGAFGK
-ESF------ILTGYFNL--TKVLEITLNNGF---DPVTGK-KI----------GV-QTE
VVE--NLHSFKALFEAFKVQLNHFIDIKIKGNNIIEKLYAHYMPS--PFLSILIDDCIKN
AKDYNA----GGTRY-----NTNYIQ-GVGIASITDSLSAIKSHVFDDKLF-TLRQLM--
----------ETLHVDFK---------------------G-H------------------
-------------------------EPIRQL-----------------------------
------------LLNK--TPRYGNDDDYVDSIMVKVFDAFYQAV-NGR--KTM--R----
--GGTYRINMLPTTC-HVYFGSVIGATPDGRKAGRPLSE-GISPVQGTDKKGPTAVIKS-
-ASKMDQ--LKTG-------------GTLLNQKFTPNMLEGEAG--LENVVHLVRSYFR-
----LDGHHIQFNVVDAATLKKAQANPEAYQNLIVRVAGYSDYFNNLNKGLQDEIIARTE
HQAM-----------
>gi|170760792|ref|YP_001788503.1| formate acetyltransferase [Clostridium botulinum
A3 str. Loch Maree]
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----MMTGRVK-------------------------------------------------
------------------------------------------------------------
---------------------------KLR---------EES-LK-AVPR-ISMERTRIV
TYVYKKY-EGTVSIP------VL----RALVLRELMERKELCIYDG-ELIVGERGEA-AA
ATPTYPELC---CHTVEDFDI---MDKREKI--S--------------------------
---FKTTDEDKEIQE-ELIIPFW-----EKRSMRHKILEK---MTP--------------
-EWKACY----------------EAGIFTEFM---EQRGP--------------------
------GHTAGG-DKYY--KMGFLDIKEQIKEAISKLDYL------NDDEAL---DKKEQ
LDAMDIACDAIMIYGKRYSEYAAKLAQKE-ADPVRKKELMEISEVCSWVPAHAPRTFREA
IQMYWFVHLCVISELNPWDA-FNPGRLDQHLYPFYKKEIE-E--ETLDREQ-----AREL
LQCFWVKFNN-QPAPPKVGITLKESGTYTDFANIN---SGGM-KA-DGS--DGVNDVSYL
VLEVIDEM-KLLQPSSNVQIS-KKTPQRFLKKACEVIR-KGWGQPSIFN-ADSVVQELVR
--------A------G---KSIEDARCGGTS-GCVE------------------AGAFGR
-EAY------ILTGYFNL--PKILEITLLNGV---DSQTGK-QL----------GI-KTG
DIS--ALKTYEDLLDAFKKQLKYFVDIKVNGNRVIERLYATLMPA--PFLSVVTDDCIAK
GKDYNA----GGARY-----NTSYIQ-GVGIGTITDSLSAIKYQVFDEKNI-TMEELM--
----------EALRSNFE---------------------G-H------------------
-------------------------EDIYNL-----------------------------
------------VKNK--TPKYGNDDDYADEIMKEVFDAYYNEV-NGR--PNG--R----
--GGCYRIDMLPTTC-HVYFGSVINATPDGRKAHIPVSE-GISPSKGADVNGPTGVIKS-
-AAKMDH--LRTG-------------GTLLNQKFVPSVVQGEEG--IDNMANLVRAYFT-
----MDGHHIQFNIVSKETLLKAQQNPDEYKDLIVRVAGYSDYFNNLDKVLQNEIIERTE
QEFN-----------
>gi|57640224|ref|YP_182702.1| pyruvate-formate lyase [Thermococcus kodakarensis
KOD1]
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------------------------------------MSEAIETCCTNSHGKIEKELERRR
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SSIRPINERVA-------------------------------------------------
------------------------------------------------------------
---------------------------KLR---------EES---VNTEVRISSERARLI
TEFYKSDLAKGKSIP------VQ----RALAFKYLLEHCSLPVEDG-QLIVGIRGTG-VK
EVPTYPEIT---VHSIEDLEI---LNSRENM--P--------------------------
---YRVDEETKELYE-REIIPFW-----KGRAMRDIIFEN---LPQ--------------
-EWIDAY----------------EAGVWTEFM---EQRAP--------------------
------GHTAGG-ERIF--KMGVLDIKEEIRRKMEELDP-------SDPEYY---EKMEE
LKAMDIVADAILIYARRYAEKLEKMAEEE-TDPKRKEELKQMAEICRWVPAHPPRTFWEA
LQHYWFIHVGVTYETNPWDS-FNPGRIDQHLYPFYKKDIE-E--GRLTREK-----AKEL
LQCFWLKFNN-QPAVPKVGVTAEESFTYNDFSKLN---VGGL-KE-DGS--DGVNELSYL
ILEVLGEM-RTLQPNTAVLVS-EKNPDCLLIEALKVVG-PGFGEPPFFNFDGVIVKMLRQ
---------------G---KSLEDARTSGVS-GCVE------------------SGAFGK
-EAY------ILTGYFNL--PKILEITLNNGV---DPRTGK-KI----------GL-ETG
DPR--DFKSFEELWEAFMKQVKHFLDIKMKGNDIIEALYAKYLPV--PFLSLWIEDCVEK
AKDYNC----GGARY-----NTQYIQ-VVGLGTIADSLAAIKYHVFDKKTF-TMDALL--
----------KALKNNWK---------------------G-Y------------------
-------------------------EIMREI-----------------------------
------------LRNPDKTPKFGNDDDYVDEIAKRVVDEVVDLI-ESY--PPSPVR----
--KASKRAYFLPTTV-HVYFGKVTGATPDGREAGFPVSE-GVSPVQGMDRKGIAAVFRS-
-VAKCDW--DKTG-------------GALLNQKLTPDIFDSEEN--IKKLAQLIRTFFR-
----LGGHHVQFNVVSAELLREAQRKPQDFQDLMVRVAGYSDYFVNLPEGLQEEIVQRTE
QELL-----------
>gi|39997199|ref|NP_953150.1| formate acetyltransferase [Geobacter sulfurreducens
PCA]
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------------------------------------------------------------
-----MTERTR-------------------------------------------------
------------------------------------------------------------
---------------------------ELR---------RRS-LE-ARPA-ISAERALLL
TEFYREN-EGKYSVP------VM----RALSFLHICRHKTIWIGEG-ELVVGERGPE-PK
AVPTYPELT---CHSLEDLRI---LDSRPLT--S--------------------------
---YAVSAECLAAYE-ETVIPYW-----RGRSLRDKMFGE---LAP--------------
-EWHEAY----------------AAGIFTEFM---EQRAP--------------------
------GHTVLD-EKPF--RRGLLDFKADIAREIGRLDFV------QDGAAW---EKREQ
LRAMAISCDAAILFAERHAGLADEMAARE-TDPHRKRELERIAEVCRHVPAHAPRDFHEA
LQAYWFCHLAIITELNGWDA-MSPGHLDQHLLPFYEQGLA-H--GSLSRDA-----AREL
LECFFVKFNN-HPAPPKVGVTAAESGTYTDFANIN---LGGL-LP-DGS--DGSNEVSHL
LLDIIDEM-HLLQPSSNIQLS-RKSPDAFLSHALRVIR-NGYGFPSIFN-ADSVVEEQLR
--------Q------G---KSLVDARAGGCS-GCVE------------------VGAFGK
-EAY------ILTGYFNL--VKLLELALHNGV---DPRTGR-QL----------GP-ASG
DPS--GFASFDDLYAAFEAQLRHFIEIKMAGNQLIEQIYCRLMPA--PFLSVLIDDCIAT
GRDYNA----GGARY-----NNTFIQ-GVGIGSITDSLSAIKALVYDSGHI-ALPDLV--
----------AALDADFA---------------------G-Q------------------
-------------------------EPLRQR-----------------------------
------------LLNR--TSKYGNDDDYADDLMRRVFESFFRTV-DGR--PNS--K----
--GGQYRIEMLPTTC-HVYFGSVTGATPDGRRAGTPLSE-GISPVQGADRSGPTAVIKS-
-AGKMDH--IRTG-------------GTLLNMKFAPSLVEGEQG--ISTMASLVRSYFR-
----MDGHHVQFNVVRADTLRAAQADPDAHRDLIVRVAGYSDYFCDLSRELQDEIITRTE
HDSL-----------
>gi|170290137|ref|YP_001736953.1| formate C-acetyltransferase [Candidatus
Korarchaeum cryptofilum OPF8]
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--------------------------------------MTLTTPEASCEVKISKEVEKRR
SVIRPINERIA-------------------------------------------------
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------------------------------------------------------------
---------------------------RLR---------EES---VNAQVKVSLERAKLI
TEFYKSDIPKGKSIP------VQ----RALAFKYLMERVSLPIEEG-QLIVGLRGTG-VK
EVPTYPEIC---VHSLEDLEI---LDKRKNM--P--------------------------
---YKVDEETKEFYE-REAIPFW-----RGRAMRDIIFES---LPE--------------
-EWIDAY----------------EAGVWTEFM---EQRAP--------------------
------GHTAGG-ERIF--RMGVLDIKEQIRRKMESLDP-------SDPEYY---EKMEE
LKAMDIVADAIMIYARRYAEKLEQMAKEE-KDPERKKELEQMAEICRWVPAHAPRTFWEA
LQHYWFVHVGVTYETNPWDS-FNPGRIDQHLYPFYKRDIE-E--GRLTRER-----AKEL
LQAFWLKFNN-QPAVPKVGVTAEESFTYNDFSKLN---LGGL-TK-DGK--DGVNELSYL
ILEVLDEM-RTLQPNTAVLIS-EKNPDSFLIKALKVVG-PGFGEPPFFNFDGVIVKMLRQ
---------------G---KSLEDARTSGVS-GCVE------------------SGSFGK
-ECY------ILTGYFNL--PKILEITLNNGV---DPRTGK-KI----------GL-ETG
DPR--EFKSFEDLWNAFIKQVKYFLDIKMKGNDIIEALYAKYLPV--PFLSLWIDDCVEK
AKDYNA----GGARY-----NTQYIQ-VVGLGTITDSLAAIKYHVFEKGTV-SMSELL--
----------DALSKNFE---------------------G-Y------------------
-------------------------EFLREI-----------------------------
------------LRNPDKTPKFGNDDDYADSIAKEVVDRIVELI-ESY--PRSPVR----
--KASRRAYFLPTTV-HVYFGKVTGATPDGRVAGFPVSE-GISPVQGMDRRGIAAVFRS-
-VAKCDW--DKTG-------------GALLNQKLTPDIFDNEEN--LRKLAQLIRAFFR-
----LGGHHVQFNVVSAELLREAQRRPQDFQDLMVRVAGYSDYFVNLPKGLQDEIIERTE
HKSL-----------
>gi|77918545|ref|YP_356360.1| pyruvate-formate lyase [Pelobacter carbinolicus DSM
2380]
----------------------------------------------MAGSCCG-------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------------------GIAEGAT
RKKFELPERIQ-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------DAY-LQ-VKPS-IAIGRALAF
TEVTRQN-PGM-PEI------LR----RALAFKKACEDAPLLIQTD-ELIVGHPCGK-PR
AGAFSPDIA--WKWVRDELDT---IGTRSQD--P--------------------------
---FVFSEEDKKIMR-EEIFPFW-----EGRSLDEICETQ---YRE--------------
-AGLWEF--------------AAEAFVSDLSY--HQVNGG--------------------
------GDTCPGFDVILF-TKGVSGIKAEAEAHLAKLSM-------DVPDDI---DRIYF
YKAAIQTCEGIVTYANRVSAYAKELAEKE-QDPKRKAELEKIAEVNARVPANPPSSFQEA
LQSIWTIESLFVIEENQTG--LSLGRLDQYVYPCYEADIK-A--GVIDEDQ-----AFEL
MSCFIIKCAE-MMWL-TSELAAKYFAGYQPFINLC---VGGQ-KR-EGG--DATNDLTYL
VMDVVRKL-GVYQPSLACRIH-NQSPQKYLQKIVEVVK-AGLGFPACHF-DDAHIKMMLR
--------K------G---YDFEDARDYCLM-GCVE------------------PQKSGR
-IYQ-W----TSTGYTQW--PVAIEFVLNRGV---MKWHGT-KQ----------GI-DTG
DLD--QFATYEQFDAAVKEQIEYICKLSAVGTVISQRVHRDVAPK--PMMSLFVEGCMET
GKDVSA----GGAVL-----NHGPGLIFSGLATYADSMASIKKLVYDDKKY-TLADFQ--
----------KALDANWE---------------------G-Y------------------
-------------------------EQMRQ------------------------------
------------DCLD--APKYGNDDDYADKIAADLVEFTEKAC-RQF--KML--Y----
---STMSHGTLSISN-NTPIGEITGATADGRLAFTPLSD-GISPVQGADKMGPTAIIKS-
-VSKMNS-ESMNI-------------GMVHNFKLMEGILETPEG--EAGLITLLRTASI-
----LGNGQMQFSYVDNEVLKQAQQSPEEYRDLMIRVAGYSAFFVELCKEVQDEIISRTT
LSGF-----------
>gi|188587082|ref|YP_001918627.1| Formate C-acetyltransferase [Natranaerobius
thermophilus JW/NM-WN-LF]
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-------------------------------------------------------MENNS
RNSESMSPRVK-------------------------------------------------
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---------------------------KLR---------EQS-VS-KNPK-VSVERAILV
TQAYKKY-DGNVSIP------IL----RALTFKHILENKSISINDG-ELIVGERGPA-PQ
EVPTYPELC---THSITDLEI---IHDREKV--F--------------------------
---FEVDETVKKIQD-SDIIPFW-----KGKSMREKIFDN---MSR--------------
-EWLDCY----------------EAGIFT-EF--MEQRAP--------------------
------GHTVAD-GKIY--QKGLLDFRDDIDLELKNIDEI------NDPQAY---EKSEQ
LKAMRVCIDALIEFAQRYANIAEELAQEV-DDSHRKEELLKIAEICKRVPAKAPRNFWEA
LQYYWFVHLGVITELNTWDS-FCPGRLDQHLYPFYLQDLN-A--GELTRGS-----AKEL
LQCFWIKFNN-QPAPPKVGTTLKESGTYTDFCNIN---IGGV-TP-EGF--DGVNDVSYL
LLEVIDEM-QLVQPSTNIQVS-KQNPNEFIKEAGKIIR-KGWGQPSVFN-TDAVISELLN
--------Q------G---KDLVDARCGGTS-GCVE------------------AGTFGK
-ESY------ILTGYFNL--TKILELTLYRGV---DPRSGK-QI----------GL-KTD
DPE--TFDSFQDLIDAFNEQLNYFIDIKIRGNNIIEKLYDKYMPS--PFLSVIIDDCIKK
AKDYNS----GGARY-----NTRYIQ-GVGIGTITDSLSAIKHHIFEKQNY-TWNELL--
----------TALQNNFE---------------------G-F------------------
-------------------------KQMRGF-----------------------------
------------LKNK--TPRYGNDDDSADDLMKEVFQRFYDAV-NGR--KTM--T----
--GGTYRINMLPTTC-HVYFGSVIGATPEGRLRGTPLSE-GISPVQSADQEGPTAALKS-
-AAKMDH--IKTG-------------GTLLNLKFTPQVLQGEEG--LLNLVYLVRSYFR-
----MNGHHVQFNVVDAETLKDAQRNPDSYRNLIVRVAGYSDYFNNLNENLQNEIIKRTE
HSIG-----------
>gi|126700901|ref|YP_001089798.1| putative formate acetyltransferase [Clostridium
difficile 630]
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------------------------------------------------------------
-MARGTFERTK-------------------------------------------------
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---------------------------KLR---------EES-IN-AEPH-ISIERAVLM
TEAYKKY-EGSVEIP------VL----RALSFKHYIENRTLSINDG-ELIVGEKGDS-PN
GAPTYPEIC---CHTMEDLEV---MHNRDII--N--------------------------
---FSVSEEARKIHK-EEIIPFW-----KKRQTRDKIINA---MTP--------------
-EWLAAY----------------EAGMFTEFM---EQRAP--------------------
------GHTVCG-DTIY--KKGFLDLKKDIEARLKELDFL------NDLDAY---NKKAD
LEAMAIACDAMVILGKRYAEKARQMAEEE-TDEAKKKDLLLIAETCDVVPAHKPETYHQA
IQMYWFVHIGVTTELNIWDA-FTPGRLDQHLNPFYERDVE-N--GILDRDR-----AQEL
LECLWVKFNN-QPAPPKVGITLKESSTYTDFANIN---TGGI-NP-DGQ--DGVNEVSYI
ILDVMDEM-KLIQPSSNVQIS-KKTPQKFLKRACEISR-KGWGQPAFYN-TEAIVQELME
--------A------G---KTIEDARLGGTS-GCVE------------------TGCFGK
-EAY------VLTGYMNI--PKILELTLNNGY---DPISKK-QI----------GI-ETG
DPR--NFQSYEELFEAFKKQLHYMIDIKIEGNAVIENICAKHMPC--PLMSTIVDDCIEK
GKDYQR----GGARY-----NTRYIQ-GVGIGTITDSLTAIKYNVFDKKKF-DMDTLL--
----------KALDVNFE---------------------G-Y------------------
-------------------------EAILNL-----------------------------
------------VSNK--TPKYGNDDDYADEIMQEIFNAYYNEV-TGR--PTV--C----
--GGEYRVDMLPTTC-HIYFGEIMGASPNGRLCAKPVSE-GISPEKGGDTNGPTAVIKS-
-CAKMDH--IKTG-------------GTLLNQRFAPSVVQGEKG--LDNMANLVRAYFN-
----MDGHHIQFNVFDKNVLLEAQKNPQDYKDLIVRVAGYSDHFNNLSRTLQDEIIGRTE
QTF------------
>gi|78356320|ref|YP_387769.1| formate C-acetyltransferase [Desulfovibrio
desulfuricans subsp. desulfuricans str. G20]
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------------------------------------------------------------
-------------------------------------MQCCTTPLSPHEQRLQDKIAGKE
DSFRKSHERVF-------------------------------------------------
------------------------------------------------------------
---------------------------NIL---------DSF--DGKRPR-IDVERAKLF
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TDSMKET-EGQ-PLV------LR----WAKAMKHVAEHITVYIDDD-QLICGRGGCP-GR
YGVLYPELD--GDFLDLAIED---LPNRTES--P--------------------------
---FTITEADARVVV-EEIAPYW-----KGKTYHEDLNLA---LPS--------------
-DVHKLT---------YDDPQGLKSRFIVNET--SSFRSS--------------------
------IQWVHDYEKVL--KRGFRGLKEEAQEKIAGLDPL------SPRDNV---EKRPF
LEAIVIVCDAIILWANRHAKLAADMAAAE-TNPVRKAELETMAEICAWVPENPARNFYEA
VQAQWFTQMFSRLEQKTGTI-VSNGRMDQYFWPFYRKDIE-E--GRITEES-----ALEL
LECMWVGMAQ-YVDLYISPAGGAFNEGYAHWEAVT---IGGQ-TP-QGL--DATNDLTYL
FLKSKREF-PLHYPDLAARIH-SRSPERYLHDVAETIK-FGSGFPKLIN-DEEIVPLYVS
--------K------G---ASFEEALDYAVS-GCTE------------------ARMPNR
DTYT------SGGAYINF--AAALEMVLYNGR---MLKYGENEL----------GL-ETG
DPT--RFETWEEFWNAYVLQHEHFLRAAFIQQHIINNVRARHFAQ--PMGSALHDLCMKH
CLDLHTPQIPEGI-------NLGYFE-YMGFGTVVDSLAAIKKLVFEDKKL-TMQEVI--
----------EALKCNFE---------------------G-K------------------
-------------------------EDVQQ------------------------------
------------MLKS--APCYGNNDEYADSIAREIDAISVKYG-RRYS-PEL-------
--GMHNDVRYVPFTS-HVPFGKVVSATPNGRLAWTPLSD-GSSASHGADVNGPTAVLQSN
FSSKNYG-YRDRA-------------ARMLNIKFTPKCVEGDEG--TEKLVSFIRTFCD-
----LKLWHVQFNVINRDTLIAAQKDPEKYRSLIVRIAGYSAYFVDLSPDLQNDLIARTQ
HDAM-----------
>gi|150389759|ref|YP_001319808.1| formate C-acetyltransferase [Alkaliphilus
metalliredigens QYMF]
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----MITERIE-------------------------------------------------
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---------------------------SSR---------QNY-IN-AKPA-ISYERARIW
TESHKKT-EGE-SVV------IR----RAKAFRDTCEQINVTIFGE-ELIVGSIGEF-RK
CGILTPEFS--WTWVDREMDN---FDERVQD--P--------------------------
---YVMTDEQRTFVR-KKIFPYW-----KGKSLEEAFLAQ---LPE--------------
-KTAKVA--------------V-DTGIVDNDS--KWRQAV--------------------
------GEMTPDYQDVLF-KKGFGGIIKEAKEHIIKLSL-------TSAEDM---KKKDF
YNSIIITSEGMITLANRYGQKATEMADIE-NNPIRKGELLKIADICGRIPENPPDTFYEA
IQFVWFTQVGGIISENPLA--LNIGRFDQFMYPYYKSDVD-K--GIITKDE-----AQEL
IEALWIKLSE-WVWT-ISANTAEFFAGYNQFQNLT---VGGK-TR-EGK--DATNDLSYM
CLKATERV-KTHQPGLSVRVH-QDSPRSFLDAVTHLVS-KGTGFPAIHN-DTAGYQMLIN
--------A------G---YEPEDARDWNNC-GCVV------------------PHFRKT
--GE-W----TSAVNINF--TAALEFALNQGE---SRITGE-KI----------GM-DED
KPT--TFQSYEEVEKAFYKQFDNLIEHSIIATLLAQKLHKEMVPR--PFLSSCIEECMIK
GKDLVD----AGAKY-----NLGPVLTGIGLAVTSNSLAVIKKLVFEDKMT-TMETLI--
----------KALDANWE---------------------G-Y------------------
-------------------------EKLRQ------------------------------
------------LAVS--VPKYGNNVDYVDDIAIKIANYYYKQG-HKY--KDI--N----
--GNNFNTAFMGISN-YLPTGKVVGATPCGRKAKEPLSE-GVSPFAGSDTSTPLEAMRS-
-AAKLNQ-DVHSG-------------GTLLNLRLNEDLVNTKRG--QSNLGFMIQSFFA-
----LGAFHVQFNTISTDTLRKAQNNPQDYKDLLVRVAGYSTQFVNLSKSMQEAIIARTA
HENY-----------
>gi|224371979|ref|YP_002606145.1| PflD2 [Desulfobacterium autotrophicum HRM2]
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-----MNPRIA-------------------------------------------------
------------------------------------------------------------
---------------------------TLR---------EQS-FT-AIPA-ISIERALLQ
TQFYREN-LGKYATP------IL----RALNFKNLCEKKTIYIGDQ-ELIVGERGPR-PK
