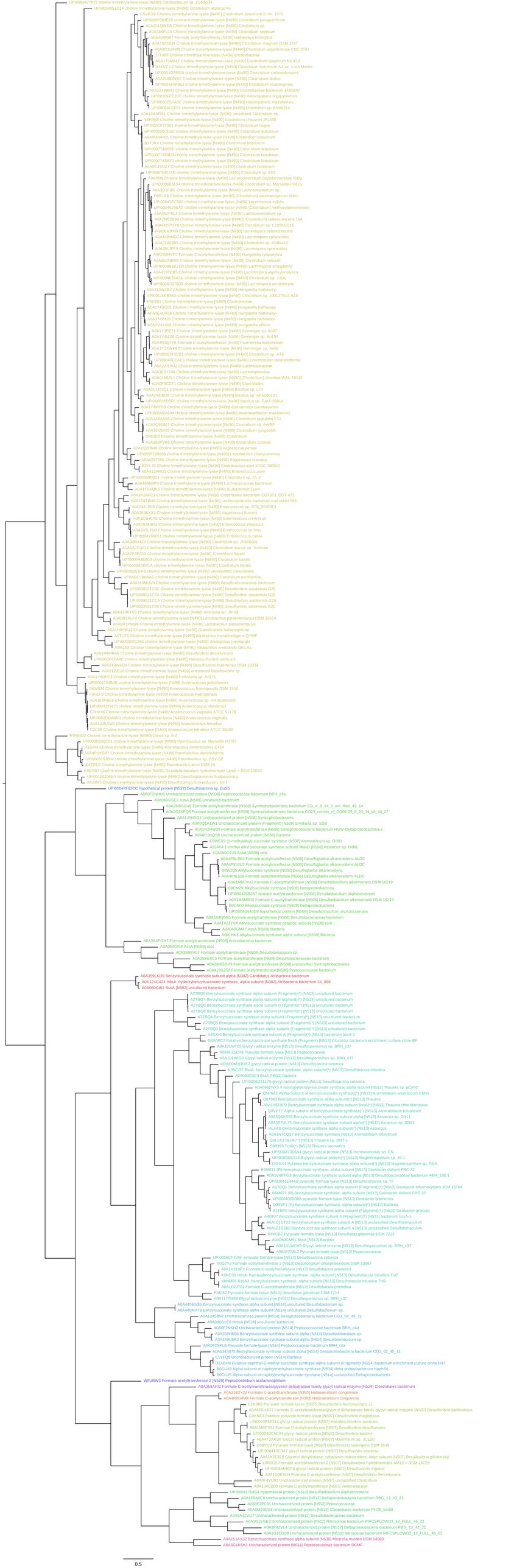
UP000647872 Choline trimethylamine-lyase [N490] Cetobacterium sp. ZOR0034
UP000049511C1A Choline trimethylamine-lyase [N490] Clostridium algidicarnis
CSVR49 Choline trimethylamine-lyase [N490] Clostridium botulinum D str. 1873
UP000C080E2F Choline trimethylamine-lyase [N490] Clostridium paraputrificum
UA3519WM5 Choline trimethylamine-lyase [N490] Clostridium sp.
A3A386P315 Choline trimethylamine-lyase [N490] Clostridium septicum
A0AU9R167 Formate acetyltransferase [N490] Hathewaya histolytica
A0A162SB34 Choline trimethylamine-lyase [N490] Clostridium magnum DSM 2767
A0A0C1U4W8 Choline trimethylamine-lyase [N490] Clostridium argentinense CDC 2741
J7T069 Choline trimethylamine-lyase [N490] Clostridiaceae
A0A175M642 Choline trimethylamine-lyase [N490] Clostridium botulinum B2 433
B1KVC2 Choline trimethylamine-lyase [N490] Clostridium botulinum A3 str. Loch Maree
UP000010395O8 Choline trimethylamine-lyase [N490] Clostridium carboxidivorans
A0A2UBDWX2 Choline trimethylamine-lyase [N490] Clostridium drakei
UP000048AF953 Choline trimethylamine-lyase [N490] Clostridium scatologenes
A0A224WB41 Choline trimethylamine-lyase [N490] Clostridiaceae bacterium 1450207
UP0010FCE2DC Choline trimethylamine-lyase [N490] Haloimpatiens lingqiaoensis
UP000C3SFA6C Choline trimethylamine-lyase [N490] Haloimpatiens massiliensis
UP000D6F7F61 Choline trimethylamine-lyase [N490] Clostridium sp. KNHs214
A0A126ARA1 Choline trimethylamine-lyase [N490] uncultured Clostridium sp.
