Content:

1. *Pseudomonas* as alternative host:

DAME oxygenation activity of different *Pseudomonas* strains was investigated in resting cell assays. The best performing strain *P. fluorescens* CHAO (pBT10) was further investigated in the two-liquid phase setup as described in the original article. Fig. S1 shows product formation (A) and specific activities (B) achieved in this setup.
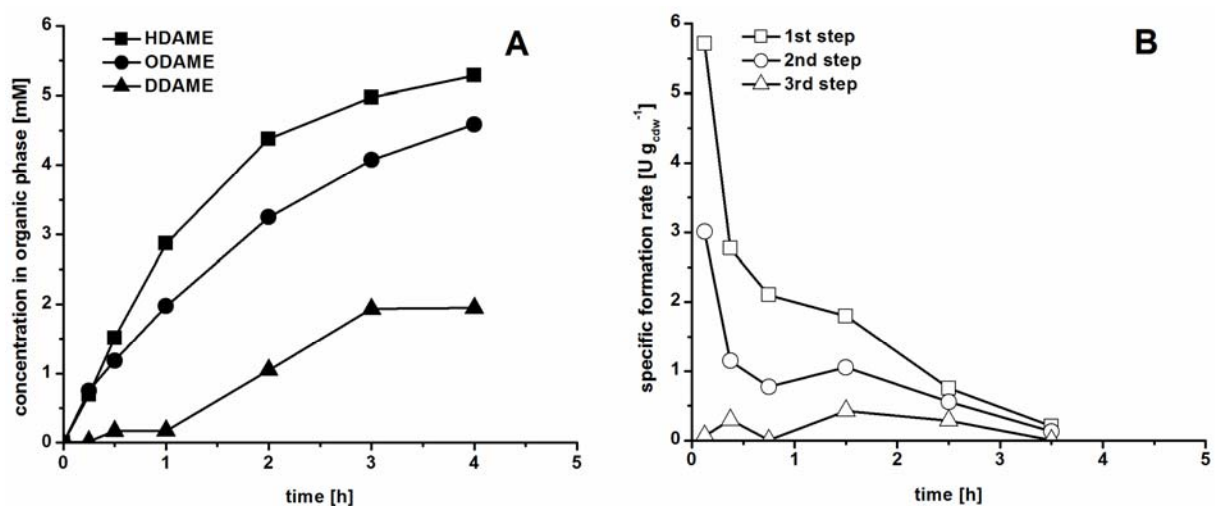

Figure S1. Two-liquid phase biotransformation of DAME using 8.5 g_{cdw} L^{-1} resting cells of *P. fluorescens* CHA0 (pBT10) fed with citrate. The substrate was applied as organic phase at a phase ratio of 1:3 (organic phase : total volume). Product concentrations in the organic phase (A) and specific activities for the different oxygenation steps (B) are given. Specific activities are calculated based on product formation.

2. Homology analysis of AlkL, OmpW, and OprG

The aligment of AlkL from *P. putida* GPo1, OmpW from *E. coli*, and OprG from *P. aeruginosa* was performed using BlastP (Tables S1 and S2). For visualisation of the homology, the three amino acid sequences were aligned using Clustal W2 (Fig. S3).

a) AlkL vs OmpW:

Table S1. Results of BlastP-analysis for alignment of AlkL from *P. putida* GPo1 and OmpW from *E. coli*

Max score	Total score	Query coverage	E value	Max ident
82	82	68%	2e-23	29%

B) AlkL vs OprG:

Table S2. Results of BlastP-analysis for alignment of AlkL from *P. putida* GPo1 and OprG from *P. aeruginosa*

Max score	Total score	Query coverage	E value	Max ident
59.7	59.7	86%	1e-15	23%

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OmpW      MKK--LTVAALAVTT--------------LLSGSAFAHEAGEFFMRAGSATVRPTEGAG- 43
OprG      MRKSWLTASLLALTVA-----------SPFAAADIQGHKAGDFIIRGGFATVDPDDSSSD 49
AlkL      MSFSNYKVIAMPVLVANFVLGAATAWANENYPAKSAGYNQGDWVASFNFSKVYVGEELGD 60
          *        ..  :.: .               ...  .:: *::.   . :.*   :  .

OmpW      ----GTLGSLGGFSVTNNTQLGLTFTYMATDNIGVELLAATPFRHKIGTRATG-----DI 94
OprG      IKLDGAKQRGTKATVDSDTQLGLTFTYMFADKWGVELVAATPFNHQVDVKGLGPGLDGKL 109
AlkL      LNVGGGALPNADVSIGNDTTLTFDIAYFVSSNIAVDFFVGVPARAKFQGEKSISSLG-RV 119
              *        :: .:* * : ::*: :.: .*::....* . :.  .        :

OmpW      ATVHHLPPTLMAQWY-FGDASSKFRPYVGAGINYTTFFDNGFNDHGKEAGLSDLSLKDSW 153
OprG      ADIKQLPPTLLLQYYPMGGTNSAFQPYGGLGVNYTTFFDEDLASNRKAQGFSSMKLQDSW 169
AlkL      SEVDYGPAILSLQYH--YDSFERLYPYVGVGVGRVLFFDK------TDGALSSFDIKDKW 171
          : :.  *. *  *::   .: . : ** * *:. . ***:        .  .:*.:.::*.*

OmpW      GAAGQVGVDYLINRDWLVNMSVWYMDIDTTANYK----LGGAQQHDSVRLDPWVFMFSAG 209
OprG      GLAGELGFDYMLNEHALFNMAVWYMDIDTKASINGPSALGVNKTKVDVDVDPWVYMIGFG 229
AlkL      APAFQVGLRYDLGNSWMLNSDVRYIPFKTDVTGT----LGPVPVSTKIEVDPFILSLGAS 227
          . * ::*. * :.. :.*  * *: :.* ..  .    **      .: :**::  :. .

OmpW      YRF 212
OprG      YKF 232
AlkL      YVF 230
          * *
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Figure S2. Alignment of AlkL from *P. putida* GPo1, OmpW from *E. coli*, and OprG from *P. aeruginosa* (Clustal W2; http://www.ebi.ac.uk/Tools/msa/clustalw2/)