ATPTFPELN---CHSVEDLET---LHNREMT--P--------------------------
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---FRVDPGDMKIYR-DEIIPYW-----RGRSMRDRVFEH---LPL--------------
-PWQKAY----------------GAGLFTEFM---EQRAP--------------------
------GHTALD-GTIY--QKGMTDFKQEIAQGLEALDYL------HDPQAQ---ERSDA
LTAMDISCDAAILFAQRHARLAEEMAAQE-TRPARKKELLEIARVCRRIPAERPTSLWEA
IQMYWFVHLGTITELNGWDA-MSPGHLDQHLYPFYMRELE-L--GTMDADG-----AKEL
ISCLWIKINN-HPAPPKVGVTAKESGTYNDFTNIN---LGGL-TR-QGA--DAVNDLSYI
MLDVIDEL-KLLQPQSNVQIS-ERTPYHFLKAACRVIR-NGYGYPSVFNADQVVLEQVRV
---------------G---KRIEDAREGGCS-GCIE------------------TGAFGK
-EAY------ILTGYLNL--PKLLELTLNNGR---DPLGGG-MV----------GL-ETG
DPR--GFETFDQLYDAFTRQLAHVVDLKIRVNNYIERMFAANAPA--PFLSVVIQDCIAK
GKDYYN----GGPRY-----NTNYIQ-CCGIGTITDSLSAIKKHVFDDKIV-TMELLL--
----------KALADNFK---------------------G-H------------------
-------------------------EALRLR-----------------------------
------------LLNK--TPFFGNDDDRADQIMVQVYDSLFSAI-DGQ--PNT--K----
--NGEYHLNMLSTTC-HVYFGKKLGASANGRFSGLPESD-GTSPSHGADRNGPTAVIKS-
-LGKMDQ--SKSG-------------GTLLNQRFLPGVLKTEQD--LDKLAGLIRTYFK-
----FGGHHIQFNVVDTQTLKRAQEHPDQYRNLLVRVAGYSDYFVDLDRDHQEEIISRHE
HRGL-----------
>gi|157364003|ref|YP_001470770.1| formate C-acetyltransferase [Thermotoga lettingae
TMO]
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----------------------------------------------MERTKIYEELEKRR
SAIKPINKRIK-------------------------------------------------
------------------------------------------------------------
---------------------------KLR---------DES---VSAKAKVSLERAKLI
TDFYKMA-PKNVSYP------VL----RALAFKYLMENCSLPVEDG-QLIIGIRGTG-PK
EVPTYPEIC---VHTLEDLET---LATRKNM--P--------------------------
---FQVDSQTRKVYE-EEIIPFW-----QGQAMRDILFQN---LPA--------------
-EWKRAY----------------EAGIWTEFM---EQRAP--------------------
------GHTSGG-GWIF--KTGVLDIKKRIEEKIQQLSA-------SDPEYF---EKLEE
LKAMNISCDAILIYAKRYSEKLKKLSENE-KDPQRKQELLEMSRICEKVPAHAPETFWEA
LQHYWFIHVGITYETNPWDS-FTPGRLDQHVYKFYAKDIA-S--GVLTREK-----AKEL
LQAFWLKFNN-QPSVPKVKITAEESFTYNDFSKIN---IGGL-KT-DGS--NAVNELSYL
ILEVLSEM-RTLQPNTAALIS-DKNPDAFLLKALEALS-PGFGEPPLFNYDRIVVKMLRQ
---------------G---KTLEDARESGVS-GCVE------------------TGALGK
-EAY------ILTGYLNL--PKILEITLNGGI---DPGTGK-RI----------GL-ETK
KPQ-----NFDELWDFFAKQLRYFIDIKMKGNDIIEALYAKYLPV--PFMSLWIQDCVEN
AKDYNA----GGARY-----NTQYIQ-FVGLGTVTDSLASIKWNIFDRKLF-TYEEML--
----------KALHNDFQ---------------------G-F------------------
-------------------------EYMRQI-----------------------------
------------FLNK--TPKYGNDNDYADDIAKKLVDYIVQIV-ESY--EPSPVR----
--KASRRCYFLPTTV-HVYFGSVTGATPDGRKAGMPVSE-GISPVQGVDRKGIAAVFNS-
-VCKCDW--DKTG-------------GALLNQRLTPDLVKEKDN--LEKLGKLIRTYFR-
----MGGHHVQFNVVSSELLREAQKKPADFEDLMVRVAGYSDYFVSLPKGLQEEIIARTE
QDEL-----------
>gi|120601541|ref|YP_965941.1| formate C-acetyltransferase [Desulfovibrio vulgaris
subsp. vulgaris DP4]
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------------------------------------------------------------
--------------------------------------MQCCNQLSPHEQRLQDKIEGKV
DRYRATHERVF-------------------------------------------------
------------------------------------------------------------
---------------------------TIL---------ESF--DNTRPR-IDVERAKYF
TESMKAT-EGQ-PLP------LR----WAKALMHIAENMTVYIDDH-QLICGRAGYQ-GR
YGVLYPELD--GDFLGTAIED---LPNRAES--P--------------------------
---FAITPEDARVVV-EEIAPFW-----KGKTYHEALNLA---LPA--------------
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-DVHKLT---------YDDPQGLMSRFIVNET--SSFRSS--------------------
------IQWVHDYEKVL--KRGFRSIKEEALEKIAALDPM------SPCDNV---EKRPF
LEAIVIVCDAIILWAKRHAKLAAELAAKE-TDPTRKRELETMAEICAWVPENPARTFHEA
VQAQWFTQVFSRIEQKTGTI-VSNGRMDQYFWPFYEKDLA-E--GRITEDS-----ALEL
LECMWVGMAQ-YVDLYISPTGGAFNEGYAHWEAVT---IGGQ-TP-EGR--DATNDLTYL
FLKSKREF-PLHYPDLAARIH-SRSPERYLWEVAETIK-DGSGFPKLIN-DEEVVPLYVS
--------K------G---ATFAEALDYAVS-GCTE------------------ARMPNR
DTYT------SGGAYINF--AAALEMVLYNGK---MLKYGDTDL----------GA-HTG
DPR--EFKTWEEFWNAYVTQHQLFLKTAFVQQHIINNLRARHFAQ--PMGSSLHDLCMKH
CLDLHTPQIPEGI-------NLGYFE-YMGFGTVVDSLSAIKKLVFEDKKL-TMDELI--
----------EALKCNFE---------------------G-K------------------
-------------------------EDIQQ------------------------------
------------LLKS--APCYGNNDDYADSIACDIDALSVKYG-RRYS-PEL-------
--GMHNDVRYVPFTS-HVPFGRVVSATPNGRKAWSALSD-GSSASHGADVNGPTAILQSN
FNSKNYG-MRDRA-------------ARMLNIKFTPKCVEGEEG--SQKLVSFIRTFCD-
----LKLWHVQFNVINKETLLAAQRDPEKYRNLIVRIAGYSAYFVDLSPDLQNDLIARTG
HDVM-----------
>gi|220904704|ref|YP_002480016.1| Formate C-acetyltransferase [Desulfovibrio
desulfuricans subsp. desulfuricans str. ATCC 27774]
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------------------------------------------------------------
------------------------------------MSMTTCECRSPQEQRLYDKIEGRE
DRFRKTHPRVF-------------------------------------------------
------------------------------------------------------------
---------------------------RLL---------ERF--EGQKPR-IDIERALYF
TQSMQET-EGQ-PLV------LR----WAKALMHIARNMTVYVQED-QLLLGRAGCD-GR
YGILYPELD--GDFLDIAVRD---LPTRKTS--P--------------------------
---ATITPEDARRVV-EEIAPYW-----KGKTYHEALNAA---LPA--------------
-EVHKLT---------YDDPEGLISRFIVNET--SSFRSS--------------------
------IQWVHDYEKIL--KRGFNSIKKEAREKLAALDPL------SAKDDR---EKRPF
LEAVMIVCDAIVLWAKRHAVLAREMAEKE-SDPVRKAELLRMAENAEHVPGEPARDFWEA
CQSQWFTQMFSRIEQKTGTT-ISNGRMDQYFQPYYKQDRE-A--GKITEAQ-----AMEL
LECMWVGMAE-FIDMYISPTGGAFNEGYAHWEAVT---VGGQ-TP-DGR--DASNDLTYL
ILKSKREF-PLHYPDLAARIH-SRAPERYLWDVAETIK-YGSGFPKLIN-DEEIVPLYVS
--------K------G---ATFEEALDYAVS-GCTE------------------ARMPNR
DTYT------SGGAYINF--AAAVEMVLRNGR---MKKYGDQKL----------GV-ETG
DPR--SFTTWDQFWNAYVEQHLLFLKTAFTQQYIINKLRAEHFAQ--PMGSAMHDLCMKH
CIDLHQEQIPEGI-------NLGYFE-YMGLGTVVDSLAAVKKLVFEEKKL-SMDKLI--
----------AAIDADFE---------------------G-Y------------------
-------------------------EDVRA------------------------------
------------LLRS--APCYGNNDEYADAIGRDIDRISVEYG-NKYSMSDL-------
--GIHNDVRYVPFTS-HVPFGKVVSATPNGRTDGFPLSD-GSSASHGADVNGPTAVLLSN
CTTKNMG-LRDRA-------------ARMLNIKFTPKCVEGEQG--TEKLVSFIRTFCD-
----LKLWHVQFNVVNKGTLVAAQKDPQKYRNLIVRIAGYSAYFVDLSPDLQNDLIARTE
HDVM-----------
>gi|206895494|ref|YP_002247822.1| pyruvate-formate lyase [Coprothermobacter
proteolyticus DSM 5265]
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------------------------------------------------------------
-----------------------------------MTDSNNQPDADKTTLTIEQEIQKRR
EAVRPINERIA-------------------------------------------------
------------------------------------------------------------
---------------------------RLR---------EES-VN-AQVK-ISTERARLV
TEFYQSGVADNLSIP------VQ----RAMAFKYLLEHCSLPVEEG-QLIVGLRGTG-PK
EVPTYPEIC---AHSLEDLDI---LDTRENM--P--------------------------
---YHNTAEDKQLYE-STILPFW-----QGKTIREKLFQR---MPE--------------
-EWLQCY----------------EAGIWTEFM---EQRAP--------------------
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------GHTAGG-ERIF--QKGILDIKEEIKRRMAQLDK-------SDSAYE---EKLEE
LKAMDIAADALLIYAQRYAEKLEQLAQEE-TNVDRKAELLHMASICRKVPAHAPETFWEA
LQHYWFIHVGITYETNPWDS-FNPGRLDQHLRPFYEKEIS-E--GTLTREK-----AKEL
LEAFWVKFNN-QPAVPKVGVTAEESFTYNDFTKIN---IGGL-KV-DGS--DGTSDVSYL
LLEVLDEM-RTLQPNTAVLIS-NKTPDRLLRKALEVIG-PGFGEPPLFNADGIIVKMLRQ
---------------G---KTLEDARTAGVS-GCVE------------------TGSFGK
-ESY------ILTGYFNL--PKILEITLNNGV---DPITGK-KI----------GL-ETG
DPI--TFQTYEELWDAYLKQIKYFMDIKMKGNDIIEELYATELPV--PFMSLWIEDCVKR
AKDYNS----GGARY-----NTQYVQ-LVGLGTVTLSLSSIKYHVFENHTF-TMEELL--
----------KALTNDFE---------------------GPY------------------
-------------------------EMMRQV-----------------------------
------------ILTR--TPKFGEDNDFADSIAKALVDETVWLI-ESY--PPTPVR----
--KASRRAYWLPTTV-HVYFGKVMEASPDGRKAGMPVSE-GVSPVQGSDRKGIAAVFRS-
-VSKCDW--DKTG-------------GALLNQKLTPDIVEDPET--LRKLGQLVRSFFN-
----MGGHHVQFNVVSAELLREAQKRPADFQDLMVRVAGYSDYFVNLPKGLQEEIIARTE
HETV-----------
>gi|46581228|ref|YP_012036.1| formate acetyltransferase [Desulfovibrio vulgaris
subsp. vulgaris str. Hildenborough]
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------------------------------------------------------------
--------------------------------------MQCCNQLSPHEQRLQDKIEGKV
DRYRATHERVF-------------------------------------------------
------------------------------------------------------------
---------------------------TIL---------ESF--DNTRPR-IDVERAKYF
TESMKAT-EGQ-PLP------LR----WAKALMHIAENMTVYIDDH-QLICGRAGYQ-GR
YGVLYPELD--GDFLGTAIED---LPNRAES--P--------------------------
---FAITPEDARVVV-EEIAPFW-----KGKTYHEALNLA---LPA--------------
-DVHKLT---------YDDPQGLMSRFIVNET--SSFRSS--------------------
------IQWVHDYEKVL--KRGFRSIKEEALEKIAALDPM------SPCDNV---EKRPF
LEAIVIVCDAIILWAKRHAKLAAELAAKE-TDPTRKRELETMAEICAWVPENPARTFHEA
VQAQWFTQVFSRIEQKTGTI-VSNGRMDQYFWPFYEKDLA-E--GRITEDS-----ALEL
LECMWVGMAQ-YVDLYISPTGGAFNEGYAHWEAVT---IGGQ-TP-EGR--DATNDLTYL
FLKSKREF-PLHYPDLAARIH-SRSPERYLWEVAETIK-DGSGFPKLIN-DEEVVPLYVS
--------K------G---ATFAEALDYAVS-GCTE------------------ARMPNR
DTYT------SGGAYINF--AAALEMVLYNGK---MLKYGDTDL----------GA-HTG
DPC--EFKTWEEFWNAYVTQHHLFLKTAFVQQHIINNLRARHFAQ--PMGSSLHDLCMKH
CLDLHTPQIPEGI-------NLGYFE-YMGFGTVVDSLSAIKKLVFEDKKL-TMGELI--
----------EALKCNFE---------------------G-K------------------
-------------------------EDIQQ------------------------------
------------LLKS--APCYGNNDDYADSIARDIDALSVKYG-RRYS-PEL-------
--GMHNDVRYVPFTS-HVPFGRVVSATPNGRKAWSALSD-GSSASHGADVNGPTAILQSN
FNSKNYG-MRDRA-------------ARMLNIKFTPKCVEGEEG--SQKLVSFIRTFCD-
----LKLWHVQFNVINKETLLAAQRDPEKYRNLIVRIAGYSAYFVDLSPDLQNDLIARTG
HDVM-----------
>gi|153955616|ref|YP_001396381.1| glycyl radical activating protein [Clostridium
kluyveri DSM 555]
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----MITERIE-------------------------------------------------
------------------------------------------------------------
---------------------------SLR---------QNY-IN-AKPV-ISYQRARIW
TESHKKT-EGE-SIP------IR----RAKAFRDTCQQIDVTIFDG-ELIVGAIGEF-RK
CGILTPEFS--WNWVDREMDN---FDKRVQD--P--------------------------
---YVMTDEQRAFVR-KNIFPYW-----KGKSLEEAFLAQ---LPK--------------
-ETTKVA---------------VDTGFVDNDS--KWRQAV--------------------
------GEITPDYQDVLF-KKGFGGIIRQAKENISKLFL-------TSAEDM---KKKDF
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YNSIIITSQGIITLANRYSEKAREMADAE-NDGVRKGELLKIAEICSSIPEKAPSTFYEA
IQFVWFTQVGGIISENPLA--LNIGRFDQFMYPYYKSDMD-K--GIMTKDQ-----IQEL
IELLWIKLSE-WVWT-ISANTAEFFAGYNQFQNLT---VGGK-TR-EGK--DATNDLSYM
CLKATERV-KTHQPGLSVRIH-QDCPGSFLDAVTYLVS-KGTGFPAIHN-DAAGYQMLIN
--------A------G---YEPEDARDWNNC-GCVV------------------PHFRKT
-GEW------TSAVNINF--TAALEFALNRGK---SRITGE-KI----------GL-DEK
NPM--NFKSYEEVEKAFYKQFDNLIEHSIIATLLAQKLHKEMVPR--PFLSSCIEECMIK
GRDLVD----TGAKY-----NIGPVLTGIGLAVTSNSLAVIKKLVFEDKVT-TMENLI--
----------KVLDANWE---------------------G-Y------------------
-------------------------EELRQ------------------------------
------------LAIA--VPKYGNDIDYVDDIAIKMANHYYKEG-HRY--KDI--N----
--GNNFITAFMGISN-YLPAGKVIGATSCGRKAREPLSE-GVSPFAGSDTSTPLAAMRS-
-AAKINQ-DVHSG-------------GTLLNLRLNEDLVSTKRG--QSNLGAMIQSFFS-
----LGAFHVQFNTISTETLRKAQNNPENYKDLLVRVAGYSTQFVNLSRAMQDAIIARTA
HENY-----------
>gi|150007435|ref|YP_001302178.1| formate C-acetyltransferase [Parabacteroides
distasonis ATCC 8503]
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------------------------------------------------------------
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------------------------------------------------------------
-----------------------------------------MNTTHHTHSCVHDTVSSVG
ANNFGMNDRIK-------------------------------------------------
------------------------------------------------------------
---------------------------RLR---------RQT-FE-AQPS-LSIERALIE
TRFYREN-YGKYPIP------IL----RALNFLEICKQKTIYIGED-ELIVGERGPR-PK
AVPTFPELT---CHSVEDLHI---LNTRELQ--R--------------------------
---YTISQEDIDTYE-REVIPYW-----KGRTQRERIFSH---VPK--------------
-EWKEAY----------------EVGMFTEFM---EQRAP--------------------
------GHTALD-GKVY--QYGLLDLKKRIEGELSALDFM------NDPEAT---DKQEE
LTAMSISCDAAILLAERHADLADEMSLTE-KDPRRAAELRKIAEVCRWVPAHAPRTYWEA
IQMYWFVHLGTITELNGWDA-MNPGHFDQHLAPFYEKEIA-A--GTLTRDE-----AKEL
MSCFFIKVNN-HTAPPKVGITAKESGTYNDFTNLN---IGGI-RA-DGS--DGVSEVSYI
MLETIEEL-HILQPGSAIHVS-ARTPERFLRAGCKVIR-QGHGYPSVFN-PDVYVQELMR
--------Q------G---KSLRDAREGGCS-GCIE------------------VGAFGK
-EAY------VLTGYLNV--PKILEVTLHNGV---DPVSGR-KV----------GL-ETG
DPR--GFRTYEELYAAFMRQIHYFVDMKVRVSNYIDRMFAKYAPA--TFLSLFIDDCIAK
GKDYYN----CGPRY-----NTTYIQ-CTGLGTITDSLSALRKHVFEDKTF-TMEALL--
----------DAMADNFE---------------------G-H------------------
-------------------------EPMRQM-----------------------------
------------ILNR--TPFFGNDDPYADQIAVRVFDDLYDAI-EGK--PNT--K----
--GECFHLNMLSTTC-HVYFGKVMGATPNGRLAGRAISD-GTSPSHGADTHGPSAVVKS-
-LGKLDQ--VKSG-------------GTLLNQRFLPSLLRREED--ISKLASLIRSYFA-
----LGGHHIQFNIVDTETLYAAQKCPEDYRDLLVRVAGYSDYFNDMNADLQADVIARTE
QETF-----------
>gi|153952960|ref|YP_001393725.1| glycyl radical activating protein [Clostridium
kluyveri DSM 555]
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------------------------------------------------------------
-----------------------------------------------------MTNSTLE
QTKRGSTERIR-------------------------------------------------
------------------------------------------------------------
---------------------------RLR---------EIS-DKKCKPS-ISMERAVLL
TEAYKMY-EGKFSIP------VL----RGLAFKYIMENRTLYIEKG-AIIIGEKGHK-PW
AAPTFPELC---CHTLKDFDN---MNNREKV--F--------------------------
---FKVSEEDKRIQK-EVIIPYW-----KDRALMTRMNKL---LPD--------------
-EWHKLF----------------DAGLYTEFL---MQRGP--------------------
------GHTVAD-GKIY--RKGYIDFINDIQYEIDHLDYN------NDVLAL---NKKEE
LEGMKLVCEGMIIFGERYADQARALASVE-NDPQWKEELLELAEVCDVVPKHAPRTFRQA
```

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VQMYWFTHIGVTTEMNNWDA-YSPGKLDQHLEPFYEKDIE-E--GRLTREE-----ALEI
LENLWIQFNN-QPTPPKVGITLKESATYTDFCNIN---TGAL-RP-DGT--TGVSEVSYL
ILEVMDEM-KLLQPSSNVQIS-RKTPEKFLREALKISR-KGWGQPAFYN-SEAIIQELLF
--------L------G---KSIDDARESGIASGCVE------------------TGTAGK
-EAY------VLTGYLNI--PKIFELVLNRGF---DSYTKK-QV----------GL-DLG
DPR--KFKSYQEVYDAFYKQLEYVVNVKIAGNNLIERMYMEYMPV--PLLSVITDDCIKS
GVDYNA----GGARY-----NTSYIQ-CVGIATITDSLVSIKKNVFEDKKF-SMDELL--
----------KACKADFK---------------------G-Y------------------
-------------------------DEIFET-----------------------------
------------VYNH--TPKYGNDDDYADDILRDVSQSLQDAI-AGR--TTP--K----
--GSTTVVEFLPTTC-HVYFGQVMEASPNGRHAGIPLPG-GISPEKGADRNGPTSVVKS-
-ASKIDQ--LKTG-------------GALLNQKFTPSVVQGEEG--ISNMATLVRSYFS-
----MDGHHIQFNVIDRKTLLDAQKHPEEYENLIVRVAGYSDYFNNLDRALQDEIINRTE
QSFA-----------
>gi|219853618|ref|YP_002470740.1| hypothetical protein CKR_0275 [Clostridium
kluyveri NBRC 12016]
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------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------------------MTNSTLE
QTKRGSTERIR-------------------------------------------------
------------------------------------------------------------
---------------------------RLR---------EIS-DKKCKPS-ISMERAVLL
TEAYKMY-EGKFSIP------VL----RGLAFKYIMENRTLYIEKG-AIIIGEKGHK-PW
AAPTFPELC---CHTLKDFDN---MNNREKV--F--------------------------
---FKVSEEDKRIQK-EVIIPYW-----KDRALMTRMNKL---LPD--------------
