

# ChemBioChem

Supporting Information

## **Production of the Carboxylate Reductase from *Nocardia otitidiscaviarum* in a Soluble, Active Form for *in vitro* Applications**

Douglas Weber, David Patsch, Annika Neumann, Margit Winkler, and Dörte Rother\*

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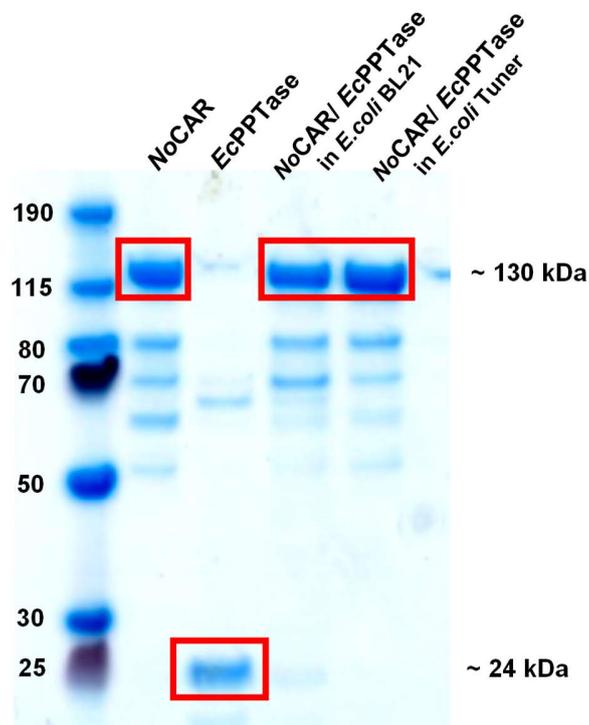
## 1. Enzymes

The NoCAR and EcPPTase enzymes used in this work are listed in Table S1. The production and purification procedures are described in the experimental section of the main manuscript.

**Table S1:** Enzymes used in this study.

Entry	Enzyme	Organism of origin	Type	Accession Nr.	Size (kDa)	pET system	Ref.
1	NoCAR	<i>Nocardia otitiscaviarum</i>	Bacterial	WP_029928026.1 <sup>[1]</sup>	130.3	pET151	[2,3]
2	EcPPTase	<i>Escherichia coli</i>	Bacterial	CAQ31055.1 <sup>[4]</sup>	23.6	pET151	[5-7]

### 1.1. SDS gel analysis of the purified enzymes



**Figure S1.** SDS gel analysis of the purified enzymes: NoCAR expressed in *E.coli* Tuner, EcPPTase expressed in *E.coli* Tuner, and the co-expressed NoCAR/EcPPTase expressed in *E.coli* BL21 or *E.coli* Tuner. It is important to mention that EcPPTase in the petDuet does not have a His-tag.

