

Supplementary Material

Table S1

Amino acid sequence similarities between the putative natural redox partners of CYP153A16 or CYP153A *P. sp.* and CamA or CamB (performed via blastp, <http://blast.ncbi.nlm.nih.gov>)

Putative natural redox partner 1: Ferredoxin reductase			CamA (422 aa): Ferredoxin reductase from <i>P. putida</i>		
Strain	Gene name	aa	Identity	Similarity	Score
<i>Mycobacterium marinum</i> M.	MMAR_3153	400	192/391 (50%)	250/391 (64%)	354
<i>Polaromonas</i> sp. JS666	Bpro_5300	405	191/408 (47%)	253/408 (63%)	357
Putative natural redox partner 2: Ferredoxin			CamB (107 aa): Ferredoxin from <i>P. putida</i>		
Strain	Gene name	aa	Identity	Similarity	Score
<i>Mycobacterium marinum</i> M.	MMAR_3155	106	43/106 (41%)	66/106 (63%)	87
<i>Polaromonas</i> sp. JS666	Bpro_5299	106	52/106 (50%)	72/106 (68%)	103

Table S2

Retention times of products analyzed by GC (FS-Supreme-5 column) as described in Materials and Methods

Product \ Chain length	Retention time [min]							
	C ₅	C ₆	C ₇	C ₈	C ₉	C ₁₀	C ₁₁	C ₁₂
2-alcohol	—	—	9,2	11,2	14,8	14,8	10,9	12,5
aldehyde	—	—	—	11,3	13,1	14,9	11,0	12,6
1-alcohol	5,5	8,5	10,6	12,5	14,2	15,8	12,1	13,5
fatty acid	—	—	—	14,3	15,7	17,2	13,4	14,5
unidentified product 1*	—	—	—	—	17,3	18,6	14,8	16,0
unidentified product 2*	—	—	—	—	17,4	18,7	14,9	16,2
α,ω-diol	—	—	—	17,0	18,4	19,4	15,7	17,1

— not detected

*unidentified products 1 and 2 were obtained only with CYP153A16. Experiments with CYP153A16 and 1-decene or α,ω-decanediol as starting substrate material showed these compounds were neither epoxidation products nor further oxidized α,ω-diols (e.g., dialdehydes or ω-hydroxyaldehydes).

Table S3

Amino acid sequence similarities between CYP153A16 or CYP153A *P. sp.* and homologous proteins from *Acinetobacter sp.* OC4 or *Mycobacterium sp.* HXN-1500 (performed via blastp, <http://blast.ncbi.nlm.nih.gov>)

CYP153s used in this study			CYP153 from <i>Acinetobacter sp.</i> OC4 (497 aa)		
Strain	CYP (Gene name)	aa	Identity	Similarity	Score
<i>Mycobacterium marinum</i> M.	CYP153A16 (MMAR_3154)	463	302/447 (68%)	357/447 (80%)	628
<i>Polaromonas sp.</i> JS666	CYP153A <i>P. sp.</i> (Bpro_5301)	418	224/409 (55%)	286/409 (70%)	444
CYP153s used in this study			CYP153A6 from <i>Mycobacterium sp.</i> HXN-1500 (420 aa)		
Strain	CYP (Gene name)	aa	Identity	Similarity	Score
<i>Mycobacterium marinum</i> M.	CYP153A16 (MMAR_3154)	463	223/408 (55%)	281/408 (69%)	436
<i>Polaromonas sp.</i> JS666	CYP153A <i>P. sp.</i> (Bpro_5301)	418	320/417 (77%)	356/417 (86%)	672

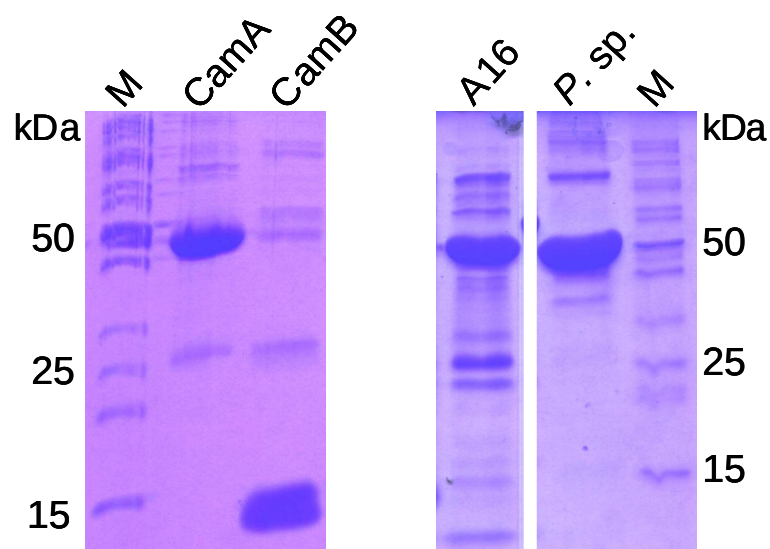


Figure S1. SDS-PAGE of purified his₆-tagged proteins. The SDS gels show CamA, 47 kDa; CamB, 13 kDa; A16 (CYP153A16), 54 kDa; *P. sp.* (CYP153A *P. sp.*), 49 kDa; M, PageRuler™ Unstained Protein Ladder. Protein solutions were analyzed on 15% acrylamide.