-EWHKLF----------------DAGLYTEFL---MQRGP--------------------
------GHTVAD-GKIY--RKGYIDFINDIQYEIDHLDYN------NDVLAL---NKKEE
LEGMKLVCEGMIIFGERYADQARALASVE-NDPQWKEELLELAEVCDVVPKHAPRTFRQA
VQMYWFTHIGVTTEMNNWDA-YSPGKLDQHLEPFYEKDIE-E--GRLTREE-----ALEI
LENLWIQFNN-QPAPPKVGITLKESATYTDFCNIN---TGAL-RP-DGT--TGVSEVSYL
ILEVMDEM-KLLQPSSNVQIS-RKTPEKFLREALKISR-KGWGQPAFYN-SEAIIQELLF
--------L------G---KSIDDARESGIASGCVE------------------TGTAGK
-EAY------VLTGYLNI--PKIFELVLNRGF---DSYTKK-QV----------GL-DLG
DPR--KFKSYQEVYDAFYKQLEYVVNVKIAGNNLIERMYMEYMPV--PLLSVITDDCIKS
GVDYNA----GGARY-----NTSYIQ-CVGIATITDSLVSIKKNVFEDKKF-SMDELL--
----------KACKADFK---------------------G-Y------------------
-------------------------DEIFET-----------------------------
------------VYNH--TPKYGNDDDYADDILRDVSQSLQDAI-AGR--TTP--K----
--GSTTVVEFLPTTC-HVYFGQVMEASPNGRHAGIPLPG-GISPEKGADRNGPTSVVKS-
-ASKIDQ--LKTG-------------GALLNQKFTPSVVQGEEG--ISNMATLVRSYFS-
----MDGHHIQFNVIDRKTLLDAQKHPEEYENLIVRVAGYSDYFNNLDRALQDEIINRTE
QSFA-----------
>gi|150003987|ref|YP_001298731.1| formate C-acetyltransferase [Bacteroides vulgatus
ATCC 8482]
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------------------------------------------------------------
----------------------------------------------------------MK
TTINGMTDRIR-------------------------------------------------
------------------------------------------------------------
---------------------------RLR---------QES-FD-TQPS-LSIERALIE
TEFYKEN-EGKYPIP------IL----RALNFLEICKRKTIYIGED-ELIVGERGPR-PK
AVSTFPELT---CHSVEDLHV---LNTRELQ--R--------------------------
---YTISQEDIDTYE-REVIPYW-----KGRTQRERIFNH---VPK--------------
-EWKEAY----------------EVGMFT-EF--MEQRAP--------------------
------GHTSLD-GKVY--QHGMLDLKERIAHELKNLDFM------NDPEAT---DKQEE
LTAMSISCDAAIIFAERHAELAEKMAGQE-TDPKRKEELKKIAEICRWVPAHAPRTYWEA
IQMYWFVHLGTITELNGWDA-MNPGHFDQHLAPFYEKDLE-E--GILTRAE-----AKEL
```

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MSCFFIKVNN-QTAPPKVGITAKESGTYNDFTNLN---IGGI-KR-DGS--NGVSEVSYI
MLETVDDL-HLLQPGSALHIS-VCTPERFLREGCKVIR-KGYGYPSVFN-PDTYVMELMR
--------Q------G---KTPEDAREGGCS-GCIE------------------VGAFGK
-EAY------ILTGYLNV--PKILEVTLHNGT---DPVSGK-KV----------GL-VTG
DPC--TFRSYEALYDAFLKQIHYFVDMKVRVSNYIDRMFAKYAPA--TFLSLFIDDCIAK
GKDYYN----CGPRY-----NTSYIQ-CTGLGTITDSLSVLKKHVFEERKF-NMEQII--
----------HATDTNFE---------------------G-Q------------------
-------------------------EAMRQF-----------------------------
------------ILNR--TPFFGNDDEYADRIAIQIFNDLYDAI-EGK--PNT--K----
--GECFHLNMLSTTC-HVYFGKMMNATPNGRLAGRAISD-GTSPSHGADTHGPSAVIKS-
-LGKLDQ--VKSG-------------GTLLNQRFLPSLLKHDED--IAKLASLIRSYFA-
----LGGHHIQFNIVDTATLHAAQKHPEEYRDLLVRVAGYSDYFNDMNTDLQYDVIARTA
QETF-----------
>gi|78358079|ref|YP_389528.1| formate C-acetyltransferase [Desulfovibrio
desulfuricans subsp. desulfuricans str. G20]
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------------------------------------------------------------
--------------------------------------------MNAVTHSYHDDTGRRQ
AAGLPLSARLR-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------AAY-LE-AKPS-ITIGRAMAY
TEIEKAY-PDL-PPV------LR----RAMGFRRACETAPVLIQDD-ELIVGHPCGA-PR
AGAFSPDTA--WKWLRDELDT---IGTRPQD--P--------------------------
---YMISEADKKIMR-EELFPFW-----EGRSLDEVCEDA---FRR--------------
-EGLWEF--------------CAEAGISDLSY--HHTSGG--------------------
------GDTSPGYDIILF-TKGINGLKAEAEAHLERLDA-------ENAGDS---SGADF
YRAAVIICEGVLLYAGRVAAHARQLAAAE-QNPARREELLAIAEVNTRVPANPPATFHEA
LQAVWTIQSLFLLEENQCS--TSLGRFDQYVYPCYEAGIR-N--GTLTREQ-----AFEL
TGCFIIKCSE-MIWY-TPGATARYFAGYMPFINMC---VGGQ-KR-EGG--DATNDLTLL
LMDAVRSV-GVYQPSLACRIH-NQSPQEYLEKIADVVR-AGTGMPACHF-DDAHIRMMLR
--------K------G---FDFDDARDYCLM-GCVE------------------PQKSGR
IHQW------TAGGFTQW--PVAVELVFNRGV---LRSYGR-RV----------AP-DTG
DPA--GFTSYAQFEAAVKTQLDYIMEMTARGTVINQKLVRDLMPT--PYMSLFVDGCMQT
GKDVTA----GGAVL-----YEGPGTIFAGLGTYADSMAAVRRLVFDEARY-TMAEMK--
----------QALAADWA---------------------G-F------------------
-------------------------EQMRR------------------------------
------------DCRN--APKYGNDDEYADGIARDIIDYTEKTI-NGF--KTL-------
--YARLIHGTLSQSF-NTPLGEMVGATPDGRAAGAPLSD-GMSPSQGADRKGPTAIIKS-
-VGRLNV-ESMSL-------------GMAHNFKLVHGCLETQEG--RAGLVSLLKTASV-
----LGNGQMQFNYVDDSMLRDAQRHPEQYRDLMVRVAGYSAFFVELCKEVQDEIISRTA
LH-------------
>gi|11499044|ref|NP_070278.1| pyruvate formate-lyase 2 (pflD) [Archaeoglobus
fulgidus DSM 4304]
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----MCMDRIE-------------------------------------------------
------------------------------------------------------------
---------------------------KLI---------KKV----SKPARLSVERCRLY
TESMKQT-EGE-PMI------IR----QAKALKHVLENIPIQILDS-ELIVGTMLPN-PP
GAIIFPEGV--GLRIINELDS---LPNRETN--R--------------------------
---LMVDEEDAKVLR-EEIAPYW-----QRKTIEAFAFPL---MPD--------------
-IMQILY----------------TGSVFV--L--TEIAGI--------------------
------SHVAVNYPYLL--RRGFRWFLEESERRIRALEE-------SGVYEG---EKYSF
YQAAKIVSEAVINYGLRYSKLAEELAESE--DGERREELLKIAEICRKVPAEKPETFWEA
VQFVWLVQSALHQENYEQA--ISMGRIDQYLYPFFKKDIG-E--GRINREL-----AFDI
LANLWIKTNE-IVPA-FDSLLEQYFSGQATNQAVT---IGGC-DI-YGN--DATNELTYL
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```
MLEVTDRL-RLRQPNVHVRIN-KGSPESFLKRLAEAIS-SGCNNLALFF-DDAAVKALKN
--------A------E---VDDRDALNYTTD-GCVE------------------IAPFGN
-SFT-S----SDAALINV--AKALEYALNEGV---DLQFGY-EF----------GA-KTE
KPK-----FLEDLLEKLREQVSHIVKLVVRGSNVLSYANAEVKPT--PLLSLCVEDCFEK
GVDVSR----GGARY-----NFTGIQ-AVGIADVGDSLVAIEGAL--NAGY-SMDDIV--
----------EACRKNFV---------------------G-Y------------------
-------------------------EKLHK------------------------------
------------LLLQ--SPKYGNDDDAADKYTKMVLEWYCEEV-NRH--RNF--R----
--GGKFAAGCYPMTT-NVGFGFFTSALPSGRKSGEPLNP-GVSPSTGMDREGVTAVINS-
-ASKLSY-ENLPN-------------GASLTINLSSDVL-GEKG--DAVIEALIKSSME-
----LGVMHVQFNILKEDLLRKAQQEPEKYRWLLVRVAGWSAYFVELSRPVQEEVIRRIS
CRI------------
>gi|197118876|ref|YP_002139303.1| pyruvate formate-lyase PFL [Geobacter bemidjiensis
Bem]
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------------------------------------------------------------
-----MTGRTE-------------------------------------------------
------------------------------------------------------------
---------------------------RLR---------QES-LD-AEAA-ISAERALLL
TEFYREN-EGRWSIP------VL----RAKSFYYLCEKKTIYLGDG-ELVVGERGPA-PK
LVPTYPELT---CHSLKDLRI---LNSREKT--S-------------------------
---YRVDDACLKAYG-ETVIPYW-----STRSLRDKIFRE---LPE--------------
-EWHEAY---------------QSGIFT-EF--MEQRAP---------------------
------GHTVLD-DKIY--NKGLLDFKKEIADAIAALDFV------SDPNAW---SKREE
LKAMDISCDAVILFAERHAKLAESMAAAC-ADAVRKQELLKIAANCRWVPAHAPTDFFEA
LQSYWFCHLAVITELNGWDA-FSPGHLDQHLYPFYRDGLA-A--GTLKKEE-----AREL
LECFFVKFNN-HPSPPKVGVTAAESGTYTDFANIN---LGGL-LP-DGS--DGSNEVSHL
LLDIIDEM-HLLQPSSNIQLS-RKSPDRFLKHTLRVVR-KGYGFPSIFN-ADSVVEEQLR
--------Q------G---KTLADARAGGCS-GCVE------------------VGAFGK
-EAY------ILTGYFNL--VKMLELALHDGV---DPATGA-QL----------GP-ATG
KTE--SFACFDDVFAAFTRQLAHFIDIKIRGNRLIEMIYAGLMPA--PFLSVLTDDCISR
GVDYNA----GGARY-----NNSFIQ-GVGIGSITDSLSAIKEHVFQEKAV-SLPDLV--
----------AKLDADFA------------------------------------------
-----------------------SDEPLRQR-----------------------------
------------LWNR--TRKYGNDDDFADDLMRQVFEAFFQQV-DGR--PNT--K----
--GGVYRIEMLPTTC-HVYFGSVTGAMPDGRRRGAPLSE-GISPVQGADRQGPTAVIRS-
-AGKMDH--IRSG-------------GTLLNLKFSPTLLAGEGG--VDGLAALVRSYFR-
----MDGHHVQFNVVDVETLKRAQADPRQYRDLIVRVAGYSDYFCDLSEELQNEIIARTE
HTSL-----------
>gi|78358095|ref|YP_389544.1| formate C-acetyltransferase [Desulfovibrio
desulfuricans subsp. desulfuricans str. G20]
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------------------------------------------------------------
------------------------------------------------------MKNVEK
VQYNKYEDRSRGN-----------------------------------------------
------------------------------------------------------------
---------------------------VMW---------DVL-NPLRYSQSMSMSRAQLL
MESYKET-ESL-HFF------RR----RGKAIRKILQEMPIRIDDH-QLLCGDFSAK-PM
GPEFFPDLA--ATWIVDYIDN-YGVEGRKGF-----------------------------
---FRWEDEEQMEIG-RSIGEYF-----RETGGKEKWIAF---LGD--------------
-EEAALE------------HKIGEAGSWIVNTVSEMFAEK--------------------
------AWNCPDLDRLV--KRGVRGLIADIDEQLEKFVM-------ITYEDY---RRHEF
WLGLKEMLLGGIDYAHRYRDLATELAAKE-TDPVRKAELEEMARVCNRVPEHPAETFQEA
LQSLVFGLLMVFYDTRTFG--MGYGRIDQIMYPQYKSDIA-S--GKIDDEY-----VVQL
FECFRVKIMG-KRQF-WPDVMTPNLSSESHFHNCV---ICGV-DPKTGR--DATNELSFA
FLEAAERV-RTTHPTISVRWH-TQIDPKFMKRALETVK-LGMGFPAFFN-DEPSIQYLLA
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```
--------R------G---YTMEEARNYALG-GCTL------------------HTVPGK
-TSS------IWPLVTSY--GRILELTMYNGW---DFISNS-QL----------GP-KTG
DFT--QMTSYEEFVAAYKAMIEYWANVSTKSGRAAKLQHGDTFPD--IMMSAFTDDCIGR
GKVCSL----GGAEHA----DSCMYIVPVAVQDVANELYVLKHGVFGENPICTPQEML--
----------DAMRANWE---------------------G-H------------------
-------------------------EELRA------------------------------
------------KCMA--MPKFGNDIPEVDQLLTDVYNWIKEIW-HAQ--PAT--D----
--GGRYEVSPHSIGF-HGGTGAKTGALPCGRKAGTSFSDGAVSPVQGTDVNGPSAVIKS-
-AGSIDQ-HDLY--------------GVLFNMRFSPSNIRGEKG--TANLASLIKTYFSD
----YKGKHIQFNVLNRDDLIAAKKEPEKYKDLMVRVAGYSAYWTDLPANIQDELIARTE
HEL------------
>gi|224367544|ref|YP_002601707.1| PflD1 [Desulfobacterium autotrophicum HRM2]
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------------------------------------------------------------
--MASLTERIL-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------EKS---RNAEVWIDPERAQII
TDFYSEN-AGKYSIP------VL----RARSFKNLMEKKELYLGDE-ELIVGERGRA-PK
LIPTFPEIA---CHSIKDLKV---LNSQNRI--P-------------------------
---YNVSPKTIKIYE-KKVIPYW-----DGAALRDRMFNQ---LSD--------------
-EWQTIY----------------NCGLITETM---EQRAP--------------------
------GSMALD-ERMF--GMGLKKAKQEIEEAIKNLDFL------NDFEAI---DKREQ
LTAMAITCDGMMIYAKRYADMLEKKSSEE-TNKKRKKEFEKMADVCRNVPANKPRDLWEV
LQMSWFMHIGVITESNGWDA-CNPGHVDRHFFPYYKKSLE-T--GQLDEES-----AKEL
LCAWWIKYNN-HPAPAKYGVSALESGTYNDFVNIS---LGGI-TT-DGK--DAVNDLSYI
FLEILDEI-EFIQPQVHVLLS-RMNPEHFLKEACKVIR-KGRGFPAMFN-AEAVIEQQLR
--------V------G---KTISDARGGGIC-GCVE------------------TTCYGK
-EAA------PLIGYINI--AKILELTLQNGF---DTRTKK-QV----------GP-KTG
NVK--DFNSYEELMEAFKKQARYIIDTKLVGSQYLIQMFAKYVPQ--PFLSVLIEGCVES
GKDYND----GGPKY-----NVSILP-GVGIGTVTDSLSAIKKHVFDESTY-SMGEVI--
----------EALNADWQ------------------------------------------
-----------------------KSEEMRLT-----------------------------
------------FANK--TPRYGNDNDYADSIMREVSDFFIDTV-DGI--KDS--R----
--GGTYRMNMLPTTC-HMYFGEVTGATCDGRRAGKPLSE-GISPVQGADLCGPTASLKS-
-AAKMDH-SRTC--------------GTLLNMKFLPDVLKGDIG--IHKLASLIRTYFT-
----YGGHHIQFNVCDAKTLQLAQKTPEDYNDLIVRVAGYSDYFNAIGKDLQDEIIQRYA
HEA------------
>gi|51244468|ref|YP_064352.1| formate C-acetyltransferase [Desulfotalea psychrophila
LSv54]
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------------------------------------------------------------
-----MNSRIE-------------------------------------------------
------------------------------------------------------------
---------------------------RLR--------QKSF----STQASISIERALLE
TEFYKEN-SGKYPLP------IL----RALCFQHLCQHKTLYIGDD-ELIVGERGPS-PK
AVPTFPELT---CHSAEDLHI---LNDRPMT--N-------------------------
---YRLSDEDINRYE-EEVIPYW-----QGRSMRDRIFKN---APE--------------
-EWRQAY----------------QAGLFT-EF--MEQRAP--------------------
------GHTALD-GTIY--REGMLDFKARIAGRIARLDFL------TDPRAA---DQREE
LQAMDISCNAAIIFAKRHAELAERMADKE--EGERRQELLEIARICRWVPAHAPRTMHEA
IQMYWFVHLGTITELNGWDA-MTPGHLDHHLHPFYENDLA-S--GILNREG-----AKEL
MACLWIKINN-HTAPPKVGVTAKESGTYNDFTQIN---LGGL-QR-NGQ--DGSNEISYI
ALEVSDEL-HLLQPQPSIHLS-QQSPTRLLASACEVVR-KGYGYPSFFN-ADGVVTQLVR
--------A------G---KSLEDAREGGTS-GCIE------------------TGAFGK
-EAY------ILTGYLNV--PKILEITLHNGI---DPLSGI-RV----------GL-ETG
```

```
EAS--FFQTFSALYKAFEQQLNHIIQLKVRMNNYIERMYGKYSPA--PFLSVVIHDCIEK
GRDYYD----AGPRY-----NSNYIQ-CCGIGTVTDSLSALKTHVFEGEL--SMEKMV--
----------KTLASNFQ---------------------G-E------------------
-------------------------EELRAD-----------------------------
------------LLNN--TPFYGNNDDLADDIMQRVYHSLFQGI-DGQ--KNT--K----
--GGEYHLNMLSTTC-HVYFGKMLGASANGRLAGLPTSD-GTSPSQGADLQGPTAVIKS-
-LGKMDQ--YKSG-------------GTLLNQRFLPAALKDESD--LKNLGHLIRTYFS-
----LGGHHIQFNVVDSKTLKKAQQHPDQYKNLLVRVAGYSDYFVDLDRAHQEEIISRTG
HGA------------
>gi|158520923|ref|YP_001528793.1| formate C-acetyltransferase [Desulfococcus
oleovorans Hxd3]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----MEDRIS-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------KVV--QEAVPG-VCPERALLW
TAYFKNRANRQKPVA------VQ----IAGAVSHVLKNKSIYIYPD-EILAGNYTSR-RV
GGIIYPESH--GISVLMEIFK---FHKRRLN--P--------------------------
---LETTPAHRWKLF--ATIPFW-----LNRNIIRKAFPT---IRQ--------------
-QLTFAV-----------------GQLTAREYQIYETGGI--------------------
------SHLTPNHEKIL--AIGLEGFLKEIEAHEQAATAP---------------EQRDF
YQAARIAAGGLIAFAERYADLARKMAKNE-ADPVRKADLERIADACKRVPRHGANTFFEA
VQAMLLTHISLFQESLGES--LCVGRMDQILWPYYQKDLS-E--GRLTRDQ-----AKEI
LGAFCVKLSE-TVPA-YPEILAKTLGGLTSYQVVT---TGGM-DK-NGE--DATNELSYI
LLELMDEL-RMRQPNSHVRIH-KNTPKAFYDKVVEVTT-GKGSAPALYN-DETIIATMQK
--------A------G---YTLADARNYVAI-GCVE------------------PTSQGK
TLGS------TDAAIINM--PLALELALNEGR----RFGARRRT----------GA-KTM
AVL--QMRTMADVTDAYRTQLRHQLGRLKNDLQAIEKAHAAFHPT--PLTSMLIDGCLEK
GKCSTS----GGAVY-----NFSGIQ-GVGVSTVGDSLYAVEKMVFEDRAM-GLAELV--
----------DHLKSGLS---------------------N--------------------
-------------------------EAVRT------------------------------
------------RLRR--LEKFGNDHAEADRWTRFVMDDYADAMAEMG--QTT--R----
--GGRYNAGLYSNTT-HIHFANFVGALPNGRRQGEPFAS-GIAPENGMDRRGPTALVNS-
-MNRLDF-TRMAN-------------GINFNIKFNALNMKDDAG--KNALGSIFRVYFD-
----RGGMQVQANMLDPEMLMAARDNPSLHPHLLVRVSGYSAYFNDLSPEMKDEIIARSF
VAA------------
>gi|50122690|ref|YP_051857.1| putative formate acetyltransferase [Pectobacterium
atrosepticum SCRI1043]
----------------------------------------------MDND------TLAP
DTNHFSF----------------------GNSIVNTEKMARRD-----------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-------------------------------------------------SSKKSSADEKV
AKQEMLTPRMQ-------------------------------------------------
------------------------------------------------------------
---------------------------RLR---------AHY-LE-ARPS-ISIYRALAF
TEVAKNN-PGL-PSI------LL----RAKSFRRACETAPILIQDE-ELIVGHPCGK-PR
AGAFSPDIA--WRWVRDELDT---MSTRPQD--P--------------------------
---FQISEEDKKTIR-EEIAPFW-----QGRSLDEVCEAQ---YRE--------------
-AGLWEF--------------SGETFVSDLSY--HQINGG--------------------
------GDTCPGYDVLLF-TKGMKGIKADAQAKLAELGM-------EDPAHI---DRIYF
YKAAIETCDGVMAYASRIAAHAREQAAQE-NDALRRAELLLIADVNENVPANPPKTLQEA
LQSIWTLESLFEIEENQTG--ISLGRVDQYCYPMYEADIQ-S--GRLTREQ-----ALEL
LQMFIIKCAE-LMWM-SSESGAKYFAGYQPFINLT---VGGQ-KR-SGG--DACNDLTYL
IMDAVRFV-KVYQPSLACRIH-NQSPHEYMEKIVDVVK-SGMGFPACHF-DDSHIKMMLR
--------K------G---FDFDDARDYCLM-GCVE------------------PQKSGR
-IYQ-W----TSTGYTQW--PIAIEFALNRGR---MILFDR-VQ----------GV-DTG
ELS--SLDTFEAFDRAVKTQIAHIIRLSAIGTVISQRVHRDIAPK--PLMSLLVEGCMEK
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```
GQDVAA----GGALI-----NHGPGLIFSGLATYVDSMMAIRKLVYEDRKY-TLEQMR--
----------DALLANFS---------------------G-Y------------------
-------------------------EMLHR------------------------------
------------ECLN--APKFGNDDNAVDPLARDITEWTEREC-RQY--KML--Y----
