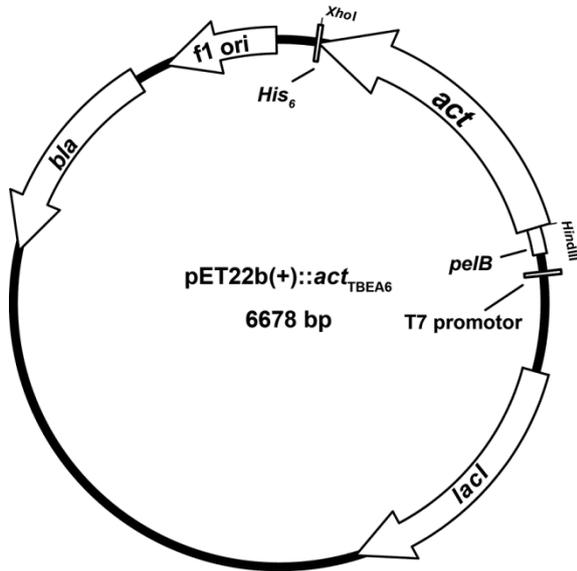
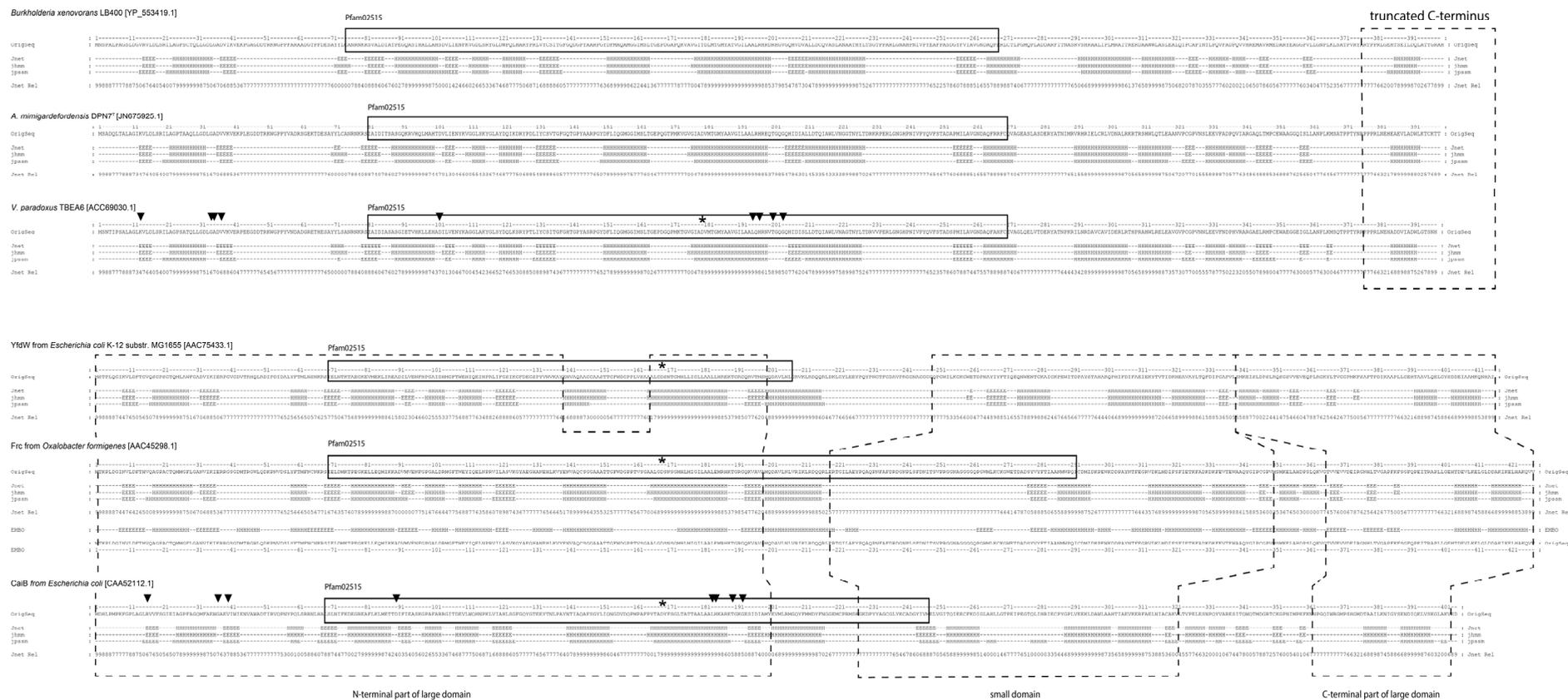


Supplemental Material



Supplemental Fig. S1

Physical map of pET22b(+):*act*_{TBEA6}. *Act*, succinyl-CoA:3-sulfinopropionate CoA-transferase from *V. paradoxus* strain TBEA6; *bla*, β-lactamase; *pelB*, pelB signal sequence for potential periplasmic localization; f1 ori, f1 origin of replication.