S6FBN5 Choline trimethylamine-lyase [N490] Clostridium chauvoei JF4335
UP000CF72561 Choline trimethylamine-lyase [N490] Clostridium cagae
UP000500CE6C Choline trimethylamine-lyase [N490] Clostridium botulinum
A0A0M0A801 Choline trimethylamine-lyase [N490] Clostridium botulinum
B2TJR4 Choline trimethylamine-lyase [N490] Clostridium botulinum
UP000774D0FE Choline trimethylamine-lyase [N490] Clostridium botulinum
UP000073399D3 Choline trimethylamine-lyase [N490] Clostridium botulinum
UP000074D6F2 Choline trimethylamine-lyase [N490] Clostridium botulinum
A0A0C2SNZ4 Choline trimethylamine-lyase [N490] Clostridium botulinum
UP000F54524D Choline trimethylamine-lyase [N490] Clostridium sp. E02
A0KP09 Choline trimethylamine-lyase [N490] Lachnoclostridium phytofermentans ISDg
UP0009883134 Choline trimethylamine-lyase [N490] Clostridium sp. Marseille-P2415
A0A3D1FIB5 Choline trimethylamine-lyase [N490] Lachnoclostridium sp.
D9R1K6 Choline trimethylamine-lyase [N490] [Clostridium] saccharolyticum WM1
UP000456EC503 Choline trimethylamine-lyase [N490] Lacrimispora indolis
UP000462 9EAE Choline trimethylamine-lyase [N490] [Clostridium] methoxybenzovorans
A0A352P8L4 Choline trimethylamine-lyase [N490] Lachnoclostridium sp.
A0A2MUZB98 Choline trimethylamine-lyase [N490] [Clostridium] celerecrescens 18A
A0A0U5P1Y8 Choline trimethylamine-lyase [N490] Clostridium sp. C105KSO15
A0A084JFX9 Choline trimethylamine-lyase [N490] Lacrimispora celerecrescens
A0A1I0HMD7 Choline trimethylamine-lyase [N490] Lacrimispora sphenoides
A0A0I02985 Choline trimethylamine-lyase [N490] Clostridium sp. ASBs410
A0A3B1JPF9 Choline trimethylamine-lyase [N490] Lacrimispora sphenoides
A0A256HYF3 Formate C-acetyltransferase [N490] Hungatella xylanolytica
A0A3E2NBN9 Choline trimethylamine-lyase [N490] Clostridium indicum
UP0000B2E7D9 Choline trimethylamine-lyase [N490] Lacrimispora amygdalina
A0A419TC85 Choline trimethylamine-lyase [N490] Lacrimispora alpidoyanolytica
UP0000463 9ASD Choline trimethylamine-lyase [N490] Clostridium sp. 12(A)
UP000047D7D09 Choline trimethylamine-lyase [N490] Lacrimispora aerotolerans
A0A419WZB7 Choline trimethylamine-lyase [N490] Hungatella hathewayi
UP000150B34D Choline trimethylamine-lyase [N490] Clostridium sp. 1001175st1 A10
R5U281 Choline trimethylamine-lyase [N490] Clostridiaceae
A0A178BG05 Choline trimethylamine-lyase [N490] Hungatella hathewayi
A0A3E4UA58 Choline trimethylamine-lyase [N490] Hungatella hathewayi
A0A374P4J9 Choline trimethylamine-lyase [N490] Hungatella hathewayi
A0A2V3Y409 Choline trimethylamine-lyase [N490] Hungatella effluvii
A0A1X3B221 Choline trimethylamine-lyase [N490] Gemmiger sp. An87
A0A1Y4IZZ8 Choline trimethylamine-lyase [N490] Gemmiger sp. An194
A0A4R1QTY6 Formate C-acetyltransferase [N490] Fournierella massiliensis
A0A1Y3XWF9 Choline trimethylamine-lyase [N490] Gemmiger sp. An50
UP000082F2E81 Choline trimethylamine-lyase [N490] Clostridium sp. AT4
UP000040ECAE9 Choline trimethylamine-lyase [N490] Enterocloster clostridioformis