---STFSHGTLSISN-NTPIGALTAASANGRLAWAPLSD-GISPTQGADKKGPTASIKS-
-VSKMNV-ESMNI-------------GMVHNFKFLKGMLDTPEG--RNGLITLLRTSSI-
----LGNGQMQFSYVDDEVLRKAQQAPEKYRDLIVRVAGYSAYFVELCKEVQDEIISRTM
IEKF-----------
>gi|218780422|ref|YP_002431740.1| Formate C-acetyltransferase [Desulfatibacillum
alkenivorans AK-01]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------MPLSTNEKQARPASPG
LFLVKKKDRVT-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------EAV-QA-ATPG-ICTERALLW
TEYFKDKANQSKHVY------VQ----MAEALAHSQKNRSIAVHPG-ELIVGNYTSR-RV
GGLLFPELH--GLVVMQDLFK---FPNRETN--P--------------------------
---LEVSRLDQARLL-S-IAPFW-----ATRMLAVKTCDS---WLD--------------
-TFSLVL-----------------NQLMGNYYIINEAAGI--------------------
------SHIAPDYETLC--RLGTDGIAAKAAKLQK-----------QSLMDA---DKWYF
YESVRIAAEGLAAFGERYAQLAGEMAERE-LDEDLAAELKGIAEVCSRVPRKGAKTFREA
LQSCFFAQIAINNESLDNS--VCPGRMDHYLYPYYEKDLK-A--GLLTREE-----AKEL
AGAFSVKMSE-IVPV-FSKYITRTHGGFFNGQIVN---VGGT-HK-NGK--DSTNELTMI
FLEVMDEL-RMRQPNYTARVH-KNSPKEYLDKVYGILS-KGANSPSIYN-DEVIVPVLKQ
--------N------G---VKIGDARNYTPV-GCVE------------------PVAQGV
-SFS-S----TDAALFNT--AIILELALNQGR----RLGRVAQI----------GA-KTK
PVS--QMTCIEDVQEAFEIQMFHGINRLLKDLQAIEIANAEYHPT--PLSSMLLDGCLEN
GACSTR----GGARY-----NFSGIQ-CVGLVDAGDSLAAIKQAVFEDKKL-SMEELV--
----------EHLKNNLS---------------------D--------------------
-------------------------DRWRH------------------------------
------------YLLN--MPKFGNDDPFADVWTAYALDVFKAAL-DGK--TST--R----
--GGKYTVGVYSVTL-HEYWGTVVSALPNGRRNGESLSN-GMSPSNGQDRKGPTAVLNS-
-MNRIDY-SKTDN-------------GINFNIKFDANTVGSPAG--CTAMKSIFSTYFK-
----RGGMQAQINVLDPKVLIEARDNPEAYPHLLVRVSGYSAYFNDLTPAMKEEMIRRTS
MGL------------
>gi|218779327|ref|YP_002430645.1| Formate C-acetyltransferase [Desulfatibacillum
alkenivorans AK-01]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---MAIHSFNQ-------------------------------------------------
------------------------------------------------------------
---------------------------CYK---------DLI-LT-APYE-ICIERARYY
TQSYRET-EGM-HPS------LR----AAKALHLTLSNMSLNILQG-EQIIGNRSGK-TL
GVVIPVERGDVNAILEMELDF---LLNRSRQ--P--------------------------
---FSIDPDDRRELE-EDILPYW-----RGRTVRDRKKVL---WKENGLNFKPAVDPLSL
YKRHKSL----------------DLQKIKKAA--KVPGGDAAYALKGMKEILHNNPALVM
NVFDVQGHLILGIKNVL--SQGFSGIMAQAEKGLAEA---------KEAGKA---DDAAF
YESVMISCEAAKILAERLAKKAEEAASEE-NDPDRQRELLAAAKRCRHSPWNPPRTFHEA
VQAMWLI-LLGGLVSHGMVGILAVGRLDQYLYPYYKKDVE-S--GRIDQAM-----AVRL
MEELLIKLGA-NLMI-LP--YVGKNTGNELGSDSCVPTIGGV-DA-QGK--DAVNPLTYA
VLEAFANV-KSLGNSFTVRLS-QESPPEFWQKALETYR-ETSG-AALFN-DEIVTPALQN
--------C------G---MTLEDARDYGVI-GCVE------------------PTGDGD
------AFGCTSGNDVSL--SAALEMALGDGY---LRVMGK-AI----------GP-KTG
NPK--KFKTFDQVLEAFKKQVEFMVDTVARAVNLKDQIYMEEYHN--PYISCTLTGCLDN
ARDMTQ----GGAKY-----NFGSIS-GRGMGTAADSLAAIKCFVFDQKTF-SMAKIL--
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----------KMLDCNFK---------------------G-Y------------------
-------------------------DKERAM-----------------------------
------------LAHR--APAFGSDDPYADDIAKEVCAFFCKTV-ASK--QTL--R----
--GGPFRPSFFSYGV-HVLEGLYIGATPNGRLAGTPVSN-SLSPTNGSEKQGPTGVLGS-
-VAKLDH-SLISN-------------GSSVNIKLMPSMFQGEER--LNKMIGLVKGFFA-
----SGGMEVQPNVVSNQTLLDAQKHPENYRDLVVRVSGYSAFFTDLGKPIQDEIIQRTE
FEGL-----------
>gi|147678771|ref|YP_001212986.1| pyruvate-formate lyase [Pelotomaculum
thermopropionicum SI]
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
---------------------------------------------------MDKIIAEEI
KKVNVMTPRLQ-------------------------------------------------
------------------------------------------------------------
---------------------------RLK---------KEW-ED-AQPT-VYVDDTLLF
TESWKET-EGL-PLD------IR----WAKAFEKKMLECPIVIRDG-ELIVGSNTKF-IR
GNSTLVAMKPREILAMCESGR---FDRKSSDISA--------------------------
---VNIDPEDLRKLK-E-DAEYWVEHMPKYDAVNEAIRAE---LGD--------------
-DHFDLMFDHGMIYEGRAVRHHRDRGLFQNWG--AFGGGN--------------------
---------CMPTKPAI--DNGLNYIIALAKDELNRMEKLGAFVQGAASNAF---RKYNL
LKAIIISCNAVIKFAERHAELARKQAESC-TDPVRKAELLKIAEVCQNVPANRPRNFWEA
VQSLRFLHLAAWKESTERPE-VGVGRIDQILYPYYKKDID-E--GTLTRQD-----AAEL
LGALWLKIRE-TENL-VTIKREHRAAPGTLLPNVT---LGGR-NE-LGE--DLINEVSWI
VLEVMRQT-KLSEPAIYIRYH-DGIDEDFMIHALECNRDFGGGNPAFLN-DELGTQRYLA
--------R------G---VPLKDAVNWNAS-GCLG------------------YHLDCG
-E--------HQGGFFSLNHAKIFEITLYNGF---DPRTGK-QL----------GL-KTG
DVT--KFTSLQQFIDAFYKQVDYFCERLRKHYFIWWCVEQEISPMSGLRAAMLYEDCIPA
GLCSRE----GGARYPSLRSSWIGDR---GITDIADSLAAIQHLVFDTKQV-TMAELL--
----------DAMRNNWE---------------------G-K------------------
-------------------------EELRQ------------------------------
------------MCLN--APKYGNDEDLPDNLFGELMFGTQRIM-QSR--PDP--I----
-TGEKPILFKGAAAG-HITQGASVGALPNGRFAYKPLNDAASSAMPGMDVNGPTAVINS-
-ATKGNY-AFEYV-------------GFTHNMKFSKQTLNTPEK--LKKLINILKTFFK-
----RGGWHIQFNIHSVEELLDAQKHPERYRNLLVRVGGYSAYFIDLPPELQEEIVQRTM
HEL------------
>gi|46580677|ref|YP_011485.1| formate acetyltransferase, putative [Desulfovibrio
vulgaris subsp. vulgaris str. Hildenborough]
------------------------------------------------------------
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------------------------------------------------------------
---------------------------------------MAALSSASNTEGQTPANKGYG
INWDTAESRVK-------------------------------------------------
------------------------------------------------------------
---------------------------ELK---------DFL-L--AAPQVMDPERLQCL
LDVYDEF-QGE-PVV------YI----RAKLLERVLLRKKIFL-DG-NPIVGTLTGV-RA
GVYAYPEWN--VSWIKEEMQM---AKMASLG--E--------------------------
---MKIPQETQELLE-K-TYKLW-----KGRTCIDLNNKM---FKE--------------
---KYGI----------------NPAPFAKAG--MYYENV--------------------
--SVASGSGIADYPLVL--NKGLRWLADDVRARFEACP--------TTLANK---EKHDL
YRAMLVTFEAVIAHSHRYAELAEKTAAEE-SDPKAKAELLEIAEICRRVPEYPARNFREA
IQSFWFIHLAIETEQMACA--TSPGRYGQYMYPFYKKDIE-E--GNLTREQ-----VLTL
LKFQWIKHLE-LGEY-QGASYAMTLSGHT-GQSIT---IGGV-DA-NGD--DASTELEEV
LLDTQIQM-KNIQPTLTLLYH-PKLKDSYMKKVVECIR-GGSGQPQILN-NNVVIQRNLA
--------RFAQYEGG---ITLEDARNCGNY-GCVS------------------TGICGK
-GSF-I----TQEDQPCL--AKVVELMLNNGK---CPVTKK-QV----------GV-ESG
DPT--TFTTFEEVYEATKKQLDHLFNISRKHSDLSQMARLQVVPS--VFRSAMYDGCIDK
GMCEEA----GGTRYP----QVNPIM-TAGI-DAANSLLAIRYLVFETKQV-TMEKLL--
----------EALKANFE---------------------G-Y------------------
```

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-------------------------EDIRK------------------------------
------------MCFE--APKHGNDYPEVEHFVQRFYRDVDAIHSAQG--PDC--F----
--GYRTPLDAYSLSY-HNYFGSLMGALPNGRKAGVALTDGSVSAMPGTDHEGITALIKS-
-GAEAID-TVRYG-------------ANHFNVKFNPSVIEGPAG--ARTLVSLIKTYCD-
----FGGSHIQFNCVSSDTLKDAQCKPQEYADLVVRVAGFSAYFTRLDKGVQNEIIKRTE
YKN------------
>gi|120602027|ref|YP_966427.1| formate C-acetyltransferase [Desulfovibrio vulgaris
subsp. vulgaris DP4]
------------------------------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
---------------------------------------MAALSSASNTEGQTPANKGYG
INWDTAESRVK-------------------------------------------------
------------------------------------------------------------
---------------------------ELK---------DFL-L--AAPQVMDPERLQCL
LDVYDEF-QGE-PVV------YI----RAKLLERVLLRKKIFL-DG-NPIVGTLTGV-RA
GVYAYPEWN--VSWIKEEMQM---AKMASLG--E--------------------------
---MKIPQETQELLE-K-TYKLW-----KGRTCIDLNNKM---FKD--------------
---KYGI----------------NPAPFAKAG--MYYENV--------------------
--SVASGSGIADYPLAL--NKGLRWLADDVRARFEACP--------TTLANK---EKHDL
YRAMLVTIEAVIAHSHRYAELAEKTAADE-SNPKAKAELLEIAEICRRVPEYPARNFREA
IQSFWFTHLAIETEQMACA--TSPGRYGQYMYPFYKKDIE-E--GNLTREQ-----VLTL
LKFQWIKHLE-LGEY-QGASYAMTLSGHT-GQSIT---IGGV-DA-NGD--DASTELEEL
LLDTQIQM-KNIQPTLTLLYH-PKLKDSYMKKVVECIR-GGSGQPQILN-NNVVIQRTLA
--------RFAQYEGG---ITLEDARNCGNY-GCVS------------------TGVCGK
-GSF-I----TQEDQPCL--AKVVELMLNNGK---CPVTKK-QV----------GV-ESG
DPT--TFTTFEEVYEATKKQLDHLFNISRKHSDLSQMARLQVVPS--VFRSVMYDGCIDK
GMCEEA----GGTRYP----QVNPIM-TAGV-DAANSLLAIRYLVFETKQV-TMEKLL--
----------EALKANFE---------------------G-Y------------------
-------------------------EDIRK------------------------------
------------MCFE--APKHGNDYPEVEHFVQRFYRDVDAIHSAQG--PDC--F----
--GYRTPLDAYSLSY-HNYFGSLMGALPNGRKAGVALTDGSVSAMPGTDHEGITALIKS-
-GAEAID-TVRYG-------------ANHFNVKFNPSVIEGPAG--ARTLVSLIKTYCD-
----FGGSHIQFNCVSSDTLKDAQCKPQEYADLVVRVAGFSAYFTRLDKGVQNEIIKRTE
YKN------------
>gi|218782693|ref|YP_002434011.1| Formate C-acetyltransferase [Desulfatibacillum
alkenivorans AK-01]
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------------------------------------------------------------
---------------------------------------MGKTASPNSAIQEANPYLENP
CLFPQASDRIL-------------------------------------------------
------------------------------------------------------------
---------------------------AIK---------AEL-M--AEPYSICLERPSLL
FEFWESK-NGKAAKN------LHPAEARALMLAHIMRRRRPRIYNH-ELIIGNMSSK-RI
GANFYPEGG--SLNILEDLLH---LENRQI---P--------------------------
---FKLAPMEKAELL-RLGLKSIPVSIGGKALLKPGRFSH---FLD-------------F
FRAKRYF------------------------V--TEEAGI--------------------
------SHQAGNYGEVV--SHGLVKADLYARDRLKADALED-----GTRLNA---DQRAF
YKSVRTIILGIRNMASNLAAEAEKKAAAQGVALERRKELLEAAEACLHAPYYPARTFKEG
LQACWLVHMAMNLEDFEQG--LSFGRLDRILLPLYKADLK-K--GLLTYEK-----AVEI
MASFQLKTCE-TIPI-YSERIDQYFSGNGVAQGIT---VGGV-NG-GGR--DCTNELSGL
VLDAFSQI-KTREPALHVRVH-KKTPPWFLEKAAAVAA-LGCGKPSFFG-DKAVIKALEN
--------T------G---MSKPHARDYAVI-GCVE------------------MASQGR
-TYN-S----SDAALFNL--PLCLELALNQGYRFGSRRIPALRF----------GA-PTP
SVE--EMDAFDQVLRAFKTQVRDSVNEMVKVITMIEQAYRVHRTT--PVNSIITQGCLEC
GKDVTW----GGAMY-----DLTSVQ-AAGLADAGDSLYALKRVVFDEKRM-SLKAFV--
----------DILKSNWE---------------------G-Q------------------
-------------------------EKLRQE-----------------------------
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------------ISQK--FPRYGNGDKDADRMTQVAADAYTDAV-TAH--KNS--R----
--GGQYIAGIYSMTC-HHGFGKATGALPNGRPAGYRLSN-GLSPVDGVDKKGPTAVLQS-
-AASLDS-SQWGN-------------CCALNIKFDGNQFKGTKG--AKILSGLITAYMN-
----MGGMQIQPNILDAETLREAKEDPSAHPGIVVRVAGYCAYFNDLQPMVQDEVISRTS
HGAE-----------
>gi|126697725|ref|YP_001086622.1| 4-hydroxyphenylacetate decarboxylase, catalytic subunit [Clostridium difficile 630]
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------------------------------------------------------------
-------------------------MSQSKEDKIRSILEAKNIKSNFQ-NKENLSEFNEK
KASK----RAE-------------------------------------------------
------------------------------------------------------------
---------------------------DLL---------DVY-YN-TLST-ADMEFPYWY
NREYRKS-DGD-IPV------VR----RAKALKAAFSHMTPNIIPG-EKIVMQKTRH-YR
GSFPMPWVS--ESFFVAQGEQ---MREEAKKLASNTADELTKFGSGGGNVTESFGNVVSI
AGKFGMRKEEVPVLV-K-MAKEW-----VGKSVEDLGFHYEKMMPD--------------
YDLKENL-------------MSTLICMFDSGY--TLPQ----------------------
------GREVINYFYPL--NYGLDGIIEMAKECKKAVAGNASG---DGLIGM---DRLYF
YEAVIQVIEGLQTWILNYAKHAKYLESIE-TDLEAKKEYSDLVEILEHIAHKQPRTFREA
LQLTYTIHIASVNEDAISG--MSIGRFGQILYPWYEQDIE-K--GLITKEE-----VIEL
LELYRIKITC-IDCFASAGVNGGVLSG-NTFNTLS---IGGL-KE-DGS--TGANELEEL
LLEASMRC-RTPQPSLTMLYD-EKLPEDFLMKAAECTK-LGSGYPAWVN-NSNGTTFMMK
--------QFADE--G---MTVEEARAFALG-GCLETSPGCWKQLTLNGKTYSIAGGAGQ
-SAG------SGVHFIAN--PKILELVLMNGK---DYRMNI-QV----------FE-PHN
K----PLDTYEEVIEVFKDYYKQAINVLERANNIELDIWRKFDTS--IINSLLKPDCLDK
GQHIGN----MGYRY-----NATLNVETCGTVTMVNSFAALKKLVYDDKAF-TIEEMK--
----------DAILNNFG--------------FKDALEVGNY------------------
-----------SMADQVKVDKTGKYDAIYK------------------------------
------------ACLD--APKYGNNDLYADNILKNYEVWLSKVC-EEA--QSL--Y----
--AKKMYPCQISVST-HGPQGAATLATPDGRLSGTTYSDGSVSAYAGTDKNGVYALFES-
-ATIWDQ-AVVQN--------------SQMNLKLHPTTIKGQQG--TKKLLDLTRSYLR-
----KGGFHIQYNVVDSETLKDAQKNPDNYRQLMVRVAGFTQYWCELGKPIQDEVIARTE
YEGV-----------
>gi|56476471|ref|YP_158060.1| alpha-subunit of benzylsuccinate synthase [Aromatoleum aromaticum EbN1]
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------------------------------------------------------------
---------------------------MTGAQTMEYKGKVLQFTPENPAEADIPADELHE
HLQNPSTERTR-------------------------------------------------
------------------------------------------------------------
---------------------------RLK--ARCRWKHASAGEFCEKGVTAGIERMRLL
TESHWDT-RGK-PEP------IR----RALGLKNILDKCTLVLQPD-EFIVGYHAED-PN
MFPLYPELS--YMAVQDYLKS------------K--------------------------
---YSPQPAKEA----QEIVDYW-----KPFSLQARCEPY---FDP--------------
VDLRRGY----------------QVSTIEGPV---FASGY--------------------
------NSVIPPYETIL--EDGLLARIALAEKNIEHARAEMEKFPWNAPTGLEWIDKIDN
WEAMVIACKAVIAWARRHARLCKIVAERFETDPKRKAELLEIADICQRVPAEPARGLKDA
MQAKWFTFLICHAIERYAS--GYAQKEDSLLWPYYKASVIDKTFQPMEHKD-----AVEL
IEMERLKVSE-HGAG-KSRAYREIFPGSNDLFILT---LGGT-NG-DGS--DACNDMTDA
ILEAAKRI-RTTEPSIVFRYS-KKNRAKTLRWVFECIR-DGLGYPSIKN-DDLGIQQLLE
MAKYSRNGN------G---VTPEEAHYWVNV-LCMA------------------PGVAGR
RKAQ--KTRSEGGSAIFP--AKLLEITLSNGY---DWSYADMQM----------GP-ETG
HAK--DFATFDQLWEAFRKQYQYAIALAIRCKDVSRTMECRFLQM--PFVSALDDGCMEL
GMDANA-----------LSEQPNGWHNPITTIVAGNSLVAIKKLIYDEKKY-TMEQLM--
----------DALKANWE---------------------G-Y------------------
-------------------------EEMRR------------------------------
------------DFKN--APKWGNDDDAADTLISRFYEEILGGEMMKN--INY--S----
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--GGPVKPVGQAVGL-YMEVGSRTGPTPDGRFGGEAADDGGISPYSGTDKKGPTAVLRS-
-VSKVQK-NQKAN---------------LLNQRLSVPIMRSKHG--FDIWHAYMDTWHE-
----LNIDHVQFNVVSTEEMKAAQREPEKHQDLIVRVSGFSARFVDIPTYGQNTIIARNE
QDFNAQDLEFLNAEL
>gi|218780042|ref|YP_002431360.1| Formate C-acetyltransferase [Desulfatibacillum alkenivorans AK-01]
------------------------------------------------------------
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------------------------------------------------------------
----------------------------------------MTAEPAKLDVSLQEHEENQE
WWWIAEKKRSK-------------------------------------------------
------------------------------------------------------------
---------------------------RLDYLRKAVWKKGALGGNYAPGIKVDLEGPKLF
TDMWNFWKFD--PII------MR----RAKALAHVFDNISIFITDH-SQIVGYWGSA-PH
TISWRVDGA---SIVNEELYN---EPG---------------------------------
---IMPEPEEESLRKVAEINDYW-----AGQTAVDKVARI---LDP--------------
-EDAVKF----------------LSGAIGWGA---PTSAY--------------------
------GYSGKNYEYYLKGERGFEDIIADIEDHIAEAEEKTIGT--PGPDILPIYDRIQN
WEAMITVLEAAIRFAKRYARLARTMAEHLETDEKRKEELLRIAETCERVPAKAPRNLQES
FQMDMLIQTMCRFEASEGA---WPARPDYYHGPFYEKDVLQD--KTLTEEE-----ATDL
IGEFMIRAYE-VGGF-GPRWAREGMQGITGTWVWT---IGGV-KP-DGS--DACNALTTA
FLRTARLI-RVSNPTFAFRWH-PKVSDEVMRECFECIR-HGLGYPSFRH-DPILVANCMN
-------WH------G---HPVEEARTWVHQ-ACMS------------------PCPTTK
NGVQPFR---MASATANC--AKMVEYALHNGY---DHVVGM-QM----------GP-QTG
DAR--TFTDFEQLFDAWTRQMQWLLSLLVRTVNLGRYKDAEFYGR--PLLSGITERAVER
GIDAVNPEGERGNCW----------ITGFTWVENADSLAAVKKLVFDDKKY-TMDQLI--
----------TALESNWD---------------------G-Y------------------
------------------------EQMRLD------------------------------
------------FVNK--APKWGNDDDYVDDIMLRCLRTLAKHS-RVM--RCT--S----
--NNTWPISPQNVSG-NIHYSSVVGALPNGRRLGDALYDGGISPGPGLDKKGPTAVLKS-
-CGKIDH-VGDGR-------------AFLLNQRLSPTQMAGEKG--YQLWRAYMRTWAD-
----LGLDHIQFNMVSDKTLRAAQKDPEKYQEVIVRVAGYSAHFVDISRKTQDNIIQRTV
QGI------------
>gi|187935567|ref|YP_001885917.1| 4-hydroxyphenylacetate decarboxylase, catalytic subunit [Clostridium botulinum B str. Eklund 17B]