Supplemental Fig. S2

Secondary structure prediction of ACTBEA6-orthologues. Amino acid sequences were subjected to secondary structure prediction using the Jpred3 server (44). Due to their available solved crystal structures, formyl-CoA:oxalate CoA-transferase from *E. coli* (YfdW) (27, 28), its orthologue Frc from *O. formigenes* (20, 26) and crotonobetainyl-CoA:carnitine CoA transferase from *E. coli* (CaiB) (29, 30) as members of the CoA-transferase III family were included for comparison. For them, the N-terminal and C-terminal part of the large domain as well as the small domain are indicated

(dashed outline). For each sequence amino acids annotated as Pfam02515 (CoA-transferase family III) are contoured with a solid line. The truncated C-terminus found in Act_{TBEA6} is highlighted by an additional box. Jnet, final secondary structure prediction for the amino acid query sequence; H, α -helix; E, extended β -sheet; jhmm, Jnet hmm (hidden Markov model) profile prediction; jpssm; Jnet PSIBLAST pssm (position specific scoringmatrix) profile prediction. JnetRel, Jnet reliability of prediction accuracy. The latter ranges from 0 to 9 and higher values are better.

Supplemental Fig. S3

Chloroflexus aurantiacus J-10-f1 (YP_001633818.1)	1	-----MKGILHGLRIVVEGSFAVVAAPLGGMTLAQLGSDVTRFPIGGGLDYLRWVPT	51
Burkholderia xenovorans LB400 (YP_559695.1)	1	-----MGALSHRLVLDLRLVLAGPWCQAQADFGADVTKIERPQVGGDDTRHWGPF	50
A. mimigardefordensis DPN77 (JN675925.1)	1	-----MSADQLTA--IAGIKVLDLRLIAGPTAAQLGDLGADVVKVEPLEGGDDTRHWGPF	55
V. paradoxus TBEA6 (ACC69030.2)	1	-----MSNTIPSA--IAGIKVLDLRLIAGPSATQLGDLGADVVKVEPLEGGDDTRHWGPF	55
V. paradoxus EPS (YP_004152464.1)	1	-----MTKPAALDGTIKVLDLRLVLAGPWCQTQIADLADGADVVKIERPVGDDTRHWGPF	53
V. paradoxus S110 (YP_002942048.1)	1	-----MTATKPAALDGTIKVLDLRLVLAGPWCQTQIADLADGADVVKIERPVGDDTRHWGPF	55
V. paradoxus B4 (contig47_RVVP05211)	1	-----MTA-KPAALDGTIKVLDLRLVLAGPWCQTQIADLADGADVVKIERPVGDDTRHWGPF	54
Verminephrobacter eiseniae EF01-2 (YP_996507.1)	1	MACPGAHGHFFPSSPTAMPSTARSITAPTSAPTTAPTSAAALGKIKVLDLRLVLAGPWCQTQIADLADGADVVKIERPVGDDTRHWGPF	90
Pseudomonas putida KT2240 (NE_742328.1)	1	-----MGALSHRLVLDLRLVLAGPWCQAQADFGADVTKIERPQVGGDDTRHWGPF	50
