

SUPPLEMENTARY MATERIAL TO
PCR-based detection of alkane monooxygenase genes in the hydrocarbon and crude oil-degrading *Acinetobacter* strains from petroleum-contaminated soils

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Table S-I. The phenotypical characteristics of the strains D11, E1 and E2, in comparison with other *Acinetobacter* species

Characteristic	1	2	3	4	5	6	7	8	9	10	11
Cell shape	Cb	Cb	Cb	ND	B	Cb	B	C	B	Rs	Cb
Gram staining	-	-	-	-	-	-	-	-	-	-	-
Motility	+	+	-	-	-	-	ND	-	-	-	+
Oxygen requirement	A	A	A	ND	A	A	ND	ND	ND	ND	A
Growth temperature (°C)	20-40	20-40	20-40	ND	10-40	25-37	ND	25-45	20-40	30-39	10-45
Optimum Growth temperature (°C)	35	35	35	25-30	30	ND	28	30	30	36-37	30
Growth pH	5.0-10.0	5.0-10.0	4.0-10.0	ND	5.0-10.0	ND	ND	6.0-8.0	6.0-9.0	7.0-9.0	5.0-11.0
Optimum growth pH	8.0-10.0	9.0-10.0	4.0-10.0	7.0-8.0	6.0-8.0	ND	7.0	7.0	ND	8.5	5.0
Starch hydrolysis	+	+	+	-	-	ND	ND	ND	+	ND	+
Gelatin hydrolysis	-	+	-	-	ND	+	-	ND	+	ND	+
Oxidase	-	-	-	-	-	-	-	-	-	-	-
Catalase	+	+	+	+	+	+	+	+	+	+	+
Citrate	+	+	+	+	+	+	-	+	+	+	+
Urease	-	-	-	+	ND	ND	-	ND	ND	ND	+
Indole	-	-	-	-	-	ND	-	-	ND	-	-
NaCl resistance	3	3	5	3.5	0-5	ND	ND	ND	0-9	0-3	4

+ = positive; - = negative; ND= no data available; C=cocccoid; Cb=coccobacil; Rs= short rod; B=bacil; A= aerobic; 1=Acinetobacter pittii strain D11, 2: Acinetobacter pittii E1 3=Acinetobacter calcoaceticus strain E2, 4= Acinetobacter sp. strain ADH-1 (Cormack and Fraile 1997), 5 = Acinetobacter soli, sp. Nov. (Kim et al. 2008), 6= Acinetobacter beijerinckii, sp. Nov., NIPH 838^T (Nemec et al. 2009), 7=Acinetobacter sp. strain RTE1.4 (Paisio et al. 2013), 8= Acinetobacter strain USTB-X (Yuan et al. 2014), 9= Acinetobacter junii strain VA2 (Zhang et al. 2014), 10= Acinetobacter sp. strain S2 (Sawadogo et al. 2014), 11= Acinetobacter sp. strain BT1A (Acer et al. 2016).

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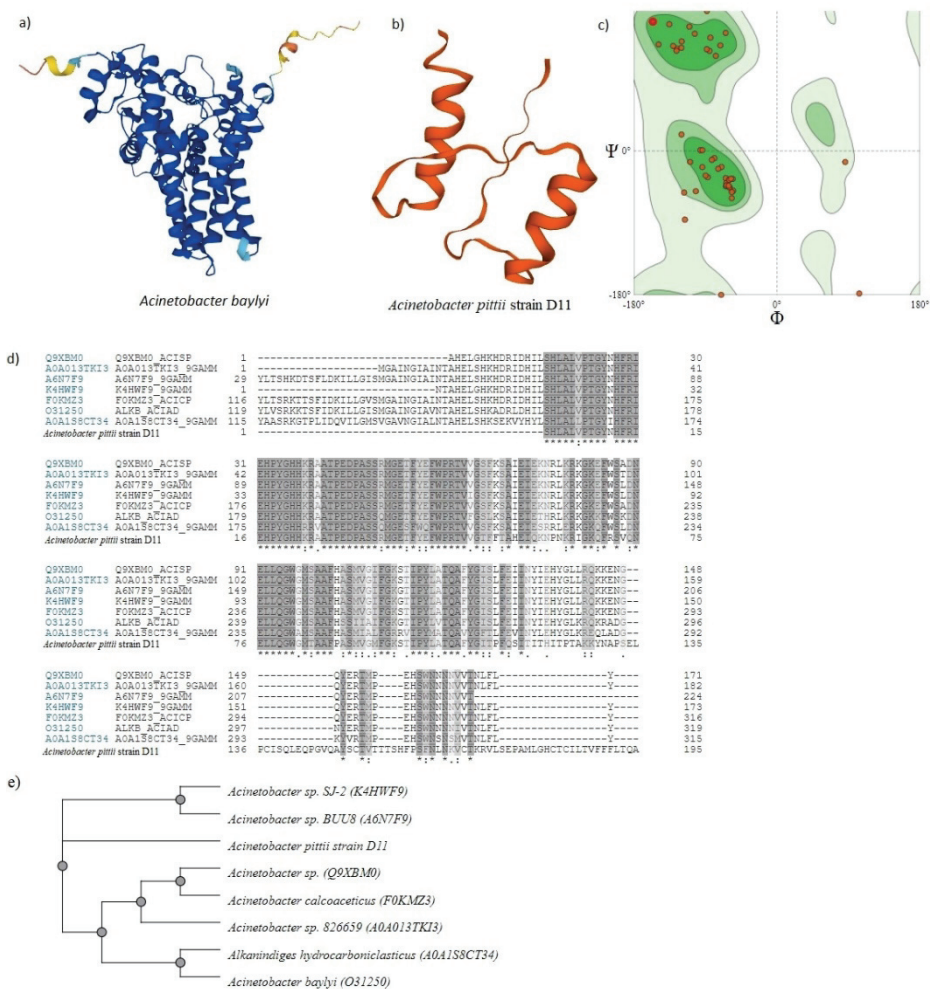