A0A227LN17 Choline trimethylamine-lyase [N490] Lachnospiraceae
A0A3E2Y709 Choline trimethylamine-lyase [N490] Lachnospiraceae
A0A0J9BZL1 Choline trimethylamine-lyase [N490] [Clostridium] citroniae WAL-19142
A0A0F0CDT1 Choline trimethylamine-lyase [N490] Clostridiales
A0A021NVQ1 Choline trimethylamine-lyase [N490] Bacillus sp. LF1
A0A2A8IBD8 Choline trimethylamine-lyase [N490] Bacillus sp. AFS006103
UP000835D5F5 Choline trimethylamine-lyase [N490] Bacillus sp. FJAT-29814
A0A174WFF8 Choline trimethylamine-lyase [N490] Caloramator quimbayensis
UP000SB2A644 Choline trimethylamine-lyase [N490] Anaerosalibacter massiliensis
A0A146AS68 Choline trimethylamine-lyase [N490] Clostridium ragsdalei P11
A0A3Q5S937 Choline trimethylamine-lyase [N490] Clostridium sp. AWRP
A0A1665K92 Choline trimethylamine-lyase [N490] Clostridium ljungdahlii
D8GID3 Choline trimethylamine-lyase [N490] Clostridium
A0A1E6PVB6 Choline trimethylamine-lyase [N490] Clostridium coskatii
A0A1Q2D648 Choline trimethylamine-lyase [N490] Vagococcus penaei
UP000F738B99 Choline trimethylamine-lyase [N490] Lactobacillus zhaoyuanensis
A0A4Q5Z505 Choline trimethylamine-lyase [N490] Vagococcus hubeiensis
I0PL79 Choline trimethylamine-lyase [N490] Enterococcus asini ATCC 700915
A0A143ARG3 Choline trimethylamine-lyase [N490] Enterococcus asini
UP000S595B23 Choline trimethylamine-lyase [N490] Clostridium sp. CL-2
A0A486NBP9 Choline trimethylamine-lyase [N490] Lachnospiraceae bacterium
A0A1TSKQK5 Choline trimethylamine-lyase [N490] [Eubacterium] yurii
A0A3P2AFC1 Choline trimethylamine-lyase [N490] Clostridiales bacterium COT073_COT-073
A0A2T4TBH8 Choline trimethylamine-lyase [N490] Lachnospiraceae bacterium oral taxon 096
A0A242L9D8 Choline trimethylamine-lyase [N490] Enterococcus sp. 6C8_DIV0013
A0A369AXX3 Choline trimethylamine-lyase [N490] Vagococcus fluvialis
A0A1E5HCT0 Choline trimethylamine-lyase [N490] Enterococcus urolyticus
A0A0S3K9F3 Choline trimethylamine-lyase [N490] Enterococcus silesiacus
A0A242LTU0 Choline trimethylamine-lyase [N490] Enterococcus termitis
UP000470265L choline trimethylamine-lyase [N490] Enterococcus crotali
A0A386H423 Choline trimethylamine-lyase [N490] Clostridium sp. JN500901
A0A0AFTU0 Choline trimethylamine-lyase [N490] Clostridium baratii str. Sullivan
A0A0F3F5Z6 Choline trimethylamine-lyase [N490] Clostridium baratii
UP000S9A60D8 choline trimethylamine-lyase [N490] Clostridium baratii
UP000S9A3D0A choline trimethylamine-lyase [N490] Clostridium baratii
UP000065530F6 choline trimethylamine-lyase [N490] unclassified Clostridiales
UP000C7BBBAC choline trimethylamine-lyase [N490] Clostridium minhonense
A0A316MUV0 Choline trimethylamine-lyase [N490] Desulfovibrionaceae bacterium
UP000852 1C9C Choline trimethylamine-lyase [N490] Desulfovibrio alaskensis G20
UP000852 1CE6 Choline trimethylamine-lyase [N490] Desulfovibrio alaskensis G20
UP000852 1CCA Choline trimethylamine-lyase [N490] Desulfovibrio alaskensis G20