## 2. Molecular biology

### 2.1. Vector maps

#### 2.1.1. NoCAR

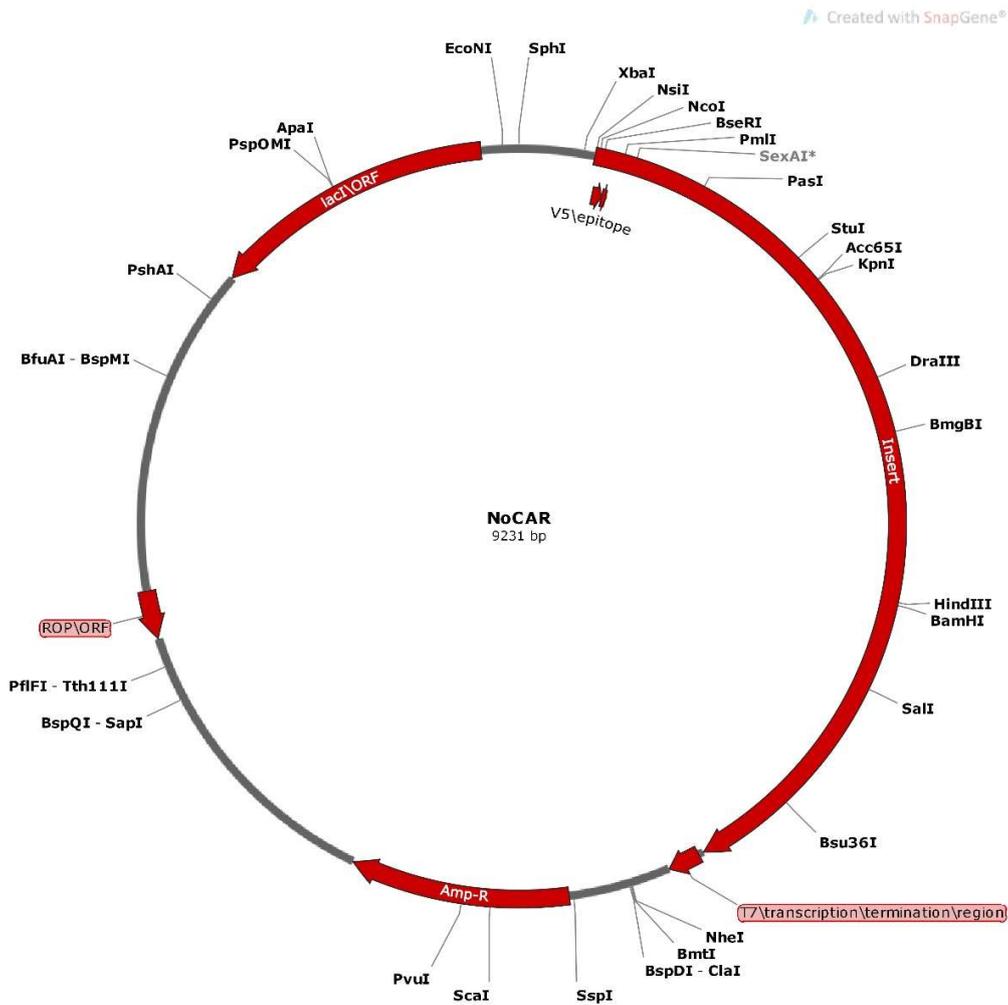
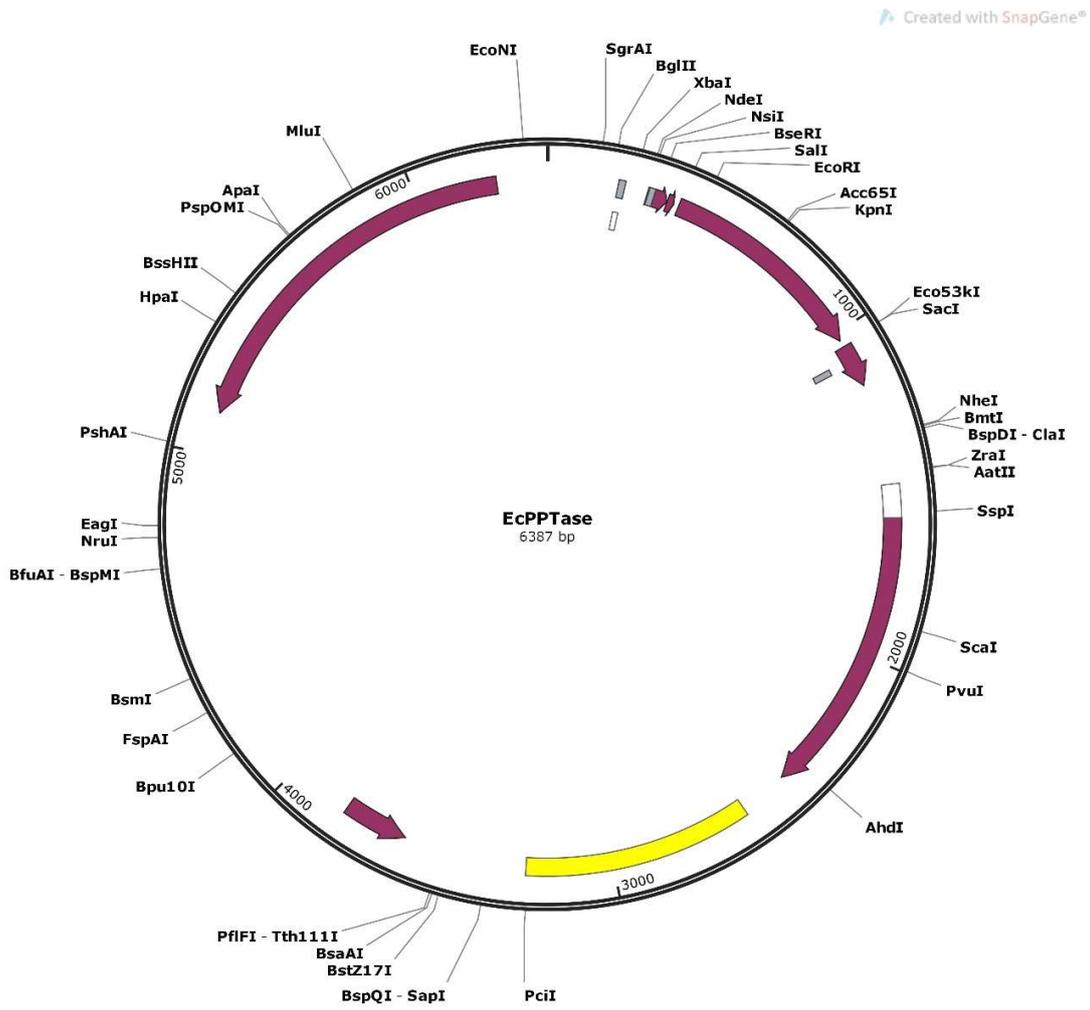


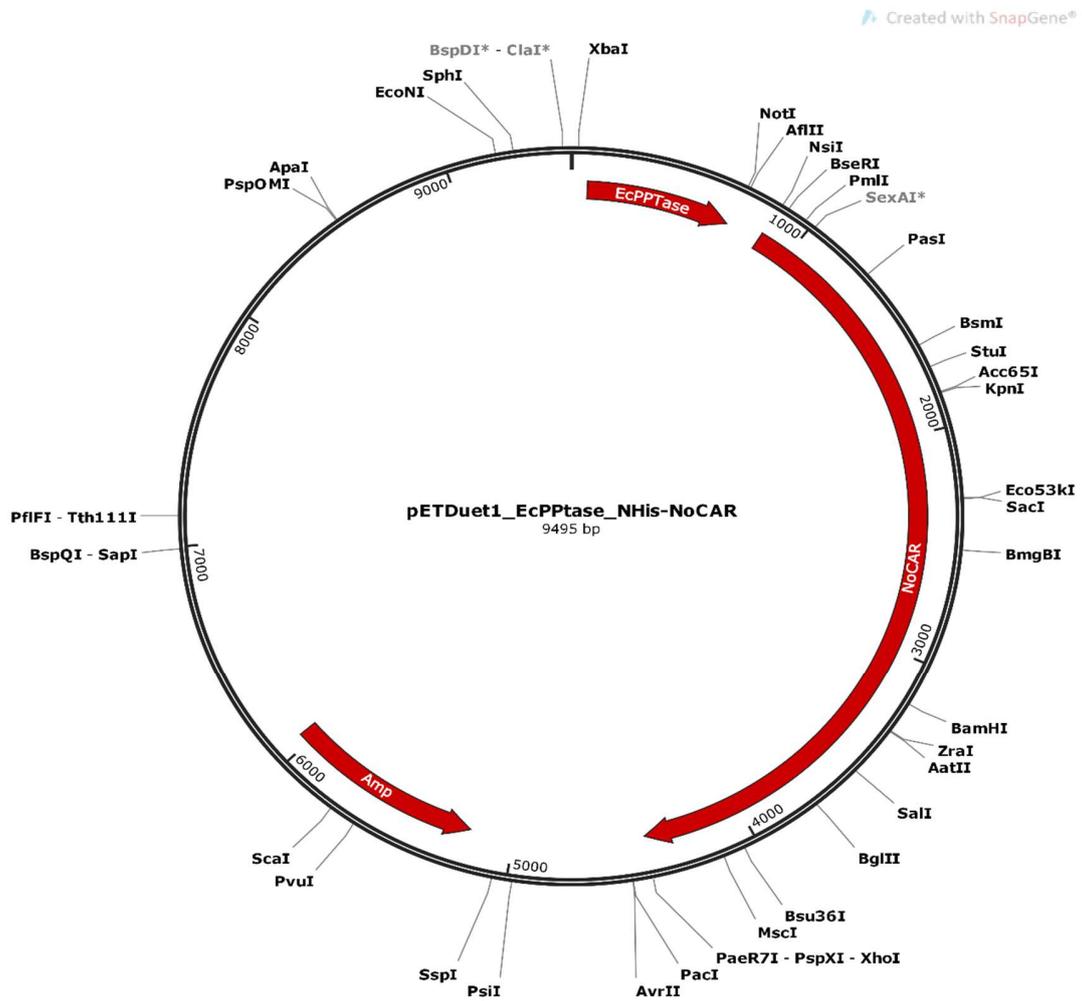
Figure S2. Illustration of the expression vector pET151 harboring the gene of interest coding for NoCAR.