Figure S-1. 3-D models of *alkM* protein of *A. baylyi* (a) and strain D11 (b) generated by the Swiss-Model server (c) Graphs obtained by using the Ramachandran-Prochek software for each *alkM* protein model generated (d) Alignment of region linked to substrate specificity for the *alkM* from D11 and other related species by the UniprotKB server (e) Phylogenetic tree

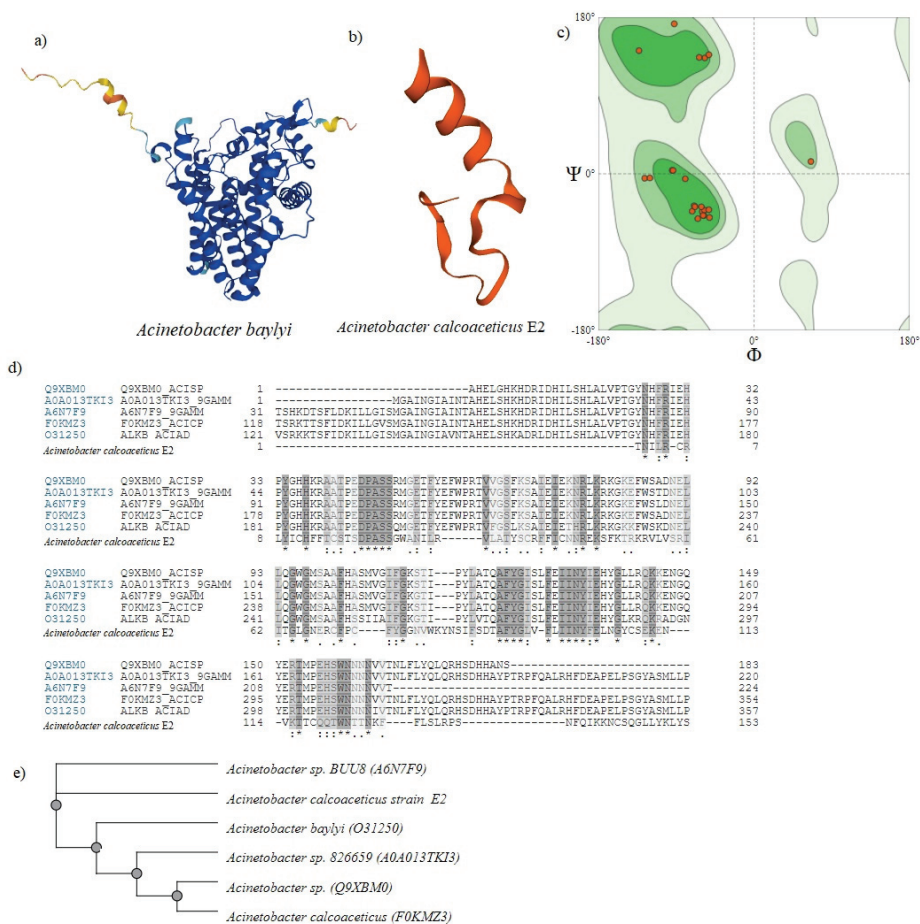


Figure S-3. 3-D models of *alkM* protein of *A. baylyi* (a) and strain E2 (b) generated by the Swiss-Model server (c) Graphs obtained by using the Ramachandran-Prochek software for each *alkM* protein model generated (d) Alignment of region linked to substrate specificity for the *alkM* from E2 and other related species by the UniprotKB server (e) Phylogenetic tree