UP000852 1C85 Choline trimethylamine-lyase [N490] Desulfovibrio alaskensis G20
A0A149PTV0 Choline trimethylamine-lyase [N490] Animipila sp. JN-18
A0A0R1KLF0 Choline trimethylamine-lyase [N490] Lactobacillus paralimentarius DSM 19674
A0A0R1PMD8 Choline trimethylamine-lyase [N490] Lactobacillus paralimentarius
A0A1H9HBU3 Choline trimethylamine-lyase [N490] Granulicatella balaenopterae
A6TUT5 Choline trimethylamine-lyase [N490] Alkaliphilus metalliredigens QYMF
UP000035053A0 choline trimethylamine-lyase [N490] Alkaliphilus oremlandii
A0MJE6 Choline trimethylamine-lyase [N490] Alkaliphilus oremlandii OhILAs
A0A1MSHRA6 Choline trimethylamine-lyase [N490] Desulfotomaculum desulfuricans
UP000 3F6FA4C choline trimethylamine-lyase [N490] Halodesulfovibrio aestuarii
A0A1T4W4Q4 Choline trimethylamine-lyase [N490] Desulfovibrio bizertensis DSM 18034
A0A212J116 Choline trimethylamine-lyase [N490] uncultured Desulfovibrio sp.
A0A1Y4DRT3 Choline trimethylamine-lyase [N490] Colinsella sp. An271
UP000672480B choline trimethylamine-lyase [N490] Anaerococcus jeddahensis
W9WL94 Choline trimethylamine-lyase [N490] Anaerococcus hydrogenalis DSM 7454
H0H1F9 Choline trimethylamine-lyase [N490] Anaerococcus hydrogenalis
A0A1E8R8C6 Choline trimethylamine-lyase [N490] Anaerococcus sp. HMSC065G05
UP000312171 choline trimethylamine-lyase [N490] Anaerococcus obesiensis
C7HVX6 Choline trimethylamine-lyase [N490] Anaerococcus vaginalis ATCC 51170
UP0002DDA0DD choline trimethylamine-lyase [N490] Anaerococcus vaginalis
A0A133KAW7 Choline trimethylamine-lyase [N490] Anaerococcus tetradius
C2CI8 Choline trimethylamine-lyase [N490] Anaerococcus tetradius ATCC 35098
R9MND2 Choline trimethylamine-lyase [N490] Dorea sp. 5-2
UP000D1062D1 choline trimethylamine-lyase [N490] Paenibacillus sp. Marseille-P3787
H3SIR4 Choline trimethylamine-lyase [N490] Paenibacillus dendritiformis C454
A0A4R5YSR7 Choline trimethylamine-lyase [N490] Paenibacillus dendritiformis
UP000315130B4 choline trimethylamine-lyase [N490] Paenibacillus sp. OSY-SE
K4ZDE0 Choline trimethylamine-lyase [N490] Paenibacillus alvei DSM 29
X8DYB7 Choline trimethylamine-lyase [N490] Desulfotomaculum hydrothermale LamS = DSM 18033
UP001018 20FBA choline trimethylamine-lyase [N490] Desulfosporosinus fructosivorans
A4J9M5 Choline trimethylamine-lyase [N490] Desulfotomaculum reducens MI-1
UP000047F62CC hypothetical protein [N527] Desulfosarcina sp. BuS5
A0A0F2NHU6 Uncharacterized protein [N508] Peptococcaceae bacterium BRH_c4a
A0A060GS E2 AssA [N508] uncultured bacterium
A0A2M8GDA9 Formate acetyltransferase [N508] Syntrophobacterales bacterium CG_4_8_14_3_um_filter_49_14
A0A2G9XFQ8 Formate acetyltransferase [N508] Syntrophobacterales bacterium CG23_combo_of_CG06-09_8_20_14_all_48_27
A0A1J5HSQ1 Uncharacterized protein [N508] Syntrophobacterales
A0A0Q1A1W1 Uncharacterized protein (Fragment) [N508] Smithella sp. SDB
A0A2N2HW30 Formate acetyltransferase [N508] Deltaproteobacteria bacterium HGW-Deltaproteobacteria-2
A0A0C1RQS8 Uncharacterized protein [N508] Bacteria