## 2.1.2. *EcPPTase*



**Figure S3.** Illustration of the expression vector pET151 harboring the gene of interest coding for *EcPPTase*.

### 2.1.3. NoCAR/EcPPTase



**Figure S4.** Illustration of the expression vector pETDuet harboring the genes of interest coding for NoCAR and EcPPTase.

## 2.2. Gene sequences

**Table S2:** Gene sequences used in this study. Inserts are highlighted in red and/or green.

Gene	Sequences
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	<p>TTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCT  TTTTACGGTTCCTGGCCTTTTGTGGCCTTTTGTCTACATGTTCTTTCTGCGTTATCCCTGATTCTGTGGA  TAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGAGCCGAACGACCGAGCGCAGCGAGTC  AGTGAGCGAGGAAGCGGAAGAGCGCCTGATGCGGTATTTTCTCTTACGCATCTGTGCGGTATTTACAC  CGCAATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGTATACACTCCGCTATCGC  TACGTGACTGGGTCATGGCTGCGCCCCACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGCT  GCTCCCGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTGACAGGTTTTACCCG  TCATCACCGAAACGCGGAGGCAGCTGCGGTAAGCTCATCAGCGTGGTCTGAAGCGATTACAGATG  TCTGCCTGTTATCCGCTCCAGCTCGTTGAGTTTCTCCAGAAGCGTTAATGTCTGGCTTCTGATAAAGCG  GGCCATGTTAAGGGCGGTTTTTCTGTTTGGTCACTGATGCCTCCGTGAAGGGGGATTCTGTTTCATG  GGGGTAATGATACCGATGAAACGAGAGAGGATGCTCACGATACGGGTTACTGATGATGAACATGCCCCG  GTTACTGGAACGTTGTGAGGGTAAACAACCTGGCGGTATGGATGCGGCGGGACCAGAGAAAAATCACTC  AGGGTCAATGCCAGCGCTTCGTTAATACAGATGTAGGTGTTCCACAGGGTAGCCAGCAGCATCTCGCA  TGCAGATCCGGAACATAATGGTGCAGGGCGCTGACTCCGCGTTTCCAGACTTACGAAACACGGAAC  CGAAGACCATTATGTTGTTGCTCAGGTCGACAGCCTTTTGCAGCAGCATCGCTTACAGTTCCGCTCGCG  TATCGGTGATTCACTCTGCTAACCAGTAAGGCAACCCCGCCAGCCTAGCCGGTCTCAACGACAGGAGC  ACGATCATGCGCACCCGTGGCCAGGACCAACGCTGCCCGAGATGCGCCGCGTGGCGGTCTGGAGATG  GCGGACGCGATGGATATGTTCTGCCAAGGGTTGGTTTGCATTACAGTTCTCCGCAAGAATTGATTGG  CTCCAATTCTGGAGTGGTGAATCCGTTAGCGAGGTGCCGCGGCTTCCATTAGGTGCGAGGTGGCCCCG  GCTCCATGCACCGGACGCAACGCGGGGAGGCAGACAAGGTATAGGGCGGCGCCTACAATCCATGCCA  ACCCGTTCCATGTGCTCGCCGAGGCGGCATAAATCGCCGTGACGATCAGCGGTCCAATGATCGAAGTTA  GGCTGGTAAGAGCCGCGAGCGATCCTTGAAGCTGTCCCTGATGGTCTCATCTACCTGACCTGGACAGCAT  GGCCTGCAACGCGGGCATCCGATCCGCGGAAGCGAGAGAAGAATCATAATGGGAGCCCATCCAGC  CTCGCTCGCGAACGCCAGCAAGACGTAGCCAGCGCTCGGCCGCTGACCGGCGATAATGGCCTGCT  TCTCGCGAAACGTTTGGTGGCGGGACAGTGACGAAGGCTTGGAGCGAGGGCGTGCAAGATCCGAAT  ACCGCAAGCGACAGGCGCATCATGCTCGCTCCAGCGAAAGCGGTCTCGCGAAAATGACCCAGAGC  GCTGCCGCGACCTGCTCTACGAGTTGCATGATAAAGAAGACAGTCATAAGTGGCGGCGACGATAGTCATG  CCCCGCGCCACCGGAAGGAGCTGACTGGGTTGAAGGCTCTCAAGGGCATTGCTGCGAGATCCCGGTGCC  TAATGAGTGAGCTAACTTACATTAATTGCGTTGCGCTCACTGCCCGCTTCCAGTCGGGAAAACCTGTCGTG  CCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGGCTATTGGGCGCCAGGGTGGTTT  TTCTTTTACCAGTGAGACGGGCAACAGCTGATTGCCCTTACCAGCTGGCCCTGAGAGAGTTGCAGCAA  GCGGTCACGCTGGTTTGCAGCAGGCGAAAATCTGTTTATGGTGTGTTTACGCGGGATATAACA  TGAGCTGCTTCGGTATCGTCTGATCCCACTACCGAGATATCCGCACCAACGCGCAGCCCGGACTCGGTA  ATGGCGCGCATTGCGCCAGCGCCATCTGATCGTTGGCAACCAGCATCGCAGTGGGAACGATGCCCTCA  TTCAGCATTGCGATGGTTTGTGAAAACCGGACATGGCACTCCAGTCGCCTTCCCGTTCCGCTATCGGCTG  AATTTGATTGCGAGTGAGATATTTATGCCAGCCAGCCAGACGCGAGACGCGCCGAGACAGAACTTAATGG  GCCCCGTAACAGCGCATTTGCTGGTGACCAATGCGACCCAGATGCTCCACGCCAGTCCGCTACCGTCT  TCATGGGAGAAAATAACTGTTGATGGGTGTCTGGTCCAGAGACATCAAGAAATAACGCCGGAACATTA  GTGCAGGCAGCTTCCACAGCAATGGCATCTGGTCCATCCAGCGGATAGTTAATGATCAGCCACTGACGC  GTTGCGGAGAGAAGATTGTGACCCGCGCTTACAGGCTTCCAGCGGCTTCCGTTTACCATCGACACCAC  CAGCTGGCACCCAGTTGATCGGCGCGAGATTTAATCGCCGCGACAATTTGCGAGCGCGCTGAGGGC  CAGACTGGAGGTGGCAACGCCAATCAGCAACGACTGTTTCCCGCCAGTGTGTTGCGCCAGCGGTTGGG  AATGTAATTGAGCTCCGCATCGCGCTTCCACTTTTTCCCGCTTTTCCGAGAAACGTTGGCTGGCCTGGT  TCACCAGCGGGAAAACGGTCTGATAAGAGACACCGGCATACTCTGCGACATCGTATAACGTTACTGGTTT  CACATTACCACCCTGAATTGACTCTCTCCGGGCGCTATCATGCCATACCGGAAAGGTTTTGCGCCATT  CGATGGTGTCCGGATCTCGACGCTCTCCTTATGCGACTCTGCAATTAGGAAGCAGCCAGTAGTAGGT  TGAGGCCGTTGAGCACCGCCCGCAAGGAATGGTGCATG</p>
<p>pETDuet_NoCAR/  <i>Ec</i>PPTase</p>	<p>GGGGAATTGTGAGCGGATAACAATTCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGA  TATACCATGGTGCATATGAAAACCTACGCATACCTCCCTCCCTTTGCGCGACATACGCTGCATT  TTGTTGAGTTCGATCCGGCGAATTTTTGTGAGCAGGATTTACTCTGGCTGCCGCACTACGCAC  AACTGCAACACGCTGGACGTAACGTAACGTAACAGAGCATTAGCCGGACGGATCGCTGCTGTTT  ATGCTTTGCGGGAAATATGGCTATAAATGTGTGCCCGCAATCGGCGAGCTACGCCAACCTGTCT  GGCCTGCGGAGGTATACGGCAGTATTAGCCACTGTGGGACTACGGCATTAGCCGTGGTATCT  CGTCAACCGATTGGCATTGATATAGAAGAAATTTTTCTGTACAACCGCAAGAGAAATTGACAG  ACAACATTATTACACCAGCGGAACACGAGCGACTCGCAGACTGCGGTTTAGCCTTTTTCTGCG  CGCTGACACTGGCATTTTCCGCGAAAGAGAGCGCATTAAAGGCAAGTGAGATCCAAACTGATG  CAGGTTTTCTGGACTATCAGATAATTAGCTGGAATAAACAGCAGGTCATCATTATCGTGAGAA  TGAGATGTTTGTGCTGTGCACTGGCAGATAAAAAGAAAAGATAGTCATAACGCTGTGCCAACACGA  TTAAGCTTGGCGCCGCATAATGCTTAAGTCGAACAGAAAGTAATCGTATTGTACACGGCCGCA  TAATCGAAAATTAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCTTCTTAGT</p>