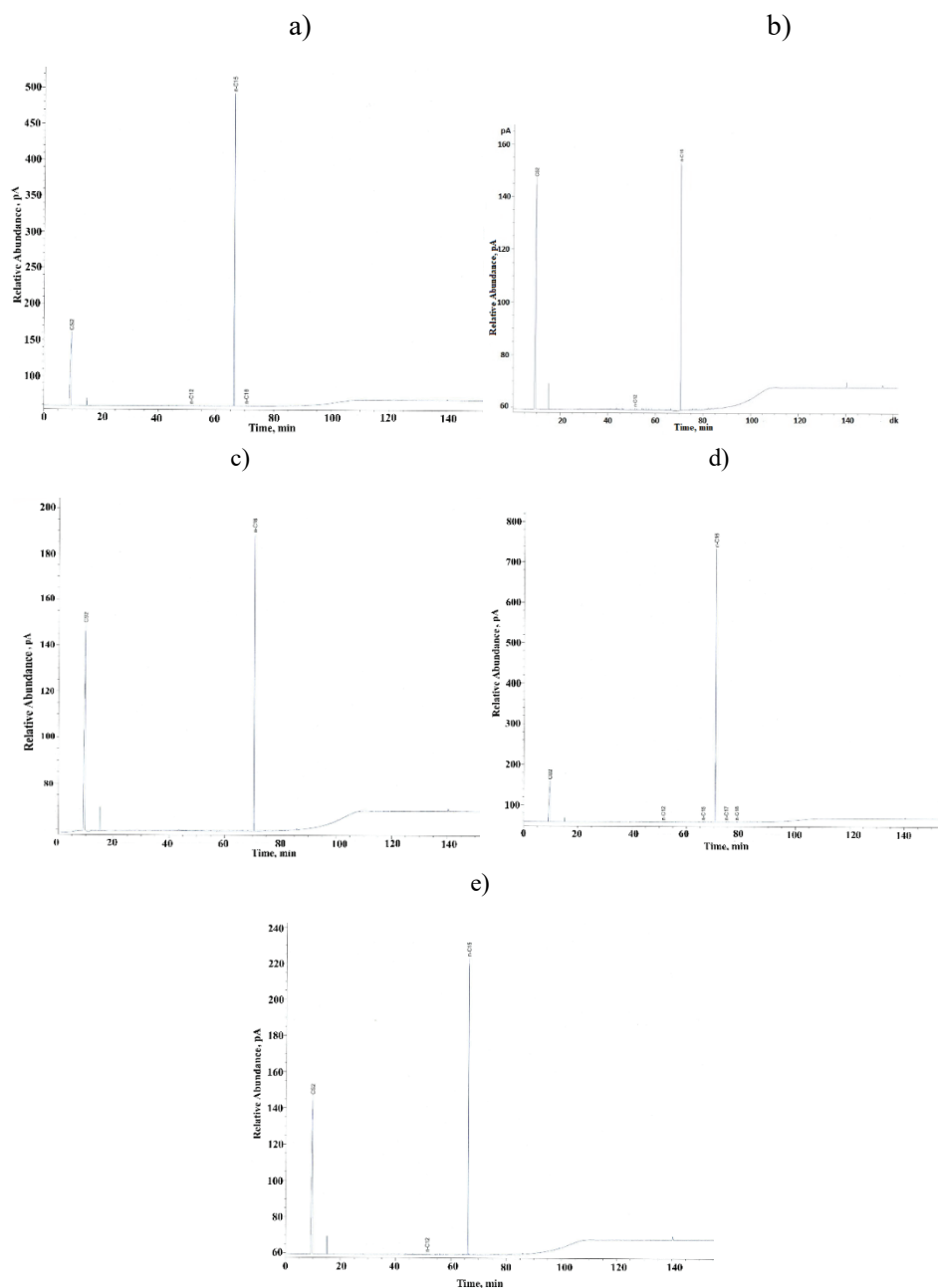


Figure S-4. a) Abiotic control of hexadecane b) Degradation of hexadecane by strain D11 c) Degradation of hexadecane by strain E1 d) Abiotic control of pentadecane e) Degradation of pentadecane by strain E2.