E0WEX9 (2-methylalkyl) succinate synthase [N508] Aromatoleum sp. OcN1
A9J4K4 1-methyl alkyl succinate synthase subunit MasD [N508] Azoarcus sp. HxN1
A0A060GTJ5 AssA [N508] root
A0A4P8L3M2 Formate acetyltransferase [N508] Desulfoglaeba alkanexedens ALDC
A0A4P8LBU2 Formate acetyltransferase [N508] Desulfoglaeba alkanexedens ALDC
D8WZ05 Alkylsuccinate synthase [N508] Desulfoglaeba alkanexedens
A0A4P8L508 Formate acetyltransferase [N508] Desulfoglaeba alkanexedens ALDC
A0A1M6CVU2 Formate C-acetyltransferase [N508] Desulfatibacillum alkenivorans DSM 16219
I6CMZ9 Alkylsuccinate synthase [N508] Deltaproteobacteria
UP000424B2A7 formate acetyltransferase [N509] Desulfatibacillum aliphaticivorans
A0A1M6M9R2 Formate C-acetyltransferase [N508] Desulfatibacillum alkenivorans DSM 16219
B5CN00 Alkylsuccinate synthase [N508] Deltaproteobacteria
UP000404GA6D9 hypothetical protein [N508] Desulfatibacillum aliphaticivorans
A0A3A4Q6M5 Formate acetyltransferase [N508] Desulfobacteraceae bacterium
A0A1422YV4 Alkylsuccinate synthase catalytic subunit [N508] root
A0A060GM47 AssA [N508] Bacteria
W6CHK3 Alkylsuccinate synthase alpha subunit [N508] Bacteria
A0A3A4PGH7 Formate acetyltransferase [N508] Acinobacteria bacterium
A0A060GS9 AssA [N508] root
A0A3B95V5 / Formate acetyltransferase [N508] Desulfotomaculum sp.
A0A355W8C5 Formate acetyltransferase [N508] Desulfobacteraceae bacterium
A0A2M8GDH9 Formate acetyltransferase [N508] unclassified Syntrophobacterales
A0A419G2S2 Formate acetyltransferase [N508] Peptococcaceae bacterium
A0A359LKD9 Benzylsuccinate synthase subunit alpha [N382] Candidatus Atribacteria bacterium
A0A124G424 HbsA: hydroxybenzylsuccinate synthase, alpha subunit [N382] Atribacteria bacterium 34_868
A0A060GI62 BssA [N382] uncultured bacterium
A2TBQ9 Benzylsuccinate synthase alpha subunit (Fragment)(*) [N513] uncultured bacterium
A2TBQ7 Benzylsuccinate synthase alpha subunit (Fragment)(*) [N513] uncultured bacterium
A2TBQ6 Benzylsuccinate synthase alpha subunit (Fragment)(*) [N513] uncultured bacterium
A2TBQ8 Benzylsuccinate synthase alpha subunit (Fragment)(*) [N513] uncultured bacterium
A2TBQ4 Benzylsuccinate synthase alpha subunit (Fragment)(*) [N513] uncultured bacterium
A2TBQ5 Benzylsuccinate synthase alpha subunit (Fragment)(*) [N513] uncultured bacterium
A2TBQ3 Benzylsuccinate synthase alpha subunit (Fragment)(*) [N513] uncultured bacterium
A6GKI6 Benzylsuccinate synthase subunit A (Fragment)(*) [N513] bacterium bssA-2
D8WWC2 Putative benzylsuccinate synthase BssA (Fragment) [N513] Clostridia bacterium enrichment culture clone BF
A0A1D1WT05 Glycyl radical enzyme [N513] Desulfosporosinus sp. BRH_c37
A0A0F2SCX8 Pyruvate formate-lyase [N513] Peptococcaceae
A0A101WIG0 Glycyl radical enzyme [N513] Desulfosporosinus sp. BRH_c37
UP000060181E7 glycyl radical protein [N513] Desulfosarcina cetonica
K0NCD2 BssA: benzylsuccinate synthase, alpha subunit(*) [N513] Desulfobacula toluolica
A0A060GSE4 BssA [N513] Bacteria