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GGCGAGCCCGATCTTCCCATCGGTGATGTGCGGATATAGCGCCAGCAACCGCACCTGTG  
CGCCCGGTGATGCCGGCCACGATCGTCCGGCGTAGAGGATCGAGATCGATCTCGATCCCC  
CGAAATTAATACGACTCACTATA

## 2.3. Cloning

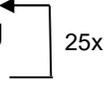
Applying the Gibson Assembly, NoCAR was cloned into a previously prepared pETDuet containing *EcPPTase* in one of the cloning sites.<sup>[8,9]</sup> The original pETDuet plasmid harbored the gene for another CAR enzyme (carboxylate reductase from *Nocardia iowensis*, NiCAR). NiCAR gene was cut with the appropriate restriction enzymes to prepare the vector backbone. All primers and DNA templates were diluted in water. The plasmid pETDuet\_NoCAR/*EcPPTase* is shown in Figure S4. The PCR program used to amplify was as follows:

- 1) Backbone (using carboxylate reductase from *Nocardia iowensis*, NiCAR):  
pETDuet1\_PPTase (5922 base pairs)

- Primers:

- Forward: CTCGAGTCTGGTAAAGAAAC
- Reverse: ATGTATACTCCTTCTTATACTTAAC

- PCR program:

- 98°C for 30 s
  - 98°C for 10 s
  - 57.2°C for 20 s annealing
  - 72°C for 2 min extension
  - 72°C for 2 min final extension
- 

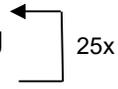
- 2) Second fragment (NoCAR):

3613 base pairs

- Primers:

- Forward: TATAAGAAGGAGATATACATATGCATCATCACCATCAC
- Reverse: GTTTCTTTACCAGACTCGAGTTAACCCTGAATCAGACC

- PCR program:

- 98°C for 30 s
  - 98°C for 10 s
  - 58.8°C for 20 s annealing
  - 72°C for 2 min extension
  - 72°C for 2 min final extension
- 

## 3. Optimization of the NoCAR production in *E. coli*

### 3.1. Medium optimization in *E. coli* BL21

**Table S3:** Protein content (mg mL<sup>-1</sup>) of soluble and insoluble fractions of NoCAR produced in different medium and induction conditions in *E. coli* BL21

Medium	Soluble fractions		Insoluble fractions	
	Samples	(mg/mL)	Samples	(mg/mL)
LB	3h	1.76	3h	1.7
	6h	1.4	6h	2.25
	24h	1.74	24h	7.3
	48h	1.94	48h	9.56
	72h	1.11	72h	9.55
AI	3h	1.55	3h	1.79
	6h	5.64	6h	1.01
	24h	7.92	24h	12.5
	48h	5	48h	12.9
	72h	7.1	72h	9.21
TB	3h	2	3h	2.27
	6h	1.93	6h	3.91
	24h	5.1	24h	9.34
	48h	7.71	48h	17.6
	72h	5.7	72h	19.1