Burkholderia xenovorans LB400 (YP_553419.1)	1	-----MNSPALPAGSLDGVRLDRLIAGPSCTQLGDLGADVVKVEKPGAGDDTRHWGPF	57
Ralstonia eutropha H16 (YP_727217.1)	1	-----MGALSHRLVLDLRLVLAGPWCQAQADFGADVTKIERPQVGGDDTRHWGPF	50
Chloroflexus aurantiacus J-10-f1 (BY35475.1)	1	-----MSSQRPFRPLDVRVLELGAFLAGFCGQLLADFGADVTKVEPFGKDDTRHWGPF	56
E. coli K-12 substr. MG1655 (AAC75433.1)	1	-----MSTPLQGIKVLDFGCVGSPSCTQMLAWGADVTKIERPVGDDTRHWGPF	50
Oxalobacter formigenes (AAC45298.1)	1	-----MTKPLDGNVLDFTVQAGPACTQMGFLGANVTKIERRSGDDTRHWGPF	50
Escherichia coli (CA52112.1)	1	-----MDHLP-MPKFGIAGLRLVFSGIEIAGKPFAGMFAENGAEVYIENWAWADTRVQPN	57
Chlostridium scindens (AAC45415.1)	1	-----MAGIKDFPKGALACGLKIDSGSNIAGPLGGGLIACGCAVTHFFGPKPKDNGRWY	58
Chloroflexus aurantiacus J-10-f1 (YP_001633818.1)	52	LDG-----KHSILWAGLNKGRSIAIDIRHRCPELLTQICAPGEHAGLFTNPARGLSYDEIKHRADLMVNVGRDGG	131
Burkholderia xenovorans LB400 (YP_559695.1)	51	YLRTPDGDADTHEAAYLAANRNRKSTVDIASPEGQRIIEAAQSDVVENYKVGQLKRYGLDYASIKGDKPDLVYCS	138
A. mimigardefordensis DPN77 (JN675925.1)	56	YVADRSGEKTDESAYVLCANRNRKSTVDIASPEGQRIIEAAQSDVVENYKVGQLKRYGLDYASIKGDKPDLVYCS	143
V. paradoxus TBEA6 (ACC69030.2)	56	YVNDADGKRETHEAAYVLCANRNRKSTVDIASPEGQRIIEAAQSDVVENYKVGQLKRYGLDYASIKGDKPDLVYCS	143
V. paradoxus EPS (YP_004152464.1)	54	FKDADGNDTDAQSMPTACNRNRKSTVDIATPEGQRIIEAAQSDVVENYKVGQLKRYGLDYASIKGDKPDLVYCS	141
V. paradoxus S110 (YP_002942048.1)	56	FKDADGNDTDAQSMPTACNRNRKSTVDIATPEGQRIIEAAQSDVVENYKVGQLKRYGLDYASIKGDKPDLVYCS	143
V. paradoxus B4 (contig47_RVVP05211)	55	FIRDAGNDTDAQSMPTACNRNRKSTVDIATPEGQRIIEAAQSDVVENYKVGQLKRYGLDYASIKGDKPDLVYCS	142
Verminephrobacter eiseniae EF01-2 (YP_996507.1)	91	FLRDAAGNDTDAQSMPTACNRNRKSTVDIATPEGQRIIEAAQSDVVENYKVGQLKRYGLDYASIKGDKPDLVYCS	178
Pseudomonas putida KT2240 (NE_742328.1)	51	FKDVEGDDTDEAAYVLCANRNRKSTVDIATPEGQRIIEAAQSDVVENYKVGQLKRYGLDYASIKGDKPDLVYCS	138
Burkholderia xenovorans LB400 (YP_553419.1)	58	FARADGTFPDESAYVLCANRNRKSTVDIATPEGQRIIEAAQSDVVENYKVGQLKRYGLDYASIKGDKPDLVYCS	145
Ralstonia eutropha H16 (YP_727217.1)	51	WLKDEGDRDTEAAYVLCANRNRKSTVDIATPEGQRIIEAAQSDVVENYKVGQLKRYGLDYASIKGDKPDLVYCS	138