UP000GED1179 glycyl radical protein [N513] Desulfosarcina cetonica
A0A0962NX3 4-isopropylbenzyl-succinate synthase alpha subunit [N513] Thauera sp. pCyN2
Q5P6A2 Alpha-Subunit of benzylsuccinate synthase(*) [N513] Aromatoleum aromaticum EbN1
Q87943 Benzylsuccinate synthase alpha subunit(*) [N513] Thauera
A0A1H5TIP9 Benzylsuccinate synthase alpha subunit BssA(*) [N513] Thauera chlorobenzoica
Q1VPT7 Alpha subunit of benzylsuccinate synthase(*) [N513] Aromatoleum toluolicum
A0A3Q8H558 Benzylsuccinate synthase subunit alpha [N513] Azoarcus sp. DN11
A0A357ULV5 Benzylsuccinate synthase subunit alpha(*) [N513] Azoarcus sp. DN11
H1HT8 Benzylsuccinate synthase alpha subunit(*) [N513] Azoarcus
A0A1N7CQ57 Benzylsuccinate synthase [N513] Aromatoleum tolulyticum
Q8LLA3 BssA(*) [N513] Thauera sp. DNT-1
O68395 TutD(*) [N513] Thauera aromatica
UP000473564 glycyl radical protein [N513] Herminiimonas sp. CN
UP000B8BC61EB glycyl radical protein(*) [N513] Magnetospirillum sp. 15-1
I7GGX4 Putative benzylsuccinate synthase alpha subunit(*) [N513] Magnetospirillum sp. TS-6
B9M011 (R)-benzylsuccinate synthase, alpha subunit [N513] Geobacter daltonii FRC-32
A0A1W8PQ3 Benzylsuccinate synthase subunit alpha [N513] Desulfobacteraceae bacterium 4484_190.1
UP000041E44D pyruvate formate-lyase [N513] Desulfuromonas sp. TF
A2TBQ1 Benzylsuccinate synthase alpha subunit (Fragment)(*) [N513] Geobacter toluenoxydans JCM 15764
B9M021 (R)-benzylsuccinate synthase, alpha subunit [N513] Geobacter daltonii FRC-32
UP000408D38A pyruvate formate-lyase [N513] Geobacter bremensis
Q39VF1 (R)-benzylsuccinate synthase, alpha subunit(*) [N513] Bacteria
A2TBP9 Benzylsuccinate synthase alpha subunit (Fragment)(*) [N513] Geobacter grbiciae
A4GKI7 Benzylsuccinate synthase subunit A (Fragment)(*) [N513] bacterium bssA-1
A0A101GT22 Benzylsuccinate synthase subunit A [N513] unclassified Desulfotomaculum
A0A101G5A0 Benzylsuccinate synthase subunit A [N513] unclassified Desulfotomaculum
R4KCB7 Pyruvate-formate lyase [N513] Desulfallas gibsoniae DSM 7213
A0A060GM51 BssA [N513] Bacteria
A0A101WCH5 Glycyl radical enzyme [N513] Desulfosporosinus sp. BRH_c37
A0A0F2SBL2 Pyruvate formate-lyase [N513] Peptococcaceae
UP1000GCF42AF pyruvate formate-lyase [N513] Desulfosarcina cetonica
S0GZY2 Formate acetyltransferase 2 [N513] Desulfotignum phosphitoxidans DSM 13687
A0A1H2EDF2 Formate C-acetyltransferase [N513] Desulfitobacula phenolica
K0ND30 HbsA: hydroxybenzylsuccinate synthase, alpha subunit [N513] Desulfobacula toluolica Tol2
K0NMG5 BssA3: benzylsuccinate synthase, alpha subunit [N513] Desulfobacula toluolica Tol2
A0A3JH2JT01 Formate C-acetyltransferase [N513] Desulfitobacula phenolica
R4KK57 Pyruvate-formate lyase [N513] Desulfallas gibsoniae DSM 7213
A0A117SH59 Glycyl radical enzyme [N513] Desulfosporosinus sp. BRH_c37
A0A445MV39 Benzylsuccinate synthase alpha subunit [N514] uncultured Desulfobacterium sp.
A0A445MVT8 Benzylsuccinate synthase alpha subunit [N514] uncultured Desulfobacterium sp.