### 3.2. Optimization in *E. coli* Tuner

As already mentioned in the main manuscript, producing soluble NoCAR in sufficient amounts turned out to be challenging, hindering purification and characterization attempts. Thus, it was essential to find cultivation conditions that could increase the amount of soluble recombinant protein expression as much as possible. Those were the cultivation temperature, OD<sub>600</sub> at induction, and IPTG concentration. All of them can be varied smoothly and without much effort, compared to co-expression of molecular chaperons or codon optimization, which would be much more time consuming.<sup>[10]</sup> After deciding on the parameters, the experiments were designed. This step was done according to a central composite design (CCD). The table below shows the cultivation conditions for a CCD in 15 experiments (great part of them were performed in duplicates). Therefore, the operational window was determined empirically or by suggestions from literature.<sup>[10,11]</sup>

**Table S4:** CCD for the optimization of the expression of NoCAR in *E. coli* Tuner

Run Nr.	T (°C)	IPTG (mM)	OD <sub>600</sub>
1	15	0.1	0.6
2	17	0.05	0.4
3	17	0.15	0.4
4	17	0.05	0.8
5	17	0.15	0.8
6	20	0.03	0.6
7	20	0.1	0.2
8	20	0.1	1.0
9	20	0.1	0.6
10	20	0.2	0.6
11	23	0.05	0.4
12	23	0.15	0.4
13	23	0.05	0.8
14	23	0.15	0.8
15	25	0.1	0.6

All the data was gathered from the small-scale cultivation (100 mL) of NoCAR. Densitometric analysis with the aid of the *ImageJ* software, in combination with protein concentrations determined by Bradford assay (described in the experimental section in the main manuscript), was used to estimate the total soluble NoCAR protein concentration (in mg/mL). For modeling and optimization, only the soluble fractions collected after 48 h of cultivation were considered. The quadratic surface obtained is shown in Figure 2A in the main manuscript. To obtain the optimal process conditions for the cultivation of soluble NoCAR, the quadratic had to be maximized using a genetic algorithm. Genetic algorithms are a group of models that are inspired by the process of natural selection and are capable of generating high-quality solutions for both, constrained and unconstrained optimization and search problems<sup>[12]</sup>. The output of this was the cultivation conditions depicted in the main manuscript (0.9-1.0 OD<sub>600</sub> at induction, 0.18 mM IPTG concentration, and a cultivation temperature of 15°C). It is essential to evaluate the performance of a model to develop an understanding of how well it generalizes to new data. Thus, a very common and popular metric for the evaluation of the performance of a regression model is the mean squared error (mse). It describes the average of the squares of errors and is an accurate measure of a model's predictive power. In other words, mse is the average squared difference between the estimated values and the actual value. In our work, the quadratic model showed an mse score of 0.19. The equation<sup>[13]</sup> used to fit the data is shown below:

$$y = \beta_0 + \sum_{i=1}^k \beta_i x_i + \sum_{i < j} \sum \beta_{ij} x_i x_j + \sum_{i=1}^k \beta_{ii} x_i^2 + \epsilon.$$

in which  $y$  corresponds to the response of interest,  $x_i$  and  $x_j$  are numbers of associated control (or input) variables,  $\beta$  is a vector of  $p$  unknown constant coefficients referred to as parameters, and  $\epsilon$  is a random experimental error assumed to have a zero mean. All this additional information were added to the SI material.

Thus, a mean squared error of 0.19 mg/mL and a standard deviation of 0.18 were determined by a 10-fold cross-validation for the quadratic system.

#### 4. Optimization of the post-translational modification of NoCAR via incubation assay

The incubation of purified NoCAR expressed in *E. coli* Tuner with purified EcPPTase and acetyl-CoA was performed under different conditions. Measuring parameters were the amount of EcPPTase, concentration of acetyl-CoA, and incubation time. In each case, the specific activity using the photometric-based assay described in the experimental section of the main manuscript. Variables, conditions tested, and the best conditions are shown in Table S5. The initial parameters that were evaluated to determine the best *in vitro* conditions for the activation of NoCAR were decided based on previous works.<sup>[7]</sup> Besides, these initial parameters were chosen because we believed they were the ones which could have the highest influence on the *in vitro* activation of NoCAR. The PPTase from *E. coli* was produced and purified to be used in this study. Here, we were limited by the protein content of the protein preparation containing the PPTase. In this case, the protein concentration of this preparation was about 0.272 mg mL<sup>-1</sup> (determined by the Bradford assay). Therefore, the operational window for this specific parameter was decided based on this limiting protein content.