Chloroflexus aurantiacus J-10-f1 (BY35475.1)	57	RYKG-----DIPDIDALFTMLNSNRKSTVDIATPEGQRIIEAAQSDVVENYKVGQLKRYGLDYASIKGDKPDLVYCS	137
E. coli K-12 substr. MG1655 (AAC75433.1)	50	-----DIPDIDALFTMLNSNRKSTVDIATPEGQRIIEAAQSDVVENYKVGQLKRYGLDYASIKGDKPDLVYCS	132
Oxalobacter formigenes (AAC45298.1)	50	-----DKPNVDSIDFTMFCNRKSTVDIATPEGQRIIEAAQSDVVENYKVGQLKRYGLDYASIKGDKPDLVYCS	132
Escherichia coli (CA52112.1)	57	-----YFQSLRRNLHLSLNTFVDEGEAFKIMETTDITFEASKGPAFARRGITDEVIWQHPNPLIAHSGSQYGTPE	133
Chlostridium scindens (AAC45415.1)	58	-----YFQNLRRNLHLSLNTFVDEGEAFKIMETTDITFEASKGPAFARRGITDEVIWQHPNPLIAHSGSQYGTPE	133
Chloroflexus aurantiacus J-10-f1 (YP_001633818.1)	131	----SEVDYTVNPLQLPFMTGFPVTP---DVVNHVLP*AVLTVTGQIALGLLAEHRHRLTGGGLKIKALIKVGMIGHLMAIEVM	214
Burkholderia xenovorans LB400 (YP_559695.1)	139	YARAGDFTVLSIGGFSITGERDQPGGGPQKAGVAIALMTGMYSTAVTALTRHRDGGGQYDMAILLQVQAMLMNMSNYLTD	229
A. mimigardefordensis DPN77 (JN675925.1)	144	YARPGDFTVLSIGGFSITGERDQPGGGPQKAGVAIALMTGMYSTAVTALTRHRDGGGQYDMAILLQVQAMLMNMSNYLTD	229
V. paradoxus TBEA6 (ACC69030.2)	144	YARPGDFTVLSIGGFSITGERDQPGGGPQKAGVAIALMTGMYSTAVTALTRHRDGGGQYDMAILLQVQAMLMNMSNYLTD	229
V. paradoxus EPS (YP_004152464.1)	142	YAEARPDFTVLSIGGFSITGERDQPGGGPQKAGVAIALMTGMYSTAVTALTRHRDGGGQYDMAILLQVQAMLMNMSNYLTD	231
V. paradoxus S110 (YP_002942048.1)	144	YAEARPDFTVLSIGGFSITGERDQPGGGPQKAGVAIALMTGMYSTAVTALTRHRDGGGQYDMAILLQVQAMLMNMSNYLTD	231
V. paradoxus B4 (contig47_RVVP05211)	143	YAEARPDFTVLSIGGFSITGERDQPGGGPQKAGVAIALMTGMYSTAVTALTRHRDGGGQYDMAILLQVQAMLMNMSNYLTD	232
Verminephrobacter eiseniae EF01-2 (YP_996507.1)	179	YAEARPDFTVLSIGGFSITGERDQPGGGPQKAGVAIALMTGMYSTAVTALTRHRDGGGQYDMAILLQVQAMLMNMSNYLTD	268
Pseudomonas putida KT2240 (NE_742328.1)	139	YARAGDFTVLSIGGFSITGERDQPGGGPQKAGVAIALMTGMYSTAVTALTRHRDGGGQYDMAILLQVQAMLMNMSNYLTD	229
Burkholderia xenovorans LB400 (YP_553419.1)	146	YARPGDFTVLSIGGFSITGERDQPGGGPQKAGVAIALMTGMYSTAVTALTRHRDGGGQYDMAILLQVQAMLMNMSNYLTD	231
Ralstonia eutropha H16 (YP_727217.1)	139	YARPGDFTVLSIGGFSITGERDQPGGGPQKAGVAIALMTGMYSTAVTALTRHRDGGGQYDMAILLQVQAMLMNMSNYLTD	229
Chloroflexus aurantiacus J-10-f1 (BY35475.1)	138	YRDKAGFSSIGGFSITGERDQPGGGPQKAGVAIALMTGMYSTAVTALTRHRDGGGQYDMAILLQVQAMLMNMSNYLTD	228