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------------------------------------------------------------
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------------------------------------------------------------
---------------------------MNKKTKLADILAEKGLPINFQFGGEAPEEMTTR
EINKEPAPRAK-------------------------------------------------
------------------------------------------------------------
---------------------------RLR---------EIY-YD-TLST-ANTEFPYWY
NRRWNEL-EGE-VDV------VR----RAESLKCAYSHLTPNIIPG-EKLVMQKTNY-YR
GSFPMPWLS--EGFFVAKEDE---LYKEALNRGSASAGELSKFGTGGGNVTKSFGSVVSI
AGKFGMRQEEIPALV-K-LAKEW-----VNRSVDDLGHKYEQMVPG--------------
YEIKENI-------------MKSLICMFDSGF--TLPQ----------------------
------GREVVNYYYPL--QYGFDGLIDMAMECKKKVAGNADG---DGLVGM---DRLYF
YEAVKITLQGIQNWILNYEKHARDLALIE-KNEVQKEEYLEIADCLGWIAHKQPRTFREA
LQLTYIIHIAVINEDAISG--LSPGRVGQVLYPWFKQDME-N--GRITEKE-----VLEL
LELHRVKFTC-IDCFASTGVVGGVLSG-NTFNNLT---LGGL-KK-DGS--SAANRLEYL
IVEAGITC-ATPQPTLSCFYD-EKLPEEFLLKCIECDK-TGSGYPAWMN-NRGAIEFMMN
--------QYSDE--G---MTIEEARSVAIG-GCLETSPCTWKELTLNGEKFDIPGGAGQ
-PTS------VGVHFIAN--PKVLELVLTNGK---DYRTNL-QV----------YP-PHN
K----KLETFEEVVNQFKEYYELTCDVLAKTNNIQHDIWRKKNMS--IVNSLLKPNCLDA
GKHIGN----LGYRF-----NATYNVESCGTINTINSLASLKKLVYDDKKY-TLDEMR--
----------EAMLHNFG--------------FKTAEEIGSY------------------
-----------SLADQEKADISSKYDDIYG------------------------------
------------DCLL--APKYGNDDSYVDSILKDYEDWFCDVC-HNY--ESL--Y----
--GKKMYACQISVST-HGAQGAATLATTDGRLAGTTYADGSMSAYPGTDKNGPYALFTS-
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-ATVWDH-SRSQN--------------SQMNLKIHPSAIKGIEG--SKKLLDLTRSYMR-
----KGGYHIQYNVVDSKVLKEAQVKPENYRDLMVRVAGFTQYWCEIGKPIQDEVISRTE
YEGV-----------
>gi|218779578|ref|YP_002430896.1| Formate C-acetyltransferase [Desulfatibacillum
alkenivorans AK-01]
------------------------------------------------------------
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------------------------------------------------------------
-----------------------------------------MVAEPAQDQSVQELEDKQE
WWWVAEKKRSK-------------------------------------------------
------------------------------------------------------------
---------------------------RLDYLRKSIWKKGALGGNYAPGIKLDLECATLF
TDMWKFWKYD--PIM------MR----RAKAIAHVLDKKTIFITDH-AQLVGYFGSL-PN
TIMWRVDGA---SMVNEEAYN---EPG---------------------------------
---IMPEPENESLQKVAELNDYW-----AGQTAVDKVARI---LDP--------------
-EDAVKF----------------LSGAIGWGA---PSSAY--------------------
------GYSGKDYEYLFAGRRGFEDIIEEINAAIEKAEDKTVGV--PGPEILDIYDRLQN
WDAMILVLEAGIRHAKRYARLARTMAENMETDEKRREELLKIAETCERVPARAPRNLQES
LQYDHFIQIFARTEAHEGA---WPARPDYYHGPYYDKDVNVD--KTLTKED-----ALDL
VGEFMIRAYE-VGGF-APRWAREGLQGITGTWVWT---LGGV-NK-DGS--DACNDLTVA
FLQAARLV-RVSNPTFGFRWH-PKVKDEVLRECFECIR-HGLGYPSMRN-DPLLIQNAMH
-------WH------G---HPLEEARTWVHQ-ACMS------------------PCPTTK
HGVQPMR---MASATANC--AKMVEYALHNGY---DHVVGM-QM----------GP-ETG
DAA--KFHDFEDLFQAWVKQMEWLTSLLVRTVNLGRYKDPEFFGR--PFLSGMSERSVES
GLDVVSPVGDRGNCW----------VTAFTWVENIDSLAAVKKLVFDDKKY-TMEQLL--
----------TALKANWD---------------------G-Y------------------
-------------------------EEMRLD-----------------------------
------------FVNN--APKWGNDDDYVDDIMLRCLRETARHS-RVM--KCP--S----
--GNSWPILPENVSG-NIHYASIVGALPNGRRCGDALYDGGISPGPGLDKKGPSAVLKS-
-CGKIDH-VSDGR-------------AFLLNQRLSPTQLAGEKG--YQLWKAYIRTWAD-
----LGLDHVQFNMVSDETLRAAQKDPEKYSEVIVRVAGYSAHFVDISRKTQDNIIQRTV
QGI------------
>gi|188589129|ref|YP_001921253.1| 4-hydroxyphenylacetate decarboxylase, catalytic
subunit [Clostridium botulinum E3 str. Alaska E43]
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------------------------------------------------------------
---------------------------MNKKTKLADILAEKGLPINFQFGGEAPEEMTKR
EINKEPTPRAK-------------------------------------------------
------------------------------------------------------------
---------------------------RLR---------EIY-YD-TLST-ANTEFPYWY
NRRWNEL-EGE-VDV------VR----RAESLKCAYSHLTPNIIPG-EKLVMQKTNY-YR
GSFPMPWLS--EGFFVAKEDE---LYKEALNRGSASAGELSKFGTGGGNVTKSFGNVVSI
AGKFGMRQEEIPVLV-K-LAKEW-----VDRSVDDLGHKYEQMVPD--------------
YEIKENI-------------MKSLICMFDSGF--TLPQ----------------------
------GREVVNYYYPL--QYGFDGLIDMAVECKKKVAGNADG---DGLVGM---DRLYF
YEAVKITLEGIQNWILNYEKHARDLALIE-KNQSQKEEYIEIADCLNWIAHKQPRTFREA
LQLTYIIHIAVINEDAISG--LSPGRVGQVLYPWFKQDIE-N--GRITEKE-----VLEL
LELHRVKFTC-IDCFASTGVVGGVLSG-NTFNNLT---LGGL-KK-DGS--SAANRLEYL
IVEAGITC-ATPQPTLSCFYD-EKLPEDFLLKCIECDK-TGSGYPAWMN-NRGAIEFMMN
--------QYGDE--G---MTIEEARSVAIG-GCLETSPCTWKELTLNGEKFDIPGGAGQ
-PTS------VGVHFIAN--PKVLELVLTNGK---DYRTNL-QV----------YP-EHN
R----KLETFEDVVNQFKEYYELTCDVLAKTNNIQHDIWRKKNMS--IVNSLLKPNCLDV
GKHIGN----LGYRF-----NATYNVESCGTINTINSLASLKKLVYDDKKY-TLDEMR--
----------EAILNNFG--------------FKTAEEIGSY------------------
-----------SLADQEKAGISSKYDDIYG------------------------------
------------DCLL--APKYGNDDPYVDSILKDYEDWFCDVC-HNY--ESL--Y----
--GKKMYACQISVST-HGAQGAATLATTDGRLAGTTYADGSMSAYPGTDKNGPYALFTS-
-ATVWDH-SKSQN--------------SQMNLKIHPSAIKGIEG--SKKLLDLTRSYMR-
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----KGGYHIQYNVVDSKVLKEAQVKPESYRDLMVRVAGFTQYWCEIGKPIQDEVISRTE
YEGV-----------
>gi|94989382|ref|YP_597483.1| formate acetyltransferase [Streptococcus pyogenes
MGAS9429]
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-----------------------------------------M------------------
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------------------------------------------------------------
------------LIND--APKYGNDDDYADSLVVEAYDTYIDEI-AKY--PNT--RYGRG
PIGGIRYSGTSSISA-NVGQGKGTLATPDGRHAGTPLAE-GCSPEHSMDKKGPTSVLKS-
-VAKLPT-DEIVG-------------GVLLNQKVNPQTLAKEED--KLKLMALLRTFFNR
----LHGYHIQYNVVSRETLIDAQKHPEKHRDLIVRVAGYSAFFNVLSKATQDDIIERTE
HTL------------
>gi|218778683|ref|YP_002430001.1| Formate C-acetyltransferase [Desulfatibacillum
alkenivorans AK-01]
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------------------------------------------------------------
---MLFQFQSNGSSKPAFSWTNLLIKNLLRLMALNFNLRPGLNQYLKSVDGWMNFSANLR
TENNSLNASIVFKDGKAFVPAVAPDPCDISLIFRDDKTVRKLLGSTPTEQIFMLLKSELR
TQGNQTYLNLLFFYLNLLLKKKAYKLIEKEKQASAKQAKELVPDSKPELSHALLDRKNHR
LKGPKVDPGIRFLDDPYLSQYSLEDFPRLS---------RFLDIHFTQKGEICPERPKIL
TDWFKEHGFEKNASGKDWIPELR----QGLVFKHLMENRKPIIRKD-DLLAGTSTTK-EV
GVIVYPDAH--GTMLWGELYT---VPHRSLN--P--------------------------
---YDVSEDTVRLLH-HEVFPYF-----THRNFKEWVRYN---YQS--------------
-PLCQAI----------------DERYAVYFV--WKQAAL--------------------
------SHTIPDFPKIL--SLGASGVINEIKGKLNQEGL-------SD-------RQKGL
LEGMIHSMEGMIAYSKNLSAQAAEEAAQE-SDPKRKAELENIAQACAQVVENPARNLDEA
VNAVWITWVGMHMENTNAG--LSMGRLDQWLQPYYETDLEKISDGKEREAY--IKHAIEL
VGCLFMRCTD-HLPL-TPDLANWYFGGSSSDQAIT---LGGV-TP-EGK--DAVNDMTYI
FLKVTEML-GIRDPNVNARYNREKNSDAYLKRLCEVNL-ITAATPSLHS-DQAVIESLKE
--------F------D---YAQEDLNNWSAT-GCVE------------------PTLSGR
HIGH------TNFQMMNM--VAALEMALNNGL---HPLMNW-RL----------GP-ETG
EPAQGAFKTFDDFFEAFTKQFAFLIDQSVEYNNLMGLAHQAIRPT--PFLSSLIDDCIST
AADVTH----GGARY-----NSSGAA-CIGLADVTDSLMAIKKLVYDDKSV-SFADLK--
----------NAVADNFQ------------------------------------------
-----------------------SEPALHAL-----------------------------
------------ITHK--VPLFGSGSEEAVEMANRVAKFAHDHY-GTH--TNY--R----
--GGKYTVGFWSMSN-HVIYGTLSGALPSGKLEGKPFTP-GLTPQPIASPN-LLDNIRD-
-VARLSP-KYITN-------------NLAFNVKIVPGPNDTHEQT-VDNMFSYVKTYFD-
----LGGMQMQLNAVTSDTLKDAMANPENYRNLLVRISGYNAYFVTLNRDMQLELIERAQ
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YGL------------
>gi|222055530|ref|YP_002537892.1| Formate C-acetyltransferase [Geobacter sp. FRC-32]
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------------------------------------------------------------
--------------------------MAMVAQSINYKGRTIDFPLENPEEMNVPDEILHE
NLCKPTTERTR-------------------------------------------------
------------------------------------------------------------
---------------------------RLK--ARCRWKHASAGEFIDKEVRAGIERMRLI
TESHKAT-AGK-PEV------IR----RALGLAHLLNNCTLVLQDD-ELIIGYHAED-PE
MFPLYPELA--YMAVQDYLMT------------D--------------------------
---YAPQPKDEA----QEILNYW-----KPFSIQAKCEPY---FDQ--------------
ADLTRMY----------------QVSTMEGPM---FASGY--------------------
------NSIVPPYETVL--EDGLLKRIELAKEKLANAQAEMEKTPWDATKQLSWIPKIDL
WKAMIIADEAVINWARRHARLAKIVAENFETNSARKEELLEISEICHRVPAEPCKGLRDA
FQSKWFVFLICHALDRYAS--GFAQKEDELLEPYYNISVKDRSFQPMTHKD-----VVEL
VECERLKISE-HGAG-KSRAYREIFPGSNDLFILT---VGGT-KP-GFV--DACSDMTDA
ILEGARNI-RTTEPSIVFRWD-PVGRVKTKRLVFECVR-DGLGYPSIMH-NRIGVEQMKF
YSQFSLNEN------G---VTDDEAHRWANV-LCMS------------------PGVCGR
RKTQ--KTRSEGGGAIFP--AKLLEIALNNGY---DWSYSGMQL----------GP-KTG
EAT--GFKTFDDLLEAFRKQYAYVTSLVIRAKDVMRHFECQVMQM--PFVSSIDDGCMEL
GIDSVE-----------LSEQPNGWHNPITTVVAANSLVAIKKLIYDEKKY-TMKQLL--
----------DALQANWE---------------------G-H------------------
-------------------------EAMRQ------------------------------
------------DFLN--APKWGNDDPYADGIISKFYEEILGGELAKV--TNF--S----
--GGPVLPVGQAVGL-YMEVGSRTGPTPDGRFGGDAADDGGISPYFGTDKKGPTAVLKS-
-VSKVQK-NQKTN---------------LLNQRLNVPMMRSIHG--FDIWKSYMDTWES-
----LNIAHVQFNCVSTAELKAAQKEPEKHQDLIVRVSGFSARFVDVPTYGQNTIIARNE
QHFGADDYEYINAPL
>gi|218778024|ref|YP_002429342.1| Formate C-acetyltransferase [Desulfatibacillum
alkenivorans AK-01]
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------------------------------------------------------------
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------------------------------------------------------------
-----------------------------------------------MAGSNAQVKEHSV
KEPKGLSPRIE-------------------------------------------------
------------------------------------------------------------
---------------------------WLR---------DYY-FQGAERAWNNEYTAWTT
GDPWDEVYDELSFYI------VP----ETYAFMQTFCSSYLQAARK-VPLNG------EF
WDLSLPERR---AWFVKKVMT----KHLPVEILP--------------------------
---GDLIAGGRFNIQ-TSMCL-------DEKQAKTRKKLV---QGK--------------
-KGSRA-----------------EMKWFHDHG--YGNAGA--------------------
--TS--GHLVPGYEDVL--KKGWKGVHDYLASRLDALG--------PENQNS---HQANQ
LKAMMTAATMPRDLAARYASLIRDMEQKE-SDPERKEELARMAANLDHTPWNPPRDFWEA
IQALWLTHMLVLSDENYPGPGVSFGRVDQYLLPYWEASMA-Q--G-MDREW-----GKEI
LKCFWIHANTAYDAMIRTGANGGITAGYGQLITLS-----GM-GP-DGT--DLTNDLTYV
FLEVIDEMSPILEPKPNVRLH-ANTPEELYDHIIDMIA-ESQGAPFLLNFDERSMAGMMR
--------E-AEKAGRQDLINESNVWQYAPV-GCLE------------------NTMVGN
-DR-------SGTVDINLNLLKAVEFALTGGA---DLLPYKDTIMGKEYPIDASGI-PTG
DPT--EFTVFEEFFAAFAKQTRHIIKKAMDLYETSESVRAAYHPT--PYLSCLVKGCAEK
GKDVTQ----GGAEL-----SFVTIE-AVTFATTVDSLLAVKYLVFDEKIC-TMAELI--
----------QALKDNWE---------------------G-H------------------
-------------------------DILMAR-----------------------------
------------AKFK--APKYGRDDDEADEMARKVMDLWTEET-WKHKTQST-------
--GRQARPGMLSWNY-WVGDGYILHASPDGRPKGQFLSN-AICPTNGADINGPTSNANS-
-VGKALG-GRKPGKGDFGDYLNSLPNGASHTITFNPSILADPLH--KEKFKAYLKGYVQ-
----NGGTALQINMLDADMLKDAQKNPADYRHLLVRITGYNAYFTSIGKELQDEVIARLS
HEGL-----------
>gi|158522202|ref|YP_001530072.1| formate C-acetyltransferase [Desulfococcus
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oleovorans Hxd3]
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------------------------------------------------------------
------------MNANRKGMTNMLANLFFRFFAANFNLRPALNRYLSCDDGPINFTFGIR
TESGSVEQAVQFENGRVRVLKKMPEKPDAQLVFVDEAAVKEAATQPPNKLMLALMENRMV
TRGNLGYLQLMNFYLSLLLKKVQVGKLQKEAKREKRDY-----DPAEASQKSINKKNKDR
LSATATDPGVRFLADPYLADYSLDDFPRLK---------TFLDIHLKTRPALCHERPEIL
TRWYRENGFETDKNGEPWVAEIR----QAHALKYLMENRKPLIREN-DLVAGTTTAQ-EI
GVVLYPDAH--GTMIWGELLT---APHRPLN--P--------------------------
---YDVSPNTIDVLH-NSVFPFW-----LNRNFREWVRDN-KGYPD--------------
---CQKL----------------DERFAACFL--WKTVAL--------------------
------SHTILDYPTLL--SLGTKGIMAQIDAEIGR----------TSEADA---EKHTT
LRAMKLTLEGINAYAKNLAAEAHRLAGME-KDPARKKELVRLADICRKVPENPAATLDEA
INAIWIVWVGVHMENTNAG--FSLGRMDQWLQPYFEADMAAL--KNENEQKDYIRRAIEL
VGCFYMRCTD-HLPL-IPDIGNYLFGGSSSDQAIT---LGGV-TP-DGE--DAVNDMTYI
FLKVTEML-SIRDPNVNARYNREKNSDAYLARLCEVNL-NTAATPSIHN-DEAVMASLAE
--------F------N---YPAEHLRDWAAT-GCVE------------------PTLSGR
HIGH------TNCMMFNM--VAALEMALNNGR---HPLMRW-DL----------GP-KTG
DVTTGHFKDFESFFEAFATQLGFLADQTCEYNNLLGQAHQTIRPT--PYISALIQGPKEK
GRDVTK----GGALY-----NSSGVA-CIGLADITDSMMVIKKLVFDGKQV-SFGDLH--
----------RALAANFE------------------------------------------
-----------------------NEPALLAI-----------------------------
------------IKNK--IPLFGSGDKEALAMANRIIRLAHDIF-GAH--TNY--R----
--GGPYTAGFWSMSN-HVAFGTLTGALPSGRLAGKAFTP-GLTPEPHSSPS-ILDNLRD-
-VAGLDP-TAMNN-------------NIAFNVKVVPAPGESHAQT-VNTLCSYTKAYTG-
----LGGMQMQLNVVSSDTLRDAMEHPENYQNLLVRISGYNAYFVSLNREMQIELIERAE
FGM------------
>gi|222055540|ref|YP_002537902.1| Formate C-acetyltransferase [Geobacter sp. FRC-32]
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------------------------------------------------------------
--------------------------MATVATSIKYDGRVIDFPLANPDENGIADEVLHE
NLARPTTERTK-------------------------------------------------
------------------------------------------------------------
---------------------------RLK--ARCRWKHASAGEFVDAEVRAGIERMRYI
TEAHKAS-AGQ-PEV------IR----RALGLANILNKSTLVLQQD-EFIIGYHAED-PE
MFPLYPELA--YMAVQDYLIS------------N--------------------------
---YSPEPKEEA----AEINEYW-----KKYSMQAKGERY---FTQ--------------
EELLQMY----------------QVSTMEAPG---FATGY--------------------
------NSICPPYETVI--QDGLLKRVELAKENIDHAKKEMQKVPWNATTGLDWIAKIDV
WKAMIIADEAVINWARRHARLARIVAEHFETNQERKEELLEIADISHRVPAEPCKGLKDA
FQAKWYTFLLCHAIDRYAS--GYAHKEDELLEPYYNISVVEKSFQPMTYTD-----VVEM
VEMERLKISE-HGAG-KSRAYREIFPGSNDLFILT---IGGT-KP-GYV--DACSDMTDA
ILEGARNI-RTTEPSIVFRWH-PNGREKTKRLVFECIR-DGLGYPSIKH-DVIGTEQLKY
YSKFSKNNN------G---ATDAEAHYWGLV-LCMS------------------PGVCGR
RKTH--KTRSEGGGSIFP--AKMMEIVLADGF---DWSYSGMQL----------GP-HTG
DPT--TFKTFEQLWEAFRTQYAYATSKVIRAKDIMRYFESKFLQM--PFVSSIDDGCMEL
GIDAME-----------LSEQPNGWHNPITTVVAANSMVAIKKLIYDDKKY-TMAELV--
----------TALRANWH---------------------G-Y------------------
-------------------------EEMRR------------------------------
------------DFLN--APKWGNDDDYADSIIKDFYEDIIGGEMAKI--TNY--S----
--GGPVLPVGQAVGL-YMEIGSRTGPTPDGRFGGEAGDDGGISPYMGTDKKGPTAVLKS-
-VSKVQK-NQKAN---------------LLNQRLSVPLMRSVHG--FDIWKSYMDAWEK-
----LRIDHVQFNCVSTAEMKAAQKEPEKHQDLIVRVSGFSARFVDIPTYGQNTIIARNE
QSFGADDLEFLNTQI
>gi|150008479|ref|YP_001303222.1| putative formate acetyltransferase
[Parabacteroides distasonis ATCC 8503]
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------------------------------------------------------------
-----------------------------------------------------------M
ANFNVEGAQNV-------------------------------------------------
------------------------------------------------------------
---------------------------EIS---------KKL-PC-EKPLIVQLEIMERY
TAVHKAC-AAL-PKE------IR----EVECLKVLYPTLFRKITNQ-DLIAGRTDFL-PI
GFGCVTSLGGVGHYCV--------FKKLRAF--Q--------------------------
---LQLDETERKRVD-A-LYDYW-----LDHDLKTQFNKE--VLTE--------------
-DTLGMF--------------------IDCEYPMIATARL--------------------
------SGMMLDYPKLL--DKGIGGLRSDLQEKLK-----------EQPDN-------NF
YKAGIQCLDIFVDCASHLQQDAREQMASA--NMKRQKELERICQALENIKEKKPGTFHEA
MQLFWLFALLAGV--------INYGRLDDYLGPYLVADLK-S--GRLTDEE-----AYRY
IHSLWTMIEN-----RRTTVNGRII-------------VGGK-GR-KHP--KEADVFLHI
AMKVAKNC-RYVEPQFTLRFD-KETSEEIWDEALDALG-AGATYPTLYN-DDVNVPAVMY
---------------GMR-VDEKTAEQYVPF-GCTE------------------FVIQGQ