**Table S5:** Post-translational modification of NoCAR<sup>a</sup>: optimization of the incubation assay

Entry	Construct	Experimental	Variable	Specific activity (U/mg)	Best condition
1	NoCAR + acetyl-CoA + PPTase	50 $\mu$ L + 25 $\mu$ L acetyl-CoA ( <b>1 mM</b> ) + 25 $\mu$ L PPTase (0.143 mg/mL) → incubation (1 h, 28°C, 600 rpm)	acetyl-CoA concentration	0.010	2 mM acetyl-CoA
2	NoCAR + acetyl-CoA + PPTase	50 $\mu$ L + 25 $\mu$ L acetyl-CoA ( <b>2 mM</b> ) + 25 $\mu$ L PPTase (0.143 mg/mL) → incubation (1 h, 28°C, 600 rpm)		0.012	
3	NoCAR + acetyl-CoA + PPTase	50 $\mu$ L + 25 $\mu$ L acetyl-CoA ( <b>5 mM</b> ) + 25 $\mu$ L PPTase (0.143 mg/mL) → incubation (1 h, 28°C, 600 rpm)		0.011	
4	NoCAR + acetyl-CoA + PPTase	50 $\mu$ L + 25 $\mu$ L acetyl-CoA (2 mM) + 25 $\mu$ L PPTase ( <b>0.075 mg/mL</b> ) → incubation (1 h, 28°C, 600 rpm)	EcPPTase concentration	0.0092	0.143 mg/mL
5	NoCAR + acetyl-CoA + PPTase	50 $\mu$ L + 25 $\mu$ L acetyl-CoA (2 mM) + 25 $\mu$ L PPTase ( <b>0.143 mg/mL</b> ) → incubation (1 h, 28°C, 600 rpm)		0.0108	
6	NoCAR + acetyl-CoA + PPTase	50 $\mu$ L + 25 $\mu$ L acetyl-CoA (2 mM) + 25 $\mu$ L PPTase ( <b>0.272 mg/mL</b> ) → incubation (1 h, 28°C, 600 rpm)		0.0107	
7	NoCAR + acetyl-CoA + PPTase	50 $\mu$ L + 25 $\mu$ L acetyl-CoA (2 mM) + 25 $\mu$ L PPTase (0.143 mg/mL) → incubation ( <b>0.5 h</b> , 28°C, 600 rpm)	Time of incubation	0.010	2 h
8	NoCAR + acetyl-CoA + PPTase	50 $\mu$ L + 25 $\mu$ L acetyl-CoA (2 mM) + 25 $\mu$ L PPTase (0.143 mg/mL) → incubation ( <b>1 h</b> , 28°C, 600 rpm)		0.011	
9	NoCAR + acetyl-CoA + PPTase	50 $\mu$ L + 25 $\mu$ L acetyl-CoA (2 mM) + 25 $\mu$ L PPTase (0.143 mg/mL) → incubation ( <b>2 h</b> , 28°C, 600 rpm)		0.022	

a] Protein concentration of NoCAR stock solution was always determined via Bradford assay prior to each incubation assay. The protein concentration ranged from 18 to 25 mg/mL.

## 5. Biocatalytic reduction reactions with *in vitro* recycling of cofactors

### 5.1. Auxiliary enzymes for the regeneration of both cofactors

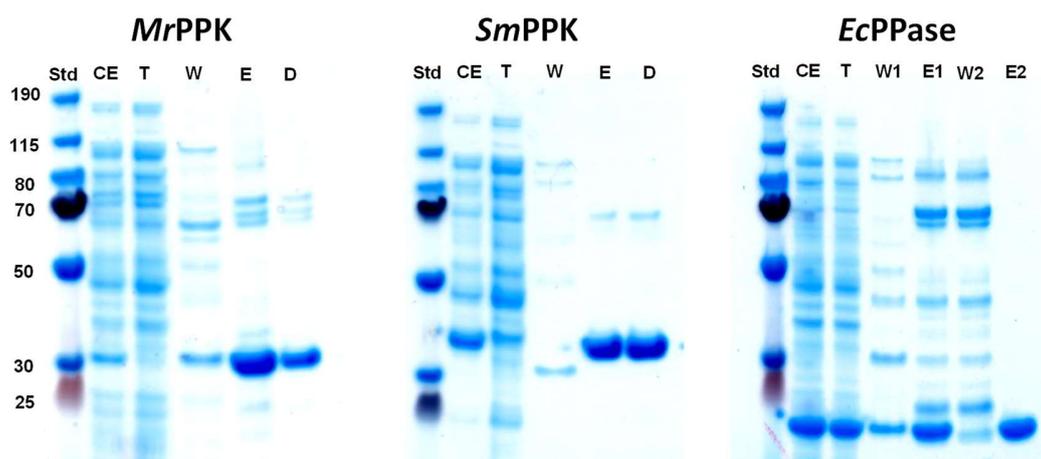
The full recycling of both cofactors was achieved using the following auxiliary enzymes: the simultaneous action of polyphosphate kinases from *Meiothermus ruber* (MrPPK) and *Sinorhizobium meliloti* (SmPPK) for the regeneration of ATP and a glucose dehydrogenase (GDH) for the regeneration of NADPH. Finally, the inhibitory effects of pyrophosphate (PP), which is generated *in situ* during the catalytic cycle of CARs, is surpassed by using the pyrophosphatase from *Escherichia coli* (EcPPase). GDH from *Pseudomonas* sp. was commercially available and obtained from Sigma-Aldrich (Steinheim, Germany).

His-tagged MrPPK was used similarly as described previously by Parnell *et al.*<sup>[14]</sup>. SmPPK was expressed from the pET28+ vector constructed previously by Mordhorst *et*

*al.*<sup>[14,15]</sup> *E. coli* BL21 (DE3) Star served as the production host. Cells were cultivated in LB medium and PPKs expression was induced by addition of 0.5 mM IPTG at 28°C. Cell disruption and purification was performed as described for NoCAR. Liquid stocks of purified PPKs were stored at -20°C. Protein concentrations were determined with the Bradford assay following the procedure described in the experimental section of the main manuscript.

Strep-tagged *EcPPase* was expressed from the pETSTREP3 vector as constructed previously by Pfeiffer et al.<sup>[16]</sup> Similarly, *E. coli* BL21(DE3) Star served as the expression host and was cultivated in LB medium at 37°C. *EcPPase* expression was induced by addition of 0.5 mM IPTG. Purification was performed under standard conditions using a gravity flow strep tacin sepharose column as the stationary phase. Protein concentrations were determined with the Bradford assay following the procedure described in the experimental section of the main manuscript.

Liquid stocks of purified *EcPPase* was stored at -20°C. Full characterization of both PPKs and *EcPPase* in terms of enzyme activity was determined and described by Strohmeier et al.<sup>[8]</sup>



**Figure S5.** SDS gel analysis for the purification steps of the ATP-recycling enzymes used in this study. Legend: CE: crude cell extract; T: throughput fraction; W: washed fraction; E: eluted fraction; D: desalted fraction. *EcPPase* had in total two washing and elution steps.

## 5.2. Reaction components and setup

The components and stock solutions prepared for the biotransformations with *in vitro* recycling of ATP and NADPH are shown in Tables S5 and S6.