E. coli K-12 substr. MG1655 (AAC75433.1)	133	YVNVKAMENADAGGAASITGDFWDPG---PLVSAALGQSNTEHMLLIGLALLHREKIRGGRGIVNENQAVNLCRVIKRLDQQR	218
Oxalobacter formigenes (AAC45298.1)	133	NEHLKVENADAGGAASITGDFWDPG---PTVSAALGQSNTEHMLLIGLALLHREKIRGGRGIVNENQAVNLCRVIKRLDQQR	218
Escherichia coli (CA52112.1)	134	YTNLFAVNTDAQPSYILIQND---VQDMPAFPTAYVFSGLTATTAALALHKAERKGRGSDIADYVYVPMQCYFMDYFNG	218
Chlostridium scindens (AAC45415.1)	134	YVTRASDNDQAPSYMSING---TTEALKINPYLSEVCGLLTCWAMLCVSTVILGKRVYDVALRIGDLMRDMQYATD	217
Chloroflexus aurantiacus J-10-f1 (YP_001633818.1)	215	INDT-----DRPQGNLYLQAGRDFETLIGKRVVWGLTDLQWALKGLTGLTADFNALGAR	272
Burkholderia xenovorans LB400 (YP_559695.1)	229	GQF-----FVRGNNAHNPVYQTFQSTGQ-WIIVAVGNDGQFRKFEVVGGLPLANDER	282
A. mimigardefordensis DPN77 (JN675925.1)	230	RKR-----PERLGNHNPVYQTFQSTGQ-WIIVAVGNDGQFRKFEVVGGLPLANDER	283
V. paradoxus TBEA6 (ACC69030.2)	230	RVV-----PERLGNHNPVYQTFQSTGQ-WIIVAVGNDGQFRKFEVVGGLPLANDER	283
V. paradoxus EPS (YP_004152464.1)	232	GKA-----PQRGNTHESLAPYQDFPTDQ-SMGLAI GNNQGFARFCAAAHAKWAADAR	285
V. paradoxus S110 (YP_002942048.1)	234	GKA-----PQRGNTHESLAPYQDFPTDQ-SMGLAI GNNQGFARFCAAAHAKWAADAR	287
V. paradoxus B4 (contig47_RVVP05211)	233	GKA-----PQRGNTHESLAPYQDFPTDQ-SMGLAI GNNQGFARFCAAAHAKWAADAR	286
Verminephrobacter eiseniae EF01-2 (YP_996507.1)	269	GQA-----PTRGNHNPVYQTFQSTGQ-WIIVAVGNDGQFRKFEVVGGLPLANDER	322
Pseudomonas putida KT2240 (NE_742328.1)	229	GQA-----PTRGNHNPVYQTFQSTGQ-WIIVAVGNDGQFRKFEVVGGLPLANDER	282
Burkholderia xenovorans LB400 (YP_553419.1)	232	GTP-----PARLGNHNPVYQTFQSTGQ-WIIVAVGNDGQFRKFEVVGGLPLANDER	285
Ralstonia eutropha H16 (YP_727217.1)	229	GQA-----PRWGNHNPVYQTFQSTGQ-WIIVAVGNDGQFRKFEVVGGLPLANDER	282
Chloroflexus aurantiacus J-10-f1 (BY35475.1)	224	GHI-----RERTGNILNVAFSNIYPTAGDSWFIIGANQDTIFRNLQAKGPELATDPR	278
E. coli K-12 substr. MG1655 (AAC75433.1)	219	DKLGLYEEYQY-PNGTFG-----DAVPRGNNAGGGGEGWLLKCKGWEVDADSYNYFTITANWQYICMIDIKPEKDDPAA	306
Oxalobacter formigenes (AAC45298.1)	219	ERTGILAEYPAQPNFADFRDGNLFDNFITSVPRGNNAGGGGEGWLLKCKGWEVDADSYNYFTITANWQYICMIDIKPEKDDPAA	306
Escherichia coli (CA52112.1)	219	GEM-----CPRMSKGRDYYAGGLYKCADG-YIMELVGTITQIECFKILGLH-LTGPET	274