-STG------TPNICINL--LKLLTIYMNDGI---DPIDGKRKS----------GPVSLK
KLE--EYQTFEEFYDGYKALLDYYLDLSVKAQYHSYEVMNQHVSF--LFTSLLTDDCIAR
GKALLD----GGVRY------LGGTNETYGNINTSDSLWVIRDLVFNQKKY-TLRQLN--
----------DAMLANFN---------------------G-Y------------------
-------------------------EALRK------------------------------
------------DCLN--CDKYGNDLETADTMANDLYEFVAKGVRDRG--IAI-------
--GMQYFLIVISNNQLNTEWGNRTAASPDGRLSCMYMNP-ANNPQGGANKSGPTAMLNS-
-LAKFD--AKYHG-------------GSVQNIKFSPSMF--NEN--RAVIKSLFKTYFA-
----KGGCHLMVTVVDKGVLEDAVEHPENYPDLIVRVSGFSAVFVDLSPNIQQELLSRVL
YDK------------
>gi|53715663|ref|YP_101655.1| putative pyruvate formate-lyase [Bacteroides fragilis
YCH46]
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
-----MNERIN-------------------------------------------------
------------------------------------------------------------
---------------------------YLK---------TYI------------------
--------LDKRHHS------QR----RTPSSIGLDKLNTIYAQQGLSPV--------ER
ATACF------AALMNAELPV---------------------------------------
-----ILPGEKIVFT---------------RTLTQVPDIY---TPE--------------
-EWNEIK----------------NKYYIHEKG------TV--------------------
------CNISPNYAYTI--QHGLEARKQEIRKRQENPSL-------NE-------KERVF
LNSMYQCIISIQKLIEKYEQYALLNNETE------------IAHTLHTIKTEGAQNFRQA
LQLLRILHFSIWEAGNYHN---TLGRFDQYMYPFYQRDLE-N--GTLTKEE-----AFDL
LEEFFLVCNK------DSDLYPGMQQGDN-GQSLV---LGGR-DP-EGK--YLFNDLSRM
CLQASYEL-KLIDPKINIRVD-PKTPDEIFSLGSRLTK-IGLGFPQYSN-DDIIIPGLIR
--------K------G---YSKEDAYNYVVA-ACWE------------------FIIPNR
--------------AMDI--PNIDAVSLIGCV---DRCLEK-------------LN----
-----TCSDYSSFYTLVEQEIQKEVNAICEKHRNLYII-----PS--PMMSLLMDGTIER
AKDISE-----GSYY-----NNYGIH-GTGIATATDTLAALKKYYFEEQSL-DYTTLL--
----------TAIRSNFK---------------------G-Y------------------
-------------------------EELQKK-----------------------------
------------LREE--APKMGQDNDYADLIAKDLLDSFDRSL-ADK--RNE--R----
--GGLYRAGTGTAMY-YIFHSNQLRATPDGRNDGEMIPA-NYSPSLFLKQKGPISVIKS-
-FTKQHL-DRVVN-------------GGPLTLEFDQSVFSNDET--IEKLGMLVKTYIV-
----LGGHQLQLNTVSRETLLHARKHPEQHKNLIVRVWGWSGYFVELDECYQNHVINRIE
FSL------------
>gi|60683602|ref|YP_213746.1| putative formate acetyltransferase (pyruvate
formate-lyase) [Bacteroides fragilis NCTC 9343]
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------------------------------------------------------------
-----MNERIN-------------------------------------------------
------------------------------------------------------------
---------------------------YLK---------TYI------------------
--------LDKRHHS------QR----RTPSSIGLDKLNTIYAQQGLSPV--------ER
ATACF------AALMNAELPV---------------------------------------
-----ILPGEKIVFT---------------RTLTQVPDIY---TPE--------------
-EWNEIK----------------NKYYIHEKG------TV--------------------
------CNISPNYAYTI--QHGLEARKQEIRKRQENPSL-------NE-------KERVF
LNSMYQCIISIQKLIEKYEQYALLNNETE------------IAHTLHTIKTEGAQNFRQA
LQLLRILHFSIWEAGNYHN---TLGRFDQYMYPFYQRDLE-N--GTLTKEE-----AFDL
LEEFFLVCNK------DSDLYPGMQQGDN-GQSLV---LGGR-DP-EGK--YLFNDLSRM
CLQASYEL-KLIDPKINIRVD-PKTPDEIFSLGSRLTK-IGLGFPQYSN-DDIIIPGLIR
--------K------G---YSKEDAYNYVVA-ACWE------------------FIIPNR
--------------AMDI--PNIDAVSLIGCV---DRCLEK-------------LN----
-----TCSDYSSFYTLVEQEIQKEVNAICEKHRNLYII-----PS--PMMSLLMDGTIER
AKDISE-----GSYY-----NNYGIH-GTGIATATDTLAALKKYYFEEQSL-DYTTLL--
----------TAIRSNFK---------------------G-Y------------------
-------------------------EELQKK-----------------------------
------------LREE--APKMGQDNDYADLIAKDLLDSFDRSL-ADK--RNE--R----
--GGVYRAGTGTAMY-YIFHSNQLRATPDGRNDGEIIPA-NYSPSLFLKQKGPISVIKS-
-FTKQHL-DRVVN-------------GGPLTLEFDQSVFSNDET--IEKLGMLVKTYIV-
----LGGHQLQLNTVSRETLLHARKHPEQHKNLIVRVWGWSGYFVELDECYQNHVINRIE
FGL------------
>gi|52424456|ref|YP_087593.1| PflD protein [Mannheimia succiniciproducens MBEL55E]
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------------------------------------------------------------
----------------------------------------MAELTEAQKKAWEGFVPGEW
QNGVNLRDFIQ-------------------------------------------------
------------------------------------------------------------
---------------------------KNY---------TPYEGDESFLADATPATSELW
NSVMEGIKIENKTHA------PL--DFDEHTPSTITSHKPGYINKDLEKIVGLQTDA-PL
KRAIMPYGG--IKMIKGSCEV---YG----------------------------------
---RKLDPQVEFIFT-E-----------YRKTHNQGVFDV---YTP--------------
-DILRCR----------------KSGVLTGLP---DAYGR--------------------
------GRIIGDYRRLA--VYGIDYLMKDKKAQFDSLQ-----------------PRLEA
GEDIQATI-----------QLREEIAEQH----RALGKIKEMAASYGYDISGPATNAQEA
IQWTYFAYLAAVKSQNGAA--MSFGRTSTFLDIYIERDLK-R--GLITEQQ-----AQEL
MDHLVMKLR--MVRFLRTPEYDQLFSGDPMWATET---IAGM-GL-DGR--PLVTKNSFR
VLHTLYTMGTSPEPNLTILWS-EQLPEAFKRFCAKVS--IDTSSVQYEN-DDLMRPDFNN
---------------D----------DYAIA-CCVS------------------PMVVGK
-QMQ------FFGARANL--AKTMLYAINGGI---DEKNGM-QV----------GP-KTA
PITD-EVLNFDTVIERMDSFMDWLATQYVTALNIIHFMHDKYAYE--AALMAFHDRDVFR
TMACGI----------------------AGLSVAADSLSAIK---YAKVKP-IRGDIKDK
DGNVVA----SNVAIDFE------------------------------------------
------------------------------------------------------------
------------IEGE--YPQFGNNDPRVDDLAVDLVERFMKKV-QKH--KTY--R----
--NATPTQSILTITS-NVVYGKKTGNTPDGRRAGAPFGP-GANPMHGRDQKGAVASLTS-
-VAKLPF-AYAKD-------------GISYTFSIVPNALGKDDEAQKRNLAGLMDGYFHH
EATVEGGQHLNVNVLNREMLLDAMENPEKYPQLTIRVSGYAVRFNSLTKEQQQDVITRTF
TQSM-----------
>gi|220933149|ref|YP_002510057.1| formate acetyltransferase [Halothermothrix orenii
H 168]
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------------------------------------------------------------
--------------------------------------------------MAYNFKAGRW
QKEIDVRDFIQ-------------------------------------------------
------------------------------------------------------------
---------------------------QNY---------TPYTGDSSFLEGPTDRTRQLW
EECQKLLWQEIEEGG------VL--DIDVDTVSDINAYEAGYINRDLEKIVGLQTDK-PL
KRTLNVYGG--IRMARQAAEA---YG----------------------------------
---YKVNEQIEKVFN-N-----------YRKTHNDGVYDV---YTP--------------
-ELREIR----------------RSGVITGLP---DAYGR--------------------
------GRIIGDYRRVA--LYGIDRLIEEKEKDLAHLPT---------------------
------------RMTEENVRLREELSEQI----KALKKLKGLGRTYGLELSRPARTAHEA
IQWTYMGYLAAIQENNGAA--MSLGRVCEFFDIYIEHDLR-K--GKLTEEE-----AQEL
IDDFVIKLR--LARQLRTPEYNKLFSGDPMWITVV---IGGT-GI-DGR--PLVTKTSFR
ILNTLYNLGPAPEPNLTVLWS-RRLPDGFKEFCCRVSR--DTSSIQYEN-DELMREYYGD
--------------------------DYAIA-CCVS------------------ALRTGK
-EMQ------FFGARCNL--PKTLLYALNGGR---DELSGV-QV----------GP-EFA
PYTG-DILEYDLVMERFDTFLDWLVEKYVDALNIIHYMHDKYAYE--RVQMALMDTEVDR
VMGFGI----------------------AGLSIVADSLSAIK---YAKVRP-VRNS----
----------DGLITSFD------------------------------------------
------------------------------------------------------------
------------VEGD--HPRYGNDDDRVDSLAVEVVRRFLTKL-KQH--KLY--R----
--NARHTLSILTITS-NVVYGTKTGATPDGREAGQPFAP-GANPMHGRDESGALASLNT-
-VAKLPY-EYCQD-------------GISNTFTIVPGALGVNEEQRINNLVAILDGYFT-
----KGGHHLNVNVLNRETLLDAVNHPEKYPQLTIRVSGYAVNFIKLTPEQQQEVIARTF
HESL-----------
>gi|158333637|ref|YP_001514809.1| formate acetyltransferase [Acaryochloris marina
MBIC11017]
------------------------------------------------------------
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------------------------------------------------------------
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------------------------------------------------------------
MQEVNVRAFIQ-------------------------------------------------
------------------------------------------------------------
---------------------------SNY---------TPYVGDETFLAAASDRTSLLW
DKVSFSMDVERQQGI------LD---ADTQVPAGITAHAPGYIAPDLEQIVGLQTDQ-PL
KRAIMPLGG--IRVVQKSLEA---YG----------------------------------
---YKLDPGTLKTFT-Q-----------YRKTHNDGVFDA---YTR--------------
-EMRLAR----------------HSGIITGLP---DAYGR--------------------
------GRIIGDYRRVA--LYGVDFLINDKRQQLLSLE----------------------
----------VDAINETVIRHREELSEQI----RALQELKEMADQYGFDIGQPAATAQEA
VQWTYFGYLGAIKEQNGAA--MSLGRVSTFLDIYIQRDLN-Q--GTLTEAE-----AQEL
IDHFVMKLR--MVRFLRTPAYNELFSGDPVWVTES---IGGM-GL-DGR--TLVTRTSFR
FLHTLYNLGPAPEPNLTVLWS-EQLPDNFKRFCAQVS--IDTSSIQYEN-DDLMRTEYGD
--------------------------DYGIA-CCVS------------------AMRIGK
-QMQ------FFGARVNL--AKALLYAINGGK---DEKSGE-QI----------AP-AYA
PITA-DILDYDEVMAKFDVLMGWLAKLYVNTLNVIHYMHDKYCYE--RLEMALHDRDVYR
TMACGI----------------------AGLSVVADSLSAIK---HTQVKV-IRDD----
----------AGLAIDYK------------------------------------------
------------------------------------------------------------
------------LMGN--YPAFGNNDERVDSIAQEVVRRFMNHV-RQH--QTY--R----
--DAVPTQSILTITS-NVVYGKKTGSTPDGRKAGEPFGP-GANPMHGRDTKGAIAACES-
-VAQLPY-QHAQD-------------GISYTFSIVPQALGKGETDQDRNLVGLLDGYFH-
----NTGQHININVLNRDTLLDAMEHPEQYPQLTIRVSGYAVNFIKLTREQQRDVVSRTF
HSRF-----------
>gi|150015895|ref|YP_001308149.1| formate acetyltransferase [Clostridium
beijerinckii NCIMB 8052]
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-----------------------------------------------MFKQWDGFKNGTW
QESIDVRNFIQ-------------------------------------------------
------------------------------------------------------------
---------------------------KNY---------KLYEGDSTFLEDKTEKTSKVW
ARAYELIVEEVKKGI------ID---VANDRVSGIDNYEPGYIDKDNEVIVGLQTDA-PL
KRIVNPFGG--MRMVQSSLKE---YG----------------------------------
---YELDKNIEEYFP-K-----------YRKTHNEGVFDA---YTK--------------
-EIRAAR----------------SAGLLTGLP---DAYGR--------------------
------GRIIGDYRRVA--LYGIDYLIEEKKRDLDNLG----------------------
------------DMLDELVRKREEVSMQI----RALGEVKSMASKYGIDISKPASNAREA
AQHLYFGYLAGIKENNGAA--TSFGRTSTFLDIYIERDLE-A--GLITEKE-----AQEI
VDQLIIKLR--LVRHLRTPEYNELFGGDPTWVTES---IGGV-GI-NGK--PLVTKNSFR
YLHTLINLGTSAEPNLTVLWS-DKLPESFKKYCAEIS--IKTDSIQYEN-DEVMRPVYGD
--------------------------DYAIA-CCVS------------------AMKVGK
-QMQ------FFGARANI--AKSLLYAINGGV---DELKGI-KV----------VP-GIE
KLTDEEILDFNKVKSNYFKVLEYVAKVYVDTMNIIHFMHDKYAYE--AGQMALHDTAVER
LMAFGI----------------------AGLSVAIDSLSAVK---YAKVKP-IRNE----
----------EGITVDFE------------------------------------------
------------------------------------------------------------
------------VEGD--FPKYGNDDDRADDLGVELVTKFSNEL-KKH--PLY--R----
--DAKHTLSALTITS-NVMYGKKTGTTPDGRKKGEPLAP-GANPMHGRDINGALASLNS-
-VAKIPYNEICQD-------------GVSNTFSIVPDALGKDENQKITNLVAILDGYFT-
----QGAHHLNVNVLNRQTLIDAMENPDKYPTLTIRVSGYAVNFSRLSKEQQLEVISRTF
HESI-----------
>gi|187933107|ref|YP_001886762.1| formate acetyltransferase [Clostridium botulinum B
str. Eklund 17B]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------------MFKQWEGFKNGTW
QEGIDVRNFIQ-------------------------------------------------
------------------------------------------------------------
---------------------------KNY---------NVYEGDSSFLEGISEKTSRVW
DKAYELIVEEVKKGI------ID---IATDRVSGINNYEAGYIDKDNEVIVGLQTDA-PL
KRIVNPFGG--FRMVQTSLKE---YG----------------------------------
---YELDKDIEKHFS-R-----------YRKTHNEGVFDG---YTK--------------
-EIRLAR----------------TAGLLTGLP---DAYGR--------------------
------GRIIGDYRRVA--LYGIDYLIEEKKNDLDNLQ----------------------
--------------GDMLDELVRKREEVS-MQIRALGEIKEMAAKYGCDISKPASNAKEA
VQALYFGYLAGIKENNGAA--TSFGRTSTFLDIYIERDLE-T--GLITEKE-----AQEL
VDQLIIKLR--LVRHLRTPEYNDLFGGDPTWVTES---IGGM-GI-NGK--SLVTKNSFR
YLHTLINLGASAEPNLTVLWS-DKLPENFKKYCAEIS--IKTDAVQYES-DEVMRPIYGD
--------------------------DYAIA-CCVS------------------AMKVGK
-QMQ------FFGARCNI--AKSLLYAINGGC---DELKGM-KV----------IP-GIE
VMND-EVLDFNKVKENYFKVLEYVAKIYVDTMNIIHHMHDKYAYE--AGQMALHDTMVDR
LMAFGI----------------------AGLSVAIDSLSAIK---YAKVKP-IRNE----
----------EGLAIDFE------------------------------------------
------------------------------------------------------------
------------VQGD--FPKYGNDDDRADDLGVELVTKFSNEL-KRH--PLY--R----
--DAKHTLSALTITS-NVMYGKKTGTTPDGRKKGEPLAP-GANPMHGRDVNGALASLNS-
-VAKIPYNEVCQD-------------GVSNTFSIVPDALGKSEEQRISNLVSILDGYFV-
----QGAHHLNVNVLNRETLIDAMENPDKYPTLTIRVSGYAVNFSRLSKEQQLEVISRTF
HESI-----------
>gi|152977893|ref|YP_001343522.1| formate acetyltransferase [Actinobacillus
succinogenes 130Z]
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----------------------------------------MAQLTEAQQKAWEGFVPGEW
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QEGVNLRDFIQ-------------------------------------------------
------------------------------------------------------------
---------------------------KNY---------TPYEGDESFLADATPATTELW
NSVMEGIKIENKTHA------PL--DFDEHTPSTITSHKPGYIDKDLEKIVGLQTDA-PL
KRAIMPFGG--IKMIKGSCQV---YG----------------------------------
---RTLDPKVEFIFT-E-----------YRKTHNQGVFDV---YTP--------------
-DILRCR----------------KSGVLTGLP---DAYGR--------------------
------GRIIGDYRRLA--VYGIDYLMKDKKAQFDSLQ-----------------PRLEA
GEDIQATI-----------QLREEIAEQH----RALGKIKEMAASYGYDISGPAMNAQEA
IQWTYFAYLAAVKSQNGAA--MSFGRTSTFLDIYIERDLK-R--GLITEQQ-----AQEL
MDHLIMKLR--MVRFLRTPEYDQLFSGDPMWATET---IAGM-GL-DGR--PLVTKNSFR
VLHTLYTMGTSPEPNLTILWS-EQLPEAFKRFCAKVS--IDTSSVQYEN-DDLMRPDFNN
---------------D----------DYAIA-CCVS------------------PMVVGK
-QMQ------FFGARANL--AKTMLYAINGGI---DEKNGM-QV----------GP-KTA
PITD-EVLNFDTVIERMDSFMDWLATQYVTALNIIHFMHDKYAYE--AALMAFHDRDVFR
TMACGI----------------------AGLSVAADSLSAIK---YAKVKP-IRGDIKDK
DGNVVA----SNVAIDFE------------------------------------------
------------------------------------------------------------
------------IEGE--YPQFGNNDPRVDDLAVDLVERFMKKV-QTH--KTY--R----
--NAVPTQSILTITS-NVVYGKKTGNTPDGRRAGAPFGP-GANPMHGRDQKGAVASLTS-
-VAKLPF-AYAKD-------------GISYTFSIVPNALGKDDDAQKRNLAGLLDGYFHH
EATVEGGQHLNVNVLNRETLLDAIDHPEKYPQLTIRVSGYAVRFNSLTREQQQDVITRTF
TQAM-----------
>gi|188590176|ref|YP_001921720.1| formate acetyltransferase [Clostridium botulinum
E3 str. Alaska E43]
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------------------------------------------------------------
------------------------------------------------------------
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-----------------------------------------------MFKQWEGFKNGTW
QEGIDVRNFIQ-------------------------------------------------
------------------------------------------------------------
---------------------------KNY---------KVYEGDSSFLEGISEKTSRVW
DKAYALIVEEVKKGI------ID---IATDRVSGINNYEAGYIDKDNEVVVGLQTDA-PL
KRIVNPFGG--FRMVQTSLKE---YG----------------------------------
---YELDKDIEKHFS-R-----------YRKTHNEGVFDG---YTK--------------
-EIRLAR----------------TAGLLTGLP---DAYGR--------------------
------GRIIGDYRRVA--LYGIDYLIEEKKNDLDNL-----------------------
-------------QGDMLDELVRKREEVS-MQIRALGEIKEMAAKYGCDISKPASNAKEA
VQALYFGYLAGIKENNGAA--TSFGRTSTFLDIYIERDLE-A--GLITEKE-----AQEL
VDQLIIKLR--LVRHLRTPEYNDLFGGDPTWVTES---IGGM-GI-NGK--SLVTKNSFR
YLHTLINLGASAEPNLTVLWS-DKLPENFKKYCAEIS--IKTDAVQYES-DEVMRPIYGD
--------------------------DYAIA-CCVS------------------AMKVGK
-QMQ------FFGARCNI--AKSLLYAINGGC---DELKGM-KV----------IP-GIE
VMND-EVLDFNKVKENYFKVLEYVAKIYVDTMNIIHHMHDKYAYE--AGQMALHDTMVDR
LMAFGI----------------------AGLSVAIDSLSAIK---YAKVKP-IRNE----
----------EGLAIDFE------------------------------------------
------------------------------------------------------------
------------VEGD--FPKYGNDDDRADDLGVELVTKFSNEL-KKH--PLY--R----
--DAKHTLSALTITS-NVMYGKKTGTTPDGRKKGEPLAP-GANPMHGRDANGALASLNS-
-VAKIPYNEVCQD-------------GVSNTFSIVPDALGKSEEQRISNLVSILDGYFV-