**Table S5:** Components and stock concentrations for the NoCAR-catalyzed biotransformations

<b>Reaction mixture preparation</b>		
<b>Key components</b>	<b>Concentration in reaction (mM)</b>	<b>Concentration in stock (mM)</b>
4xMOPS buffer pH 7.5	100	400
Sodium benzoate	5	250
NADPH	0.5	50
ATP	1	50
MgCl <sub>2</sub>	6.25	50
Sodium polyphosphate	4 mg/mL	50 mg/mL
β-D-(+)-glucose	50	200
<b>Auxiliary enzymes</b>	<b>Concentration in reaction (μg/mL)</b>	<b>Concentration in the stock (μg/mL)</b>
<i>Mr</i> PPK	100	2220
<i>Sm</i> PPK	40	1100
<i>Ec</i> PPase	25	754
GDH	0.2	50

**Table S6:** Reaction mixture for the NoCAR-catalyzed biotransformations

<b>Mastermix for all reactions</b>	
<b>Components</b>	<b>Volume/reaction (μL)</b>
H <sub>2</sub> O Milli-Q	36.4
4xMOPS buffer containing MgCl <sub>2</sub> and β-D-(+)-glucose	62.5
Coenzyme stock (GDH and ATP-recycling enzymes)	98.6
NADPH	2.5
ATP	5
Sodium polyphosphate	20
Bromothymol blue (indicator)	5
<b>Reaction vial/eppi</b>	<b>Volume (μL)</b>
Mastermix	230
Substrate (250 mM stock)	5
NoCAR/ <i>Ec</i> PPase (2.5 mg/mL stock)	10
Addition of KOH (1 M)	5
<b>Total</b>	<b>250</b>

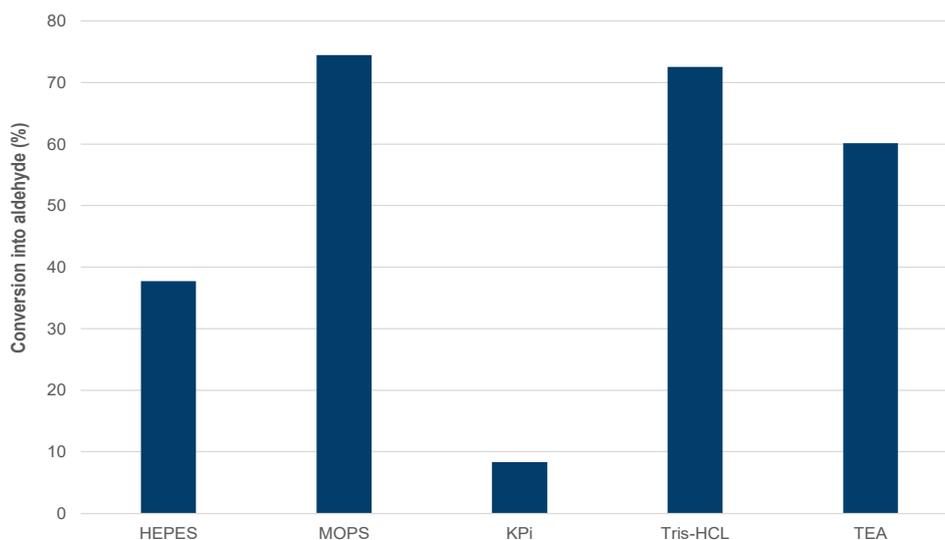
The components MgCl<sub>2</sub> and β-D-(+)-glucose were added to the 4x buffer. The total volume of reaction was 250 μL. 5 μL of 1 M KOH was added after starting the reaction for pH adjustment.



**Figure S6.** Reaction mixture (250  $\mu$ L total volume) performed in a 1.5 mL Eppendorf tube. The blue colour results from the dissociation of Bromothymol blue in solutions that are more basic.

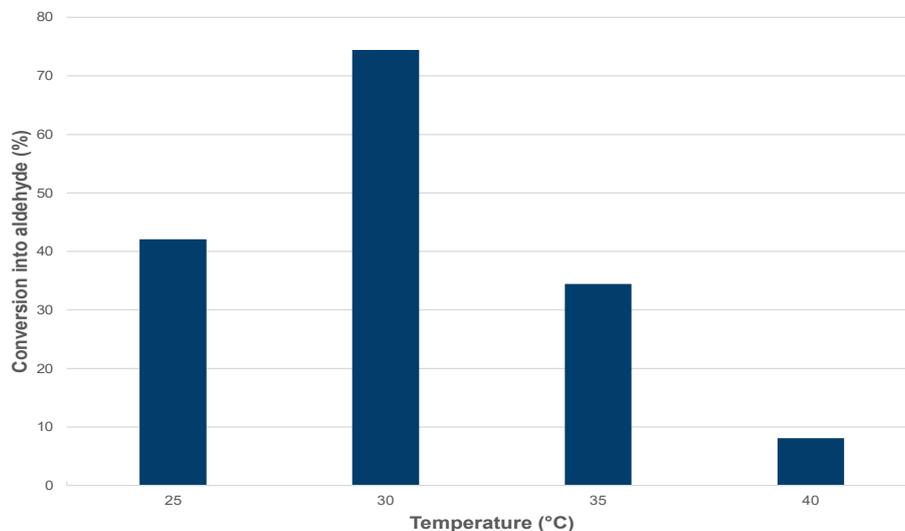
### 5.3. Investigation of optimal reaction conditions