Chlostridium scindens (AAC45415.1)	218	GVK-----MPTRTGN-KDAQALFSFYTCGRITFIGMTGAEVCKRGPFIIGLVPFGTGDGDF	274
Chloroflexus aurantiacus J-10-f1 (YP_001633818.1)	273	LGLMDEEGDRFRARHEAALPEWFHARTLAEVRRIFEQHRITWAPYRTVREAIAGPDCSTNDMPFAMVEQPGIG--SYLMPGSP	360
Burkholderia xenovorans LB400 (YP_559695.1)	282	----FATNPARVRRHRDIPVLEADIMVYQKQWIAALEAAGPCGPNNDGVEVFE-EGVARGLQVLDLPHPSGA--TVKLVNRP	364
A. mimigardefordensis DPN77 (JN675925.1)	283	----YATNMRVRRHRDIPVLEADIMVYQKQWIAALEAAGPCGPNNDGVEVFE-EPQVIARGALRMPCEWAAG-GGILLANLPM	367
V. paradoxus TBEA6 (ACC69030.2)	283	----YATNPKRLLNRDCAVDELRTRKTRAHVLRLEAVGPCGPNNDGVEVFE-EPHVRARGALRMPCEWAAG-GEIGLLANLPM	367
V. paradoxus EPS (YP_004152464.1)	285	----FATNLRVHRGVVIPMEEELTRTRTADVWVLELDEKAVPCGPNNDGVEVFE-DAQVKARGAVLTPRDAAGDGIASITGVASPLR	370
V. paradoxus S110 (YP_002942048.1)	287	----FATNLRVHRGVVIPMEEELTRTRTADVWVLELDEKAVPCGPNNDGVEVFE-DAQVKARGAVLTPRDAAGDGIASITGVASPLR	372
V. paradoxus B4 (contig47_RVVP05211)	286	----FATNLRVHRGVVIPMEEELTRTRTADVWVLELDEKAVPCGPNNDGVEVFE-DAQVKARGAVLTPRDAAGDGIASITGVASPLR	371
Verminephrobacter eiseniae EF01-2 (YP_996507.1)	322	----FASNTARVRRHRDIPMRAQVTRTRTADVWVLELDEKAVPCGPNNDGVEVFE-DAQVKARGAVLTPRDAAGDGIASITGVASPLR	407
Pseudomonas putida KT2240 (NE_742328.1)	282	----FVTKNLRVANRAEIPLRRAQVTRTRTADVWVLELDEKAVPCGPNNDGVEVFE-EPQVIARGALRMPCEWAAG--SVQVASPLR	364
Burkholderia xenovorans LB400 (YP_553419.1)	285	----FITNASRVRRHRDIPMRAQVTRTRTADVWVLELDEKAVPCGPNNDGVEVFE-EPQVHREAVMVRMDEYRAGA-GGVLGNLPLK	369
Ralstonia eutropha H16 (YP_727217.1)	282	----FATNPARVRRHRDIPVLEADIMVYQKQWIAALEAAGPCGPNNDGVEVFE-EPQVIARGALRMPCEWAAG--SVQVASPLR	364
Chloroflexus aurantiacus J-10-f1 (BY35475.1)	278	----FATHQARGEHQAEIDDLAAWTLVYADQLQVMMDEYGVAGRYTAKEMLS-EPHFIARQSIGVHDDPLG--EIKMQNVVPL	360
E. coli K-12 substr. MG1655 (AAC75433.1)	294	----YNTAARQPHIDFPAEIKYTVLIDKHEAVYLTQDFPCAPLSSKEKLSL-EPSLRQSGSVVEVVEVDEIRG--NHLTVGCPKPE	376
Oxalobacter formigenes (AAC45298.1)	306	----YSTFEGRVKIDMDFSPFETKPADKDFEVTWAAQYQPCGPNMSKELAH-EPSLQKVTGVVEVVEVDEIRG--NHLTVGCPKPE	388
Escherichia coli (CA52112.1)	275	PEGTQLIHRTECPYGLDEEKDADWLAHAEVAVKFAELNCAKALITPELES-NPQYVARESITQWQMDGR--TCKGNMIFKE	360
Chlostridium scindens (AAC45415.1)	275	PEG-TFGWMLYTPVGRQEKAKMEKYVSEHTEVEAEVMAQHQPCQRYEEDCLN-EPHWKARGITTEWDDPMG--HITGLNLIN	359