A0A1JI5BN2 Uncharacterized protein [N514] Deltaproteobacteria bacterium CG1_02_45_11
A0A0600LE0 NmsA [N514] uncultured bacterium
A0A0F2NKH2 Uncharacterized protein [N514] Peptococcaceae bacterium BRH_c4a
A0A359H8SB Benzylsuccinate synthase subunit alpha [N514] Desulfotomaculum sp.
A0A349J8R2 Benzylsuccinate synthase subunit alpha [N514] Desulfotomaculum sp.
A0A0F2NR16 Pyruvate formate-lyase [N514] Peptococcaceae bacterium BRH_c4a
A0A1J4S875 Benzylsuccinate synthase subunit alpha [N514] Deltaproteobacteria bacterium CG1_02_45_11
E1YFQ9 Uncharacterized protein [N514] Bacteria
D2XBH8 Putative naphthyl-2-methyl-succinate synthase alpha subunit (Fragment) [N514] bacterium enrichment culture clone N47
B0CLU8 Alpha-subunit of naphthylmethylsuccinate synthase [N514] delta proteobacterium NaphS6
B0CLU5 Alpha-subunit of naphthylmethylsuccinate synthase [N514] unclassified Deltaproteobacteria
W8UBW3 Formate acetyltransferase 2 [N528] Peptococcitrobium acidaminophilum
A0A358AP42 Formate C-acetyltransferase/glycerol dehydratase family glycyl radical enzyme [N529] Clostridiales bacterium
A0A318DY22 Formate C-acetyltransferase [N383] Halanaerobium congolense
A0A4R8G8M4 Formate C-acetyltransferase [N383] Halanaerobium congolense
E1K0B6 Pyruvate formate-lyase [N507] Desulfovibrio fructosivorans JJ
A0A4P6HJG7 Formate C-acetyltransferase/glycerol dehydratase family glycyl radical enzyme [N507] Desulfovibrio carbinolicus
C4XNE3 Putative pyruvate formate-lyase [N507] Desulfovibrio magneticus
UP000GF5E214 glycyl radical protein [N507] Halodesulfovibrio aestuari
A0A1M6E7G1 Formate C-acetyltransferase [N507] Desulfovibrio desulfuricans
UP000040CAE93 glycyl radical protein [N507] Desulfovibrio basilsii
A0A4T2AKU8 Glycyl radical protein [N507] Marinifilum sp. JC120
C6BVU8 Pyruvate formate-lyase [N507] Desulfovibrio salexigens DSM 2638
UP000410C3A7 glycyl radical protein [N507] Desulfovibrio zosterae
A0A1X7E8Z8 Glycerol dehydratase, cobalamin-independent, large subunit [N507] Desulfovibrio gilichinskyi
A0RQG5 Formate acetyltransferase 2 [N507] Desulfovibrio hydrothermalis AM13 = DSM 14728
UP000S569CF8 glycyl radical protein [N507] Desulfovibrio frigidus
A0A1G9KSG4 Formate C-acetyltransferase [N507] Desulfovibrio ferrireducens
A0A0F4VJ91 Uncharacterized protein [N507] unclassified Clostridium
A0A134CD09 Formate C-acetyltransferase [N507] Veillonellaceae
UP000427D8D4 hypothetical protein [N512] Desulfitobacillum alphaticivorans
A0A1F9A0C8 Uncharacterized protein [N512] Deltaproteobacteria bacterium RBG_13_43_22
A0A0F2PC91 Uncharacterized protein [N512] Peptococcaceae
A0A0M2U0V4 Uncharacterized protein [N512] Clostridiales bacterium PH28_bin88
A0A3AAZVG7 Uncharacterized protein [N512] Desulfobacteraceae bacterium
A0A1G1EGE3 Uncharacterized protein [N512] Nitrospinae bacterium RIFCSPLOWO2_12_FULL_45_22
A0A1F8ZVL4 Uncharacterized protein [N512] Deltaproteobacteria bacterium RBG_13_43_22
A0A1G1EGS8 Uncharacterized protein [N512] Nitrospinae bacterium RIFCSPLOWO2_12_FULL_45_22
A0A151AX32 Benzylsuccinate synthase alpha subunit [N530] Moorella mulderi DSM 14980
A0A3G1KSK1 Uncharacterized protein [N531] Peptococcaceae bacterium DCMF
0.5