----QGAHHLNVNVLNRETLIDAMENPDKYPTLTIRVSGYAVNFSRLSKEQQLEVISRTF
HESI-----------
>gi|22298533|ref|NP_681780.1| formate acetyltransferase [Thermosynechococcus
elongatus BP-1]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
----------------------------------MNCTRYTTRYTELPEAAWQEFTGGDW
VERIDVRDFIQ-------------------------------------------------
```

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------------------------------------------------------------
---------------------------RNY---------TPYTGDGSFLVGASDRTQQLW
AKVRDLMALEREKGV------LD---ADTSLPSSITAHPPGYIDRELEQIVGLQTDK-PL
KRAIMPFGG--IRVVETALKA---YG----------------------------------
---YELDPRTKEIFT-K-----------YRKTHNDGVFDA---YTP--------------
-EMRRCR----------------KSGIITGLP---DAYGR--------------------
------GRIIGDYRRVP--LYGVDRLIADKQAQQASLE----------------------
----------VDVMDEETIRLREELSEQI----KALNELKDMAASYGFDISRPAANGKEA
IQWLYFGYLAAVKEQNGAA--MSLGRVSTFLDIYFERDLR-H--GTATEAD-----IQEW
IDHFVMKLR--MVRFLRTPEYNELFSGDPTWVTES---IGGM-GL-DGR--PLVTKTSFR
ILNTLYTLGPAPEPNLTVLWS-ENLPEAFKRFCAQVS--IDTSSIQYEN-DDLMRPYWGD
--------------------------DYAIA-CCVS------------------AMRVGK
-QMQ------FFGARVNL--AKALLYAINGGR---DEVSGQ-QV----------AP-MFA
PITG-DTLKWEEVLPRFEQMMAWLAKVYVNTLNVIHYMHDKYCYE--RLEMALHDRDVFR
TMACGV----------------------AGLSVVADALSAIK---YAEVKV-IRNA----
----------DGLAVDYE------------------------------------------
------------------------------------------------------------
------------IKGD--FPKYGNNDDRVDSLAVWVVETFMNEV-RKH--KTY--R----
--NAVPTQSILTITS-NVVYGKKTGSTPDGRKAGEPFAP-GANPMHGRDTKGAIASLAS-
-VAKLPY-VHAQD-------------GISNTFSIVPSALGKTREDQISNLVNMLDGYIH-
----DQGFHINVNVLNREMLLDAMDHPELYPQLTIRVSGYAVNFIKLTREQQLDVINRTF
HERF-----------
>gi|150015897|ref|YP_001308151.1| formate acetyltransferase [Clostridium
beijerinckii NCIMB 8052]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------------MFKQWEGFKNGTW
QEDIDVRNFIQ-------------------------------------------------
------------------------------------------------------------
---------------------------KNY---------KLYEGDGSFLEEKTERTSKVW
GKAYALIVEEVKKGI------ID---VATDRVSGIDNYDPGYIDRDNEVIVGLQTDA-PL
KRIVNPFGG--MRMVQSSLKE---YG----------------------------------
---YELDPEINKNFS-K-----------YRKTHNEGVFDA---YTK--------------
-EIRAAR----------------SAGLLTGLP---DAYGR--------------------
------GRIIGDYRRVA--LYGIDYLIEEKKKDLDNLNG---------------------
------------DMLDELVRKREEVSMQI----RALGEVKSMAAKYGIDISKPASNAKEA
AQHLYFGYLAGIKENNGAA--TSFGRTSTFLDIYIERDLE-A--GLITEKE-----AQEI
VDQLIIKLR--LVRHLRTPEYNELFGGDPTWVTES---IGGV-GI-NGK--PLVTKNSFR
YLHTLINLGTSAEPNLTVLWS-DKLPESFKKYCAEIS--IKTDSIQYEN-DEVMRPVYGD
--------------------------DYAIA-CCVS------------------AMKVGK
-QMQ------FFGARANI--AKSLLYAINGGV---DELKGI-KV----------VP-GIE
KFTDEEILNFDKVKANYFKVLEYVAKVYVDTMNIIHFMHDKYAYE--ASQMALHDTAVER
LMAFGI----------------------AGLSVAIDSLSAIK---YAKVRP-IRNE----
----------EGITIDFE------------------------------------------
------------------------------------------------------------
------------VEGD--FPKYGNDDDRADDLGVELVTKFSGEL-KKH--PLY--R----
--DAKHTLSALTITS-NVMYGKKTGTTPDGRKKGEPLAP-GANPMHGRDINGALASLNS-
-VAKIPYNEICQD-------------GVSNTFSIVPDALGKNEDQKITNLVAILDGYFT-
----QGAHHLNVNVLNRQTLIDAMENPDKYPTLTIRVSGYAVNFSRLSKEQQLEVISRTF
HESI-----------
>gi|220929637|ref|YP_002506546.1| formate acetyltransferase [Clostridium
cellulolyticum H10]
------------------------------------------------------------
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-----------------------------------------------MRLNISDFKPGKW
QNSIDVQDFIQ-------------------------------------------------
------------------------------------------------------------
```

```
---------------------------TNY---------TPYDGDGSFLCGASSKTRQLW
ETCRSLLVEEHLNGG------IL--DIDTETVASINSHKPGFIDEKYEVIKGLQTDT-PL
KRAFLAKTG--YRMAKQACQQ---FD----------------------------------
---AAPSPEFDKIFS-K-----------SIKTHNDGVFSA---YTN--------------
-EMRKAR----------------RCGVITGLP---DTYGR--------------------
------GRIIGDYRRVA--LYGTDVLISQKQKDLDSL-----------------------
----------IGTMTDGVIRLREEIQDQI----AALNDLAVLGGSYGFDMKRPALNAFEA
VQWTYLAFLGALKETNGAA--NSLGRLNVFFDIFIQRDIN-N--GILTEED-----AQEL
IDQFVIKLR--FIRHLRTKEYNELFAGDPVWLTES---LGGM-SS-DGR--HMVSKTSFR
FLQTLKNLGAAPEPNLTILWS-VKLPENFKKFCAEIS--IVTSAIQYEN-DDLMQPQYGD
--------------------------DYGIS-CCVS------------------AMRLGK
-DMQ------FFGARCNL--AKLLLLSLNGGR---DEISGD-QV----------AP-EIK
PYEG-EYLEYEKVMKNFLELQDWLTGLYVDTMNIIHYMHDKYAYE--RLMMALHDTDVNR
LMAFGI----------------------SGLSVLVDSLSAIK---HTRVRV-VRDQ----
----------RGIITDFE------------------------------------------
------------------------------------------------------------
------------LEGS--YPQYGNNDDRADCIAKEVVTSFYNSL-KAH--PTY--R----
--NATHTLSILTITS-NVVYGKKTGSTPDGRKKGEPFAP-GANPMHNRDKSGILAMMNS-
-VASIPY-NVCSD-------------GISLTLSVIPNALGKARETKISNLSALIDGYVM-
----SSGHHINVNVLDKETLENAIKEPMKYNQLTVRVSGYAVHFVKLTKAQQLEVLSRTF
HEAM-----------
>gi|219854351|ref|YP_002471473.1| hypothetical protein CKR_1008 [Clostridium
kluyveri NBRC 12016]
------------------------------------------------------------
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------------------------------------------------------------
-----------------------------------------MKRGAFMKKKWKNFNTGNW
TENIDVRNFIQ-------------------------------------------------
------------------------------------------------------------
---------------------------KNY---------TPYTGDESFLTSPTEKTKKVW
KKSEELILEEIKKGG------VL--DVDTNTVSGIDNFKPGYIDKENEVIVGLQTDA-PL
KRIVNPFGG--IKMAKDALTD---YG----------------------------------
---YRIDENMNNIFT-K-----------YRKTHNEGVFDS---YTE--------------
-EIRAAR----------------HVGLITGLP---DAYGR--------------------
------GRIIGDFRRVA--LYGIDYLIEEKKKDLKTL---------KSPDML--------
--------EDIL-------RQREEVSEQI----KALYKIKNMAASYGIDISNPAGNAKEA
VQFTYLGYLAGIKENNGAA--MSLGRVSTFLDIYIERDLK-E--GALTEQE-----AQEL
IDQFVIKLR--LERHLRTPDYNELFAGDPNWVTEC---IGGM-SI-DGR--TLVTKNSYR
FLNTLTNLGPAPEPNITILWS-QNLPEPFKKYCSRMS--IETDALQYEN-DDLMRPVYGD
--------------------------DYGIA-CCVS------------------AMALGK
-EMQ------FFGARCNI--AKSLLYAINQGS---DEKTFE-KI----------VP-HIE
KMED-EILNYEKVKKNYFKVLEYVAKLYVNALNTIHYMHDKYAYE--AGLMALHDTKVHR
FLACGI----------------------AGLSVAADSLSAIK---YGKVTP-IRNQ----
----------KGTAVAFK------------------------------------------
------------------------------------------------------------
------------TEGD--FPKYGNDDDRVDDIAVEIVNKFISEL-RKT--ETY--R----
--NAEHTLSVLTITS-NVMYGKKTGATPDGRKSGEPFAP-GANPMHGRDKEGALASLNS-
-VAKIPYRSVCQD-------------GVSNTFSIVPDALGKDLNTRTNNLASILDGYFS-
----KGAHHLNVNVMHRETLLDAVENPEKYPTLTIRVSGYAVHFIKLTRQQQEEVIKRTF
HQRV-----------
>gi|153953732|ref|YP_001394497.1| Pfl [Clostridium kluyveri DSM 555]
------------------------------------------------------------
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------------------------------------------------------------
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-----------------------------------------------MKKKWKNFNTGNW
TENIDVRNFIQ-------------------------------------------------
------------------------------------------------------------
---------------------------KNY---------TPYTGDESFLTSPTEKTKKVW
KKSEELILEEIKKGG------VL--DVDTNTVSGIDNFKPGYIDKENEVIVGLQTDA-PL
```

```
KRIVNPFGG--IKMAKDALTD---YG----------------------------------
---YRIDENMNNIFT-K-----------YRKTHNEGVFDS---YTE--------------
-EIRAAR----------------HVGLITGLP---DAYGR--------------------
------GRIIGDFRRVA--LYGIDYLIEEKKKDLKTL---------KSPDML--------
---------------EDILRQREEVSEQI----KALYKIKNMAASYGIDISNPAGNAKEA
VQFTYLGYLAGIKENNGAA--MSLGRVSTFLDIYIERDLK-E--GALTEQE-----AQEL
IDQFVIKLR--LERHLRTPDYNELFAGDPNWVTEC---IGGM-SI-DGR--TLVTKNSYR
FLNTLTNLGPAPEPNITILWS-QNLPEPFKKYCSRMS--IETDALQYEN-DDLMRPVYGD
--------------------------DYGIA-CCVS------------------AMALGK
-EMQ------FFGARCNI--AKSLLYAINQGS---DEKTFE-KI----------VP-HIE
KMED-EILNYEKVKKNYFKVLEYVAKLYVNALNTIHYMHDKYAYE--AGLMALHDTKVHR
FLACGI----------------------AGLSVAADSLSAIK---YGKVTP-IRNQ----
----------KGTAVAFK------------------------------------------
------------------------------------------------------------
------------TEGD--FPKYGNDDDRVDDIAVEIVNKFISEL-RKT--ETY--R----
--NAEHTLSVLTITS-NVMYGKKTGATPDGRKSGEPFAP-GANPMHGRDKEGALASLNS-
-VAKIPYRSVCQD-------------GVSNTFSIVPDALGKDLNTRTNNLASILDGYFS-
----KGAHHLNVNVMHRETLLDAVENPEKYPTLTIRVSGYAVHFIKLTRQQQEEVIKRTF
HQRV-----------
>gi|150009973|ref|YP_001304716.1| formate acetyltransferase [Parabacteroides
distasonis ATCC 8503]
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------------------------------------------------------------
------------------------------------------------------------
--------------------------------------------MKFENEYWDHFKGETW
KREINVRDFIQ-------------------------------------------------
------------------------------------------------------------
---------------------------SNY---------TPYEGDDSFLVASSEKTRKVW
NKLTEMFKVEREKGV------YD---AETKLPQGIDVYGPGYIDKENEVIVGLQTDA-PL
KRGIFPKGG--IRMVENSLEA---YG----------------------------------
---YHLDPMTKEIFT-K-----------YRKTHNEGVFSA---YTE--------------
-EMVAAR----------------RSAIITGLP---DAYGR--------------------
------GRIIGDYRRVA--LYGTAILIEEKKRFLNRLD----------------------
----------IQEITEEIIQSREEISEQI----KALKAFERMCASYGFDVTRPAQNAREA
VQFVYLAYLAAVKDQDGAA--MSIGRTSTFLDIYIEKDIR-E--GKMTEEE-----AQEL
VDQLIIKLR--IVRFLRTPEYNDLFSGDPVWVTES---LGGQ-GV-DGR--SLVTRTSYR
YLHTLYNLGPAPEPNLTVLWF-KNAPENWKRFCAKVS--IDTSAIQYEN-DDLMRPDYGD
--------------------------DYGIA-CCVS------------------PMKIGK
-QMQ------FFGARANL--AKCLLYAINGGR---DERSGV-QV----------AP-MFE
PVRS-EYLEYDEVMAKYEQMMRWLAKVYVNALKIIHYMHDKYAYE--AFEMSLHDGDVER
IRATGI----------------------AGLSIVADSLAAIRD---TKVRV-IRDE----
----------RGLAVDFE------------------------------------------
------------------------------------------------------------
------------REGE--YVPFGNNDDRTDSIAVEITEKFMEYL-RQH--ETY--R----
--HAKPTQSILTITS-NVVYGKKTGTTPDGRIGGTPFAP-GANPMNGRDTKGAIAALAS-
-VAKLPF-QHAHD-------------GISYTFAVSPATLGKEREMQINNLVSLLDGYFTP
----DGGQHLNVNVFDKDLLIDAMEHPEKYPQLTIRVSGYAVNFVKLTREQQLDVISRTI
NHSL-----------
>gi|212640611|ref|YP_002317131.1| Pyruvate-formate lyase [Anoxybacillus flavithermus
WK1]
------------------------------------------------------------
------------------------------------------------------------
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--------------------------------------MALLTVNEALMDAWRTFKGDKW
KKEIDVRDFIL-------------------------------------------------
------------------------------------------------------------
---------------------------NNV---------TVYTGDESFLEGPTEATKKLW
EQVMELSKLERERGG------VL--NMDTEIVSTITSHGPGYLNKELEKVVGFQTDE-PF
KRALMPFGG--IRMAEQACEA---YG----------------------------------
```

```
---YEVSDEVKKIFT-Q-----------YRKTHNQGVFDV---YTD--------------
-EMKAAR----------------KAGIITGLP---DAYGR--------------------
------GRIIGDYRRVA--LYGVDRLIEEKKKDLRN------------------------
--------TGARTMSEDIIRLREELAEQI----RALQELKEMAASYGYDISKPARNAHEA
FQWLYFAYLAAIKEQNGAA--MSLGRVSTFLDIYIERDLQ-E--GTLTERE-----AQEL
VDHFVMKLR--LVKFARTPEYNELFSGDPTWVTES---IGGV-AI-DGR--PLVTKNSFR
FLHTLDNLGPAPEPNLTVLWS-TQLPEAFKKYCAKMS--IQTSSIQYEN-DDLMRPEFGD
--------------------------DYGIA-CCVS------------------AMRIGK
-QMQ------FFGARANL--AKALLYAINGGV---DEKLKV-QI----------GP-EFA
PITS-EYLDYEEVMRKFDNVMEWLAELYINTLNVIHYMHDKYCYE--RIEMALHDTHILR
TMATGI----------------------AGLSVVADSLSAIK---YAKVKT-IRDE----
----------NGLAVDFE------------------------------------------
------------------------------------------------------------
------------IEGD--FPKYGNNDDRVDAIAVDIVERFMTKL-RKH--KTY--R----
--DSKHTTSILTITS-NVVYGKKTGNTPDGRRAGEPFAP-GANPLHGRDTKGALASLSS-
-VAKLPY-EYALD-------------GISNTFSIVPKALGKDDATRIQNLVAILDGYAL-
----KRGHHLNVNVFNRETLLDAMEHPEKYPQLTIRVSGYAVNFIKLTREQQIDVINRTF
HETM-----------
>gi|219870424|ref|YP_002474799.1| pyruvate-formate lyase [Haemophilus parasuis
SH0165]
------------------------------------------------------------
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------------------------------------------------------------
----------------------------------------MTQLTEAQKKAWEGFAPGEW
QTDVNVRDFIQ-------------------------------------------------
------------------------------------------------------------
---------------------------KNY---------TPYEGDESFLADVTEATTTLW
ADVMEKIKVENKTHE------PY--DIDCDIPSTITSHAPGYINKDLEKIVGLQTDA-PL
KRAIMPFGG--INMVKGSCKV---YR----------------------------------
---RELNPEVEKIFT-E-----------YRKTHNQGVFDV---YTP--------------
-DILRCR----------------KSGVITGLP---DAYGR--------------------
------GRIIGDYRRMA--LYGADFLMKDKVKQFTSLQ-----------EQL---ERGED
IQATI--------------QLREEIAEQH----RALGKMKEMAASYGFDISNPATNAQEA
VQWVYFAYLAAVKSQNGAA--MSFGRVSTFLDIYIERDLK-A--GKITEKE-----AQEL
MDHLVMKLR--MVRFLRTPEYDQLFSGDPMWATET---FAGM-GL-DGR--TLVTKNSFR
LLHTLYTMGPSPEPNLTILWS-ESLPDGFKRYAAKVS--IETSSVQYEN-DDLMRPDFQN
---------------D----------DYAIA-CCVS------------------PMIVGK
-MMQ------FFGARANL--AKTLLYAINGGV---DEKSGD-QV----------GP-KTE
PIMS-EYLDYDDVMTRLDSFMDWLAKQYVTALNIIHFMHDKYAYE--AALMALHDRDVFR
TMACGI----------------------AGLSVAADSLSAIK---YAKVKP-IRGDIEIK
NKAGEVVGVAKNVALDFE------------------------------------------
------------------------------------------------------------
------------IEGE--YPQFGNNDNRVDDIAVDLVERFMKKI-QKL--KTY--R----
--NATPTQSVLTITS-NVVYGKKTGNTPDGRRSGAPFGP-GANPMHGRDQKGAVASLTS-
-VAKLPF-AYAKD-------------GISYTFSIVPNALGKDLESQKRNLAGLMDGYFHH
ESTIEGGQHLNVNVMNREMLLDAMENPEKYPQLTIRVSGYAVRFNSLTKEQQMDVITRTF
TQSM-----------
>gi|92116483|ref|YP_576212.1| formate acetyltransferase [Nitrobacter hamburgensis
X14]
------------------------------------------------------------
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-----------------------------------MKASAALRKEAKAGDCWNDFQPGDW
LSSINVRDFIV-------------------------------------------------
------------------------------------------------------------
---------------------------RNV---------APYTGDEAFLTGPSQRTKAVW
AKLQPYFAEERKKGV------LA---VDAQTPSTLLAHKAGYIDRDNEIIVGLQTDQ-PF
KRAIFPFGG--LRMVETGLKA---AG----------------------------------
---YEPDPAVHEAFT-K-----------YRKSHNDGVFDA---YTP--------------
```

```
-EIMNCR----------------RSGIITGLP---DAYGR--------------------
------GRIIGDYRRVA--LYGIDRLLAAKRAEREQID--------------------DM
WPSDDII------------RLREELSDQM----RALEDLSSMAKLYGHDISKPARNAQEA
FQWTYFAYLGAIKEANGAA--MSIGRISSFLDIYIERDLK-Q--GVLDEGK-----AQEL
WDQLVQKLR--IVRFLRTPDYDALFSGDPYWATEC---VGGM-DL-DGR--TLVTKSSYR
MLHTLTNLGPAPEPNITVLWS-NHMPATFKRYCAKVSR--DTSSLQYEN-DDLMRQFWGD
--------------------------DYGIA-CCVS------------------AMRLGK
-QMQ------FFGARVNL--AKALLYAINGGR---DEVSGE-QV----------AP-RTL
PVAG-DFLDYDDVMAKFDTIMEWLARTYVHAMNCIHYMHDKYFYE--RLEMALHDRDILR
TMAFGI----------------------AGLSVVADSLSAIK---YGKIRV-ARDA----
----------AGLVVDYQ------------------------------------------
------------------------------------------------------------
------------NEGNKATPQFGNNDDRVDQIASDIVTSFMGKI-RKH--PTY--R----
--NATHTQSVLTITS-NVVYGKATGNTPDGRRKGEPFGP-GANPMHGRDSHGWLASCLS-
-VAKLPY-KDAQD-------------GISYTVSVAPQKTHLSEGQLIDEAVKAFDVYFD-
----RGGFHMNLNVIDRDTLEDAMKNPDKYPQLTIRVSGYAVNFVRLTPEQQRDVISRTF
HGQI-----------
>gi|15601940|ref|NP_245012.1| PflB [Pasteurella multocida subsp. multocida str.