Chloroflexus aurantiacus J-10-f1 (YP_001633818.1)	361	TAVPRLVQVAPRLGHEHDEILEVLGSEAEVGRHLDEHGVAGPDRAA-----	409
Burkholderia xenovorans LB400 (YP_559695.1)	365	SGTPPEALHPTLGEHTASLDRVLDYDEAKIALRAQSVI-----	406
A. mimigardefordensis DPN77 (JN675925.1)	368	SATPPTYNRPPRLNEHAEVADWLTKCTTT-----	399
V. paradoxus TBEA6 (ACC69030.2)	368	SQTPPTYRRPPRLNEHADDVADWLGTSNH-----	398
V. paradoxus EPS (YP_004152464.1)	371	SATPPVLRHAPPALGQHTREVIAE-FGIDGARFDALRSAGV-----	411
V. paradoxus S110 (YP_002942048.1)	373	TATPPVLRHAPPALGQHTREVIAE-FGIDGARFDALRSAGV-----	413
V. paradoxus B4 (contig47_RVVP05211)	372	TATPPVLRHAPPALGQHTREVIAE-FGIDGARFDALRSAGV-----	412
Verminephrobacter eiseniae EF01-2 (YP_996507.1)	408	SATPPVLRHAPPALGQHTREVIAE-LGLDAARIALRSAGV-----	448
Pseudomonas putida KT2240 (NE_742328.1)	365	SETPVEYRRAPPRLGHEHTEVILEVGLDAGEVQRIRDAGV-----	406
Burkholderia xenovorans LB400 (YP_553419.1)	370	SATPVRVARTPRLGHEHTEVLDQLATYGRAH-----	401
Ralstonia eutropha H16 (YP_727217.1)	365	SATPPQALRHPPRLGHEHTEVIAETLGYGPEIEALRAGVL-----	406
Chloroflexus aurantiacus J-10-f1 (BY35475.1)	361	SATPGVDWTGPPALGQHTREVIAE-FGIDGARFDALRSAGV-----	402
E. coli K-12 substr. MG1655 (AAC75433.1)	377	SATPPTDKAAP-LGHEHTAAVQEG-LQYSDDIEAAMQNHAI-----	416
Oxalobacter formigenes (AAC45298.1)	389	SGQPEITRAP-LGHEHTAETKE-LGLDARIKELHAKQV-----	428
Escherichia coli (CA52112.1)	361	KNNPQVIRWMPHSGMDTAAALRN-TGYSNDEIQELSKGLAKVED-----	405
Chlostridium scindens (AAC45415.1)	360	KRNPSIWRGAPLFGMDNRDLKD-LGVYDARIDELYEQGVINEFDLTTIKRVRIDEVTHPMRKEE	426

Supplemental Fig. S3

Multiple sequence alignment of Act_{TBEA6} and orthologues from various related species.

Identical amino acids are shaded in dark-grey. Similar amino acids are shaded in light-grey.

Accession numbers are given in parentheses. Amino acid residues considered to be highly conserved throughout class III CoA-transferases (26) are indicated with a hash. Residues corresponding to Asp169, which represents the putative active site key residue in formyl-CoA-transferase (20), are highlighted with a frame. The glycine-rich loop of formyl-CoA transferases is highlighted as well.