Pm70]
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
--------------------------------------MSMSQLNETQQKAWEGFTGGDW
QTEVNVRDFIQ-------------------------------------------------
------------------------------------------------------------
---------------------------KNY---------TPYEGDESFLADATEATTKLW
NDVMEKIKVENKTHE------PY--DIDCDTPSTITSHAPGYIDKSLEKIVGLQTDA-PL
KRAIMPFGG--INMVKGSCKV---YR----------------------------------
---RELKPEVEQIFT-E-----------YRKTHNQGVFDV---YTP--------------
-DILRCR----------------KSGVITGLP---DAYGR--------------------
------GRIIGDYRRMA--LYGADFLMKDKFNQFTSLQ-----------DKL---ERGED
IQATI--------------QLREEIAEQH----RALGKMKEMAASYGYDISGPATNAHEA
VQWTYFAYLAAVKSQNGAA--MSFGRVSTFLDIYIERDLK-A--GKITEQE-----AQEL
IDHLVMKLR--MVRFLRTPEYDQLFSGDPMWATET---LAGM-GL-DGR--TLVTKNSFR
ILHTLYTMGPSPEPNLTILWS-EKLPEGFKRYAAKVS--IDTSSVQYEN-DDLMRPDFQN
---------------D----------DYAIA-CCVS------------------PMIVGK
-MMQ------FFGARANL--AKTLLYAINGGV---DEKSGD-QV----------GP-KTD
PITS-EYLDYDDVMTRLDSFMDWLAKQYVTALNIIHFMHDKYAYE--AALMALHDRDVFR
TMACGI----------------------AGLSVAADSLSAIK---YAKVKP-VRGDIEIK
NKAGEVVGIAKDVAIDFE------------------------------------------
------------------------------------------------------------
------------IEGE--YPQFGNNDNRVDEIACDLVERFMKKI-QKL--GTY--R----
--NATPTQSVLTITS-NVVYGKKTGNTPDGRRSGAPFGP-GANPMHGRDQKGAVASLTS-
-VAKLPF-AYAKD-------------GISYTFSIVPNALGKDYEAQKRNLAGLMDGYFHH
EATIEGGQHLNVNVMNREMLLDAMENPEKYPQLTIRVSGYAVRFNSLTKEQQQDVITRTF
TQAM-----------
>gi|125973025|ref|YP_001036935.1| formate acetyltransferase [Clostridium
thermocellum ATCC 27405]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------MDAWRGFNKGNW
CQEIDVRDFII-------------------------------------------------
------------------------------------------------------------
---------------------------RNY---------TPYEGDESFLVGPTDRTRKLW
EKVSELLKKERENGG------VL--DVDTHTISTITSHKPGYIDKELEVIVGLQTDE-PL
KRAIMPFGG--IRMVIKGAEA---YG----------------------------------
---HSVDPQVVEIFT-K-----------YRKTHNQGVYDV---YTP--------------
-EMRKAK----------------KAGIITGLP---DAYGR--------------------
```

```
------GRIIGDYRRVA--LYGVDRLIAEKEKEMASLE-----------------RDYID
YETV---------------RDREEISEQI----KSLKQLKEMALSYGFDISCPAKDAREA
FQWLYFAYLAAVKEQNGAA--MSIGRISTFLDIYIERDLK-E--GKLTEEL-----AQEL
VDQLVIKLR--IVRFLRTPEYEKLFSGDPTWVTES---IGGM-AL-DGR--TLVTKSSFR
FLHTLFNLGHAPEPNLTVLWS-VNLPEGFKKYCAKVS--IHSSSIQYES-DDIMRKHWGD
--------------------------DYGIA-CCVS------------------AMRIGK
-QMQ------FFGARCNL--AKALLYAINGGK---DEMTGE-QI----------AP-MFA
PVET-EYLDYEDVMKRFDMVLDWVARLYMNTLNIIHYMHDKYAYE--ALQMALHDKDVFR
TMACGI----------------------AGLSVVADSLSAIK---YAKVKP-IRNE----
----------NNLVVDYE------------------------------------------
------------------------------------------------------------
------------VEGD--YPKFGNNDERVDEIAVQVVKMFMNKL-RKQ--RAY--R----
--SATPTLSILTITS-NVVYGKKTGNTPDGRKAGEPLAP-GANPMHGRDINGALAVLNS-
-IAKLPY-EYAQD-------------GISYTFSIIPKALGRDEETRINNLKSMLDGYFK-
----QGGHHINVNVFEKETLLDAMEHPEKYPQLTIRVSGYAVNFIKLTREQQLDVINRTI
HGKI-----------
>gi|110803366|ref|YP_698491.1| formate acetyltransferase [Clostridium perfringens
SM101]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------------MFKQWEGFKEGVW
QKGIDVRNFIQ-------------------------------------------------
------------------------------------------------------------
---------------------------KNY---------TAYEGDKSFLEGTTKRTDAVL
EKAQKLIIEEIEKGI------ID---VATDRVSGIDNYEPGYLDKDNEVIVGFQTDA-PL
KRIVNPFGG--MRMVESSLKE---YG----------------------------------
---YELDSSIREHFN-A----------YRKTHNQGVFDA---YSA---------------
-ETRAAR----------------SAGLLTGLP---DAYGR--------------------
------GRIIGDYRRIA--LYGIDYLIEEKKKDYANISF-------ESEGSV--------
---------------EEYIQLRENVSEQI----RALEAIKSMAARYGFDISKPAANAKEA
VQFLYFGYLAAVKENNGAA--MSLGRTSTFLDIFIERDLK-A--GTLTELE-----AQEL
IDQFIIKLR--LVRHLRTPEYNDLFAGDPTWVTEG---IGGM-GV-NGK--PLVTKNSFR
YLQTLINLGPAPEPNMTVLWS-DRLPEGFKKFCAEVS--IKTDSIQYEN-DELMRPIYGD
--------------------------DYSIA-CCVS------------------AMQIGK
-QMQ------FFGARTNL--AKALLYTINGGI---DEKSGKVVI-------------KGL
EPITDEVLDYDKLRANYDKVLEYVAKLYVDTMNVIHYMHDKYAYE--AGQMALHDTHVGR
LMAFGI----------------------AGLSVVADSLSAVK---FAKVKP-IRE-----
----------NGIAVDFE------------------------------------------
------------------------------------------------------------
------------IEGD--FPKYGNDDDRVDDLAVEIVRKFSSEL-KKH--PLY--R----
--GAKHTLSILTITS-NVVYGKKTGSTPDGRKAGEAFAP-GANPMHGRDNSGALASLNS-
-VAKIPYCEVCED-------------GVSNTFSIVPDALGKEEDSRIDNLVAIMDGYFK-
----QGAHHLNVNVFNRETLMDAMEHPEKYPTLTIRVSGYAVNFNRLTRNQQLEVISRTF
HDSL-----------
>gi|18310135|ref|NP_562069.1| formate acetyltransferase [Clostridium perfringens
str. 13]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------------MFKQWEGFKEGVW
QNGIDVRNFIQ-------------------------------------------------
------------------------------------------------------------
---------------------------KNY---------TAYEGDKSFLEGTTKRTDAVL
EKAQKLIIEEIEKGI------ID---VATDRVSGIDNYEPGYLDKDNEVIVGFQTDA-PL
KRIVNPFGG--MRMVESSLKE---YG----------------------------------
---YELDSSIREHFN-A----------YRKTHNQGVFDA---YSA---------------
-ETRAAR----------------SAGLLTGLP---DAYGR--------------------
------GRIIGDYRRIA--LYGIDYLIEEKKKDYANISF-------ESEGSV--------
```

```
---------------EEYIQLRENVSEQI----RALEAIKSMAARYGFDISKPAANAKEA
VQFLYFGYLAAVKENNGAA--MSLGRTSTFLDIFIERDLK-A--GTLTELE-----AQEL
IDQFIIKLR--LVRHLRTPEYNDLFAGDPTWVTEG---IGGM-GV-NGK--PLVTKNSFR
YLQTLINLGPAPEPNMTVLWS-DRLPEGFKKFCAEVS--IKTDSIQYEN-DELMRPIYGD
--------------------------DYSIA-CCVS------------------AMQIGK
-QMQ------FFGARTNL--AKALLYTINGGI---DEKSGKVVI-------------KGL
EPITDEVLDYDKLRANYDKVLEYVAKLYVDTMNVIHYMHDKYAYE--AGQMALHDTHVGR
LMAFGI----------------------AGLSVVADSLSAVK---FAKVKP-IRE-----
----------NGIAVDFE------------------------------------------
------------------------------------------------------------
------------IEGD--FPKYGNDDDRVDDLAVEIVRKFSSEL-KKH--PLY--R----
--GAKHTLSILTITS-NVVYGKKTGSTPDGRKAGEAFAP-GANPMHGRDNSGALASLNS-
-VAKIPYCEVCED-------------GVSNTFSIVPDALGKEEDSRIDNLVAIMDGYFK-
----QGAHHLNVNVFNRETLMDAMEHPEKYPTLTIRVSGYAVNFNRLTRNQQLEVISRTF
HDSL-----------
>gi|150389979|ref|YP_001320028.1| formate acetyltransferase [Alkaliphilus
metalliredigens QYMF]
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------------------------------------------------------------
------------------------------------------------------------
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SRTIDVRDFIQ-------------------------------------------------
------------------------------------------------------------
---------------------------LNY---------APYHGDASFLEKATESTKELW
KQVLSLCEQERKNNG------TL--DIDVDTISTIVSHKPGYIDENLEKIVGLQTDA-PL
KRAIMPFGG--IRTVDSACQA---YG----------------------------------
---YELSSEIKDIFY-K-----------YRKTHNDGVFDV---YTP--------------
-EMLAAR----------------KAGIITGLP---DAYGR--------------------
------GRIIGDYRRVA--LYGIDRLIEDKNIQLASLEL----------DYM--------
--------------DENTMRLREEMAEQI----RALKELKEMGKSYGFDISRPASNAFEA
IQWLYLGYLAAVKEQNGAA--MSLGRVSTFLDIYIEKDLA-D--GKLTEEQ-----AQEL
VDHFVMKLR--MVRFLRTPDYNELFSGDPTWVTEC---IGGM-SM-DGR--TLVTKTSYR
VLNTLYNLGAAPEPNLTVLWS-TELPQNFKKFCSKAS--IDTSSIQYEN-DDLMRPYWGD
--------------------------DYGIA-CCVS------------------AMRIGK
-QMQ------FFGARCNL--GKALLYAINGGR---DEMSGL-QV----------GP-KFA
PITS-EYLDYQEVMEKFNTFIDWLAKLYVNTLNVIHYMHDKYAYE--RIEMALHDKDILR
TMACGI----------------------AGLSLCADSLSAMK---YAKVKV-IRNE----
----------EGLAVDYE------------------------------------------
------------------------------------------------------------
------------IEGD--FPKYGNNDDRVDDLAIELVERFMNSI-RRN--KTY--R----
--DSIPTQSVLTITS-NVVYGKKTGSTPDGRKTGEPFAP-GANPMHGRDTKGALASLAS-
-VAKLPY-EHAQD-------------GISYTFSIVPKALGKTTEERITILSSLLDGYFV-
----QGGHHINVNVFDRETLIDAMEHPELYPQLTIRVSGYAVNFIKLSREQQLDVINRTF
HGAIY----------
>gi|170717255|ref|YP_001784371.1| formate acetyltransferase [Haemophilus somnus
2336]
------------------------------------------------------------
------------------------------------------------------------
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------------------------------------------------------------
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----------------------------------------MAQLTETQQKAWEGFVGGDW
QTEVNVRDFIQ-------------------------------------------------
------------------------------------------------------------
---------------------------KNY---------TPYEGDEAFLAEATEATSILW
ADVMEKIKVENKTHE------PY--DIDTDIPSTITSHKAGYINKDLEKIVGLQTDA-PL
KRAIMPFGG--INMVRGSCKV---YR----------------------------------
---RELNPEVEKIFT-E-----------YRKTHNQGVFDV---YTP--------------
-DILRCR----------------KSGVITGLP---DAYGR--------------------
------GRIIGDYRRMA--LYGADFLMKDKFKQFTSLQ-----------------EKLES
GEDIQATI-----------QLREEIAEQH----RALGKMKEMAASYGYDISAPAKNAQEA
```

```
VQWTYFAYLAAVKSQNGAA--MSFGRVSTFLDIFIERDLK-A--GKITEQE-----AQEL
IDHLVMKLR--MVRFLRTPEYDQLFSGDPMWATET---LAGM-GL-DGR--TLVTKTSFR
ILHTLYTMGPSPEPNLTILWS-ESLPDGFKRYAAKVS--IDTSSVQYEN-DDLMRPDFQN
---------------D----------DYAIA-CCVS------------------PMIVGK
-MMQ------FFGARANL--AKTLLYAINGGI---DEKSGD-QV----------GP-KTD
PITT-EYLDYEDVMTRLDSFMDWLAKQYVTALNIIHFMHDKYAYE--AALMALHDRDVFR
TMACGI----------------------AGLSVAADSLSAIK---YAKVKP-IRGDIEVK
NKAGDVIGISKNVAIDFE------------------------------------------
------------------------------------------------------------
------------IEGE--YPQFGNNDSRVDDIAVDLVERFMKKI-QKL--KTY--R----
--NATPTQSVLTITS-NVVYGKKTGNTPDGRRSGAPFGP-GANPMHGRDQKGAVASLTS-
-VAKLPF-AYAKD-------------GISYTFSIVPNALGKDIDAQKRNLAGLMDGYFHH
ETTIEGGQHLNVNVLNREMLLDAVENPDKYPQLTIRVSGYAVRFNSLTKDQQQDVITRTF
TTSM-----------
>gi|218439783|ref|YP_002378112.1| formate acetyltransferase [Cyanothece sp. PCC
7424]
------------------------------------------------------------
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QEEINVRDFIQ-------------------------------------------------
------------------------------------------------------------
---------------------------KNY---------TPYSGDQSFLTDASERTQTLW
TQVKLLMQQEREKGI------LD---VETKVPSSITAHKPGYINKTLEQIVGLQTDK-PL
KRAIMPYGG--IRVVQKSLEA---YG----------------------------------
---YKLDPQTEKIFT-Q-----------YRKTHNDGVFDA---YTS--------------
-QMRKAR----------------HSGIITGLP---DAYGR--------------------
------GRIIGDYRRVA--LYGIDRLIKDKREQLTSLE----------------------
----------VEVMDEDTIRLREEISEQI----RALGELKEMAADYGFDISKPAANAKEA
LQWTYFAYLGAVKEQNGAA--MSLGRTSTFFDIYIERDLK-S--GLFTETD-----IQEF
IDQFVMKLR--MVRFLRTPDYNQLFAADPVWVTEV---IGGV-GE-DGR--PLVTKTSFR
FLHTLYNLGPAPEPNLTVLWS-QQLPIAFKRYCAKVS--IDTSSIQYEN-DDLMRPEYGD
--------------------------DYGIA-CCVS------------------AMRVGK
-QMQ------FFGARVNM--AKALLYAINGGK---DEKAGE-QI----------AP-SFA
PITA-EILDYEEVTAKFDLLMDWLARLYINTLNVIHYMHDKYCYE--RLEMALHDRDVYR
TMACGM----------------------AGLSVVVDALSAIK---YATVKV-IRND----
----------QGLAQDYQ------------------------------------------
------------------------------------------------------------
------------IEGD--YPKYGNNDDRVDEIAPNLVKTFMNKI-RSN--KTY--R----
--NAVPTQSILTITS-NVVYGKKTGSTPDGRKAGEPFAP-GANPMHGRDSQGAIASCAS-
-VAKLPY-EHAQD-------------GISYTFSIMPRALGKTQDTQINNLVGVLDGYFH-
----DSGHHININVFERETLLDAMDHPEKYPQLTIRVSGYAVNFIKLNREQQLDVINRTF
HERI-----------
>gi|16272145|ref|NP_438348.1| formate acetyltransferase [Haemophilus influenzae Rd
KW20]
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
--------------------------------------MTMSELNEMQKLAWAGFAGGDW
QENVNVRDFIQ-------------------------------------------------
------------------------------------------------------------
---------------------------KNY---------TPYEGDDSFLAGPTEATTKLW
ESVMEGIKIENRTHA------PL--DFDEHTPSTIISHAPGYINKDLEKIVGLQTDE-PL
KRAIMPFGG--IKMVEGSCKV---YG----------------------------------
---RELDPKVKKIFT-E-----------YRKTHNQGVFDV---YTP--------------
-DILRCR----------------KSGVLTGLP---DAYGR--------------------
------GRIIGDYRRVA--LYGVDFLMKDKYAQFSSLQK-----------DL---EDGVN
LEATI--------------RLREEIAEQH----RALGQLKQMAASYGYDISNPATNAQEA
IQWMYFAYLAAIKSQNGAA--MSFGRTATFIDVYIERDLK-A--GKITETE-----AQEL
```

```
VDHLVMKLR--MVRFLRTPEYDQLFSGDPMWATET---IAGM-GL-DGR--TLVTKNTFR
ILHTLYNMGTSPEPNLTILWS-EQLPENFKRFCAKVS--IDTSSVQYEN-DDLMRPDFNN
---------------D----------DYAIA-CCVS------------------PMIVGK
-QMQ------FFGARANL--AKTLLYAINGGI---DEKLGM-QV----------GP-KTA
PITD-EVLDFDTVMTRMDSFMDWLAKQYVTALNVIHYMHDKYSYE--AALMALHDRDVYR
TMACGI----------------------AGLSVAADSLSAIK---YAKVKP-VRGDIKDK
DGNVVA----TNVAIDFE------------------------------------------
------------------------------------------------------------
------------IEGE--YPQYGNNDNRVDDIACDLVERFMKKI-QKL--KTY--R----
--NAVPTQSVLTITS-NVVYGKKTGNTPDGRRAGAPFGP-GANPMHGRDQKGAVASLTS-
-VAKLPF-AYAKD-------------GISYTFSIVPNALGKDAEAQRRNLAGLMDGYFHH
EATVEGGQHLNVNVLNREMLLDAMENPDKYPQLTIRVSGYAVRFNSLTKEQQQDVITRTF
TESM-----------
>gi|15894267|ref|NP_347616.1| pyruvate-formate lyase [Clostridium acetobutylicum
ATCC 824]
------------------------------------------------------------
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------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------------------------MIKEWNDFKEGTW
VNNIDVRNFIQ-------------------------------------------------
------------------------------------------------------------
---------------------------KNY---------TPYLGNEDFLQGVTDRTKGLW
NKCEKLLLDEIKNQG------IL--KADNKTVSGINSFEAGYIDKENEIIYGLQTDE-PL
KRMVNPFGG--IRMAKQALEA---YG----------------------------------
---YEIDEDVYNIFT-K-----------YRKTHNEGVFDA---YTE--------------
-EMKTAR----------------HVGLLTGLP---DAYGR--------------------
------GRIIGDFRRVA--LYGIDCLIENKKADLKELKG---------------------
------------DMTEDLIRRREEVSEQI----KALKEMKAMALKYGIDISKPAANSRQA
VQFTYLGYLAGIKENNGAA--MSLGRVSTFLDIYIERDLK-N--GVITEKE-----AQEI
IDQFIIKLR--LERHLRTPEYNELFAGDPNWVTES---IGGM-GM-NGE--TLVTKNSFR
FLHSLTNLGPAPEPNMTVLWS-NNLPEPFKKYCSKMS--IKTDAIQYEN-DDIMRPIYGD
--------------------------DYGIA-CCVS------------------AMKIGK
-QMQ------FFGARCNL--AKSLLYAINGGV---DEKKFD-LV----------VP-HIK
RIDD-EVLDYDKVKENYFKVMKYVAKLYVNTLNLIHYMHDKYAYE--KGLMALHDTDVHR
FLACGA----------------------AGLSVAVDSLSAIK---YAKVKP-IRNE----
----------DGIAVDFE------------------------------------------
------------------------------------------------------------
------------VEGD--FPKYGNDDDRVDDIAVEIVNKFMSEL-RKT--AAY--R----
--NAEHTLSMLTITS-NVMYGKKTGATPDGRKSGEAFAP-GANPMHGRDKNGALASLNS-
-VAKIPYRSVCQD-------------GVSNTFSIIPDALGKNEETRANNLSAILDGYFE-
----KGAHHLNVNVLNRETLLDAMENPEKYPTLTIRVSGYAVNFVKLTKEQQMEVVKRTF
HGRM-----------
>gi|113461279|ref|YP_719348.1| formate acetyltransferase [Haemophilus somnus 129PT]
------------------------------------------------------------
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----------------------------------------MAQLTETQQKAWEGFVGGDW
QTEVNVRDFIQ-------------------------------------------------
------------------------------------------------------------
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ADVMEKIKVENKTHE------PY--DIDTDIPSTITSHKAGYINKDLEKIVGLQTDA-PL
KRAIMPFGG--INMVRGSCKV---YR----------------------------------
---RELNPEVEKIFT-E-----------YRKTHNQGVFDV---YTP--------------
-DILRCR----------------KSGVITGLP---DAYGR--------------------
------GRIIGDYRRMA--LYGADFLMKDKFKQFTSLQ-----------------EKLES
GEDIQATI-----------QLREEIAEQH----RALGKMKEMAASYGYDISAPAKNAQEA
VQWTYFAYLAAVKSQNGAA--MSFGRVSTFLDIFIERDLK-A--GKITEQE-----AQEL
IDHLVMKLR--MVRFLRTPEYDQLFSGDPMWATET---LAGM-GL-DGR--TLVTKTSFR
ILHTLYTMGPSPEPNLTILWS-ESLPDGFKRYAAKVS--IDTSSVQYEN-DDLMRPDFQN
```

```
---------------D----------DYAIA-CCVS------------------PMIVGK
-MMQ------FFGARANL--AKTLLYAINGGI---DEKSGD-QV----------GP-KTD
PITT-EYLDYEDVMTRLDSFMDWLAKQYVTALNIIHFMHDKYAYE--AALMALHDRDVFR
TMACGI----------------------AGLSVAADSLSAIK---YAKVKP-IRGDIEVK
NKAGDVIGISKNVAIDFE------------------------------------------
------------------------------------------------------------
------------IEGE--YPQFGNNDSRVDDIAVDLVERFMKKI-QKL--KTY--R----
--NATPTQSVLTITS-NVVYGKKTGNTPDGRRSGAPFGP-GANPMHGRDQKGAVASLTS-
-VAKLPF-AYAKD-------------GISYTFSIVPNALGKDIDAQKRNLAGLMDGYFHH
ETTIEGGQHLNVNVLNREMLLDAVENPDKYPQLTIRVSGYAVRFNSLTKEQQQDVITRTF
TTSM-----------
>gi|33152127|ref|NP_873480.1| formate acetyltransferase [Haemophilus ducreyi
35000HP]
------------------------------------------------------------
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------------------------------------------------------------
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----------------------------------------MIQLDEAQQKAWAGFVAGTW
QTEVNVRDFIQ-------------------------------------------------
------------------------------------------------------------
---------------------------KNY---------TPYEGDESFLAGATPATTKLW
QEVMEKIKVENKTHE------PY--DIDCDIPSTITSHKPGYIDQSLEKIVGLQTDA-PL
KRAILPFGG--IKMVKGSCDV---YR----------------------------------
---RKLNPEVEKIFT-E-----------YRKTHNQGVFDV---YTP--------------
-DILRCR----------------KSGVITGLP---DAYGR--------------------
------GRIIGDYRRLA--VYGADFLMKDKQRQFASLQP-----------NL---EAGED
IQATI--------------QLREEITEQF----RALGQIKEMAASYGFDVSRPAENAQEA
VQWTYFAYLAAVKSQNGAA--MSFGRVSSFLDIYIERDLK-A--GKITEEE-----AQEL
IDHLVMKLR--MVRFLRTPEYDQLFSGDPMWATET---LAGM-GL-DDR--TLVTKNSFR
ILNTLYTMGPSPEPNLTILWS-EQLPEGFKRYCAKVS--IDTSSVQYEN-DDLMRPDFDN
---------------D----------DYAIA-CCVS------------------PMVIGK
-QMQ------FFGARANL--AKTMLYAINGGI---DEKSGL-QV----------GP-KST
PITD-EVLNFDDVMTRMDHFMDWLATQYVTALNIIHFMHDKYSYE--AALMAFHDRDVFR
TMACGI----------------------AGLSVAADSLSAIK---YAKVKP-VRGDIKDK
DGNIVA----TNVALDFE------------------------------------------
------------------------------------------------------------
------------IEGE--YPQFGNNDSRVDDIACDLVERFMKKI-QTH--KTY--R----
--NATPTQSVLTITS-NVVYGKKTGNTPDGRRAGAPFGP-GANPMHGRDQKGAVASLTS-
-VAKLPF-AYAKD-------------GISYTFSIVPNALGKDYEAQKRNLAGLMDGYFHH
ETSVEGGQHLNVNVLNRETLLDAVEHPEKYPQLTIRVSGYAVRFNALTKEQQMDVITRTF
TESM-----------
>gi|52080503|ref|YP_079294.1| putative formate C-acetyltransferase [Bacillus
licheniformis ATCC 14580]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------MEQWKGFTTNVW
QKEVNVRDFIL-------------------------------------------------
------------------------------------------------------------
---------------------------SNF---------EPYQGDESFLEPPTEATSALW
DHVMDLTKKERENGG------VL--DMDTEIVSTITSHGPGYLNKDLEKVVGVQTDE-PF
KRSLQPFGG--IRMAKQACES---YG----------------------------------
---FKLNEEVERIFT-D-----------YRKTHNQGVFDA---YTD--------------
-EMKLAR----------------KVGIITGLP---DAYGR--------------------
------GRIIGDYRRVA--LYGVDFLIDEKKKDAAGTSR---------------------
------------VMSEENIRLREELSEQI----RALNELKALAKSYGFDISKPAANAREA
FQWLYFAYLAAIKEQNGAA--MSLGRVSTFLDIYIERDLK-T--GVLTERE-----AQEL
VDHFVMKLR--LVKFARTPDYNELFSGDPTWVTES---IGGM-AH-DGR--ALVTKNSFR
FLHTLDNLGPAPEPNLTVLWS-VRLPQKFKNYCAKMS--IKTSSIQYEN-DDIMRPEYGD
--------------------------DYGIA-CCVS------------------AMAIGK
```

```
-QMQ------FFGARANL--AKALLYAINGGK---DEKHKM-QV----------GP-EMP
PVAS-DVLDYDEVMHKFDQTMEWLAGLYINTLNVIHYMHDKYCYE--RIEMALHDTEILR
TMATGI----------------------AGLSVVADSLSAVK---YAKVSV-VRDE----
----------NGIAVDFE------------------------------------------
------------------------------------------------------------
------------TEGD--FPKYGNNDDRVDAIAVDIVKRFMKKL-RKH--QTY--R----
--QSVQTMSILTITS-NVVYGKKTGNTPDGRRAGEPFAP-GANPMHGRDTKGTLASLSS-
-VAKLPY-SYALD-------------GISNTFSIVPKALGKDEESRAANLSSILDGYAA-
----KTGHHLNVNVFNRETLLDAMEHPEEYPQLTIRVSGYAVNFIKLTKEQQLDVISRTF
HESM-----------
>gi|187736033|ref|YP_001878145.1| formate acetyltransferase [Akkermansia muciniphila
ATCC BAA-835]
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
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----------------------------------MISIVKDLKESTALPQEWQGFKPGTW
TESIDVRDFIQ-------------------------------------------------
------------------------------------------------------------
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DELKVLLKREIDNGG------VL--DADEKVVSSITSHKPGYIDKELEVVVGLQTDA-PL
KRALMPFGG--LRMAQQALES---YG----------------------------------
---FKMCEKTADIFK-K-----------IRKTHNEGVFDA---YTS--------------
-DIRAAR----------------SAGIITGLP---DAYGR--------------------
------GRIIGDYRRVA--LYGTDKLIAERRKDLKNREH---------------------
-----------SPLTDELIRLREEMSEQI----RALEELAQLGASYGCDLTRPAANAREA
VQWTYLGYLAAVKEQNGAA--MSLGRVSTFFDIYFTRDLE-Q--GLITEEE-----VQEI
IDQFVMKLR--IVRFIRTPDYNNLFSGDPTWVTES---IGGM-GE-DGR--TLVTRSSFR
MLQTLYNLGPAPEPNLTVLWS-RNLPEAFKSFCAKVS--IETSSVQYEN-DDLMRPHWGD
--------------------------DYGIA-CCVS------------------AMRIGK
-QMQ------FFGARANL--AKCLLYALNGGV---DELKGK-QV----------AP-PSP
RYTE-EILNYDEVMTLYDKMQDWLAKTYIDALNIIHYMHDKYCYE--RIEMALHDPEILR
TMATGI----------------------AGLSVAADSLSAIK---YATVKA-IRNE----
----------EGLIVDFK------------------------------------------
------------------------------------------------------------
------------TEGE--FPCYGNNDPRVDDIACSLVSNFMEKL-RRL--HTY--R----
--NSLPTQSILTITS-NVVYGKKTGNTPDGRRAGEPFAP-GANPMHGRDRNGAVASMLS-
-VAKLSY-DDSLD-------------GISYTFSIVPQALGKEERERRVKLVSLLDAYFA-
----ATGHHINVNVLERETLLDAMDHPEKYPQLTIRVSGYAVNFIKLTREQQQEVINRTF
HTR------------
========================================
```