Supplemental Table S1.

oligonucleotide	sequence (5'-3') ^a	Source or reference
Primers for PCR:		
<i>act_HindIII_For</i>	<u>AAGCTT</u> ATGAGCAACACCATTTCCTAGC	MWG Biotech AG, Ebersberg, Germany
<i>act_XhoI_Rev_oS</i>	CTCGAGGTGGTTTGAGGTTCCGAGC	MWG Biotech AG, Ebersberg, Germany
<i>XbaI_upAct</i>	AATCTAGAGGATCGCAGTCTCTCGCGC	MWG Biotech AG, Ebersberg, Germany
<i>NdeI_upAct</i>	AAA <u>CATATG</u> CAATCATCTCCAAAAGGCC	MWG Biotech AG, Ebersberg, Germany
<i>NdeI_downAct</i>	AAAACATATGTAGAAGGAATATCACCATG	MWG Biotech AG, Ebersberg, Germany
<i>XbaI_downAct</i>	AAATCTAGACATCGACTTGTGGACCTTC	MWG Biotech AG, Ebersberg, Germany
Primers for sequencing:		
M13 <i>Forward</i>	GTAAAACGACGGCCAG	MWG Biotech AG, Ebersberg, Germany
M13 <i>Reverse</i>	CAGGAAACAGCTATGAC	MWG Biotech AG, Ebersberg, Germany
<i>act_oS_451_For</i>	CCTGGCTACGACTTCCTG	MWG Biotech AG, Ebersberg, Germany
<i>act_oS_451_Rev</i>	CAGGAAGTCGTAGCCAGG	MWG Biotech AG, Ebersberg, Germany
<i>act_oS_876_For</i>	CTTCGGATTGTGGCGTAGC	MWG Biotech AG, Ebersberg, Germany
<i>act_oS_876_Rev</i>	GCTACGCCACAAATCCGAAG	MWG Biotech AG, Ebersberg, Germany
Primers for screening of <i>V. paradoxus</i> TBEA6 Δact_{TBEA6} mutant		
up <i>act_proof</i>	CGAAGTCGGGCGGCCGATAGC	MWG Biotech AG, Ebersberg, Germany
down <i>act_proof</i>	GCGCTGGGCGTTGTAGGCGG	MWG Biotech AG, Ebersberg, Germany
<i>act_int_fwd</i>	GCAGATGTTGTCAAAGTCGAGCG	MWG Biotech AG, Ebersberg, Germany
<i>act_int_rev</i>	CGAGAATCATCGGCGAGTCG	MWG Biotech AG, Ebersberg, Germany
Primers for genomewalking		
ActWalk1	CGTGACAAATCCAGCACTTTGAGGC	MWG Biotech AG, Ebersberg, Germany
ActSeq1	GAATGGTGTGCTCATCAATCATC	MWG Biotech AG, Ebersberg, Germany
ActWalk2	CTTTCGTGTTTCAAGCCAAAAAGCG	MWG Biotech AG, Ebersberg, Germany
ActSeq2	GAAATTGGCCGAAGAGCAATTC	MWG Biotech AG, Ebersberg, Germany
ActSeq3rev	GAATTGCTCTTCGGCCAATTC	MWG Biotech AG, Ebersberg, Germany
ActSeq4rev	CAAAAGCCAAAGCTACCGCG	MWG Biotech AG, Ebersberg, Germany
ActSeq5rev	CGTTATCCCTGTCTATACGCGGC	MWG Biotech AG, Ebersberg, Germany
Act_Walk3	GGTTTGCGGCTCATTGAAATCCC	MWG Biotech AG, Ebersberg, Germany
ActSeq6	GAATTTTATCCCCTATAGGCAGCCG	MWG Biotech AG, Ebersberg, Germany
ActWalk5	GGAGAAGTACAGCTACGCCACGCC	MWG Biotech AG, Ebersberg, Germany
Act_Seq7	GATCGGGCACGATGCAACACC	MWG Biotech AG, Ebersberg, Germany