#### 5.3.1. Type of buffer



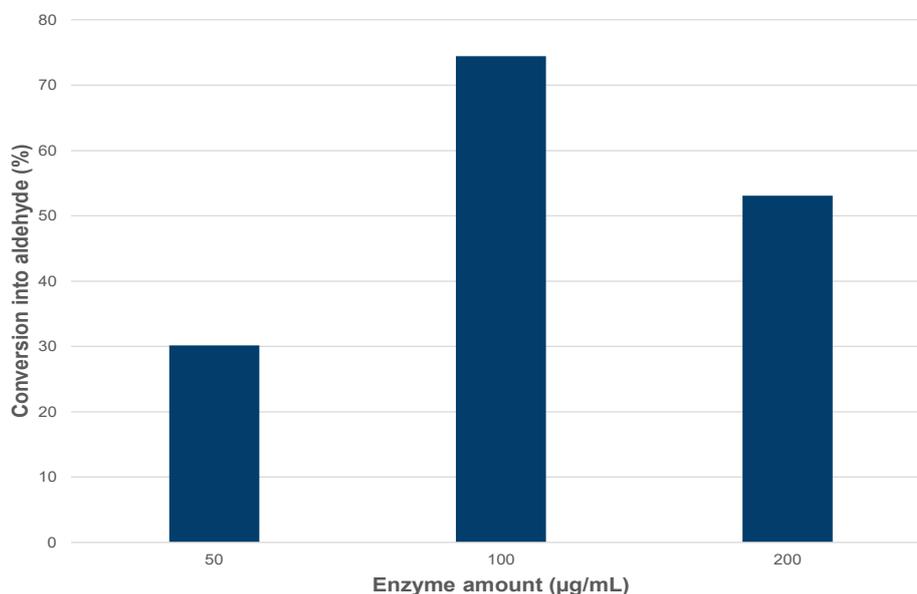
**Figure S7.** Evaluation of different types of buffer. Composition in 250  $\mu$ L reaction volume: 100 mM buffer (pH 7.5), 6.25 mM  $MgCl_2$ , 50 mM glucose, 5 mM sodium benzoate, 4 mg  $mL^{-1}$  sodium polyphosphate, 1 mM ATP, 0.5 mM NADPH, 100  $\mu$ g  $mL^{-1}$  *NoCAR/EcPPTase*, 100  $\mu$ g  $mL^{-1}$  *MrPPK*, 40  $\mu$ g  $mL^{-1}$  *SmPPK*, 25  $\mu$ g  $mL^{-1}$  *EcPPase*, 50  $\mu$ g  $mL^{-1}$  GDH, 30°C, 750 rpm. Buffers: KPi: potassium phosphate, TEA: triethanolamine. Sampling after 1 h of reaction with subsequently HPLC analysis. Values shown are mean values of technical triplicates ( $n_{biological} = 1$ ). Error bars for the technical replicates were too small to indicate.<sup>[17][18]</sup>

### 5.3.2. Temperature of reaction



**Figure S8.** Evaluation of different reaction temperatures. Composition in 250  $\mu$ L reaction volume: 100 mM MOPS buffer (pH 7.5), 6.25 mM  $MgCl_2$ , 50 mM glucose, 5 mM sodium benzoate, 4 mg  $mL^{-1}$  sodium polyphosphate, 1 mM ATP, 0.5 mM NADPH, 100  $\mu g mL^{-1}$  *NoCAR/EcPPTase*, 100  $\mu g mL^{-1}$  *MrPPK*, 40  $\mu g mL^{-1}$  *SmPPK*, 25  $\mu g mL^{-1}$  *EcPPase*, 50  $\mu g mL^{-1}$  *GDH*, 750 rpm. Sampling after 1 h of reaction with subsequently HPLC analysis. Values shown are mean values of technical triplicates ( $n_{biological} = 1$ ). Error bars for the technical replicates were too small to indicate.<sup>[17][18]</sup>

### 5.3.3. Concentration of *NoCAR/EcPPTase*

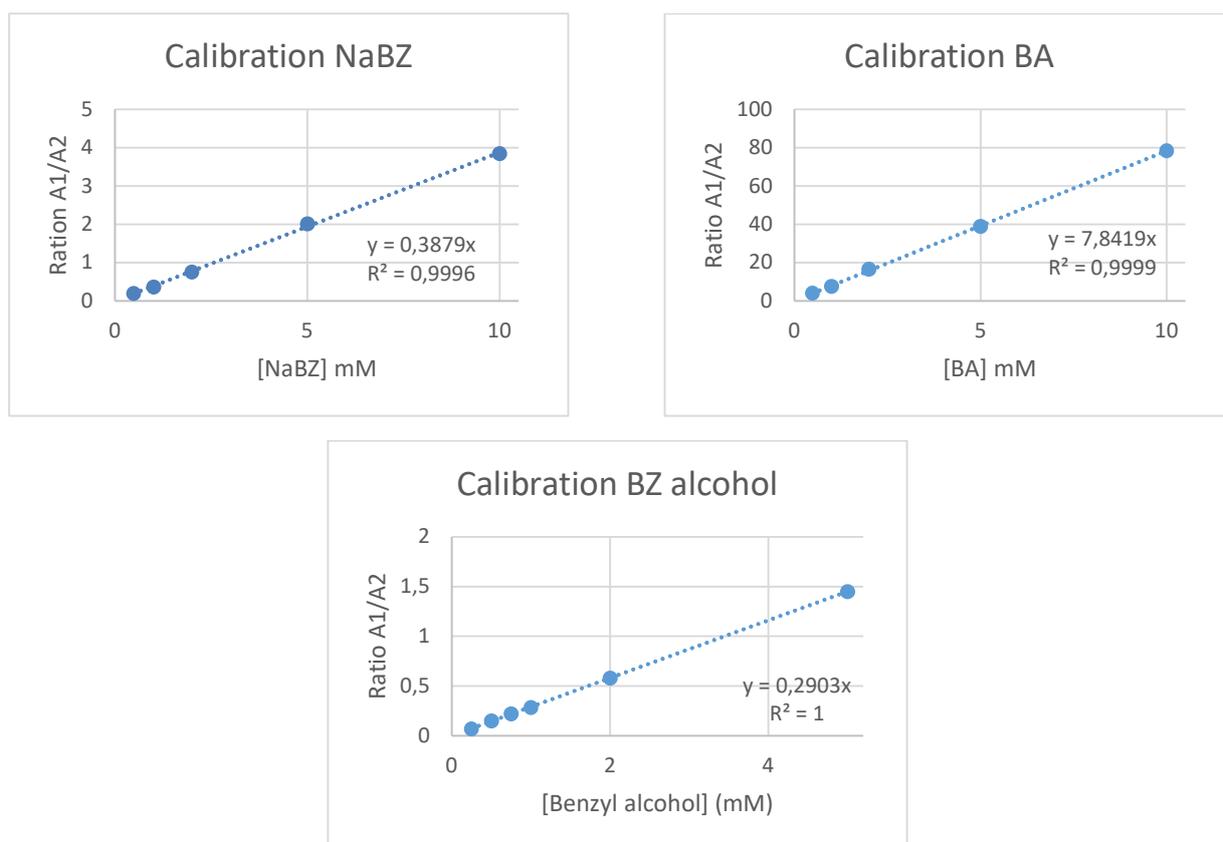


**Figure S9.** Evaluation of varying concentrations of *NoCAR/EcPPTase*. Composition in 250  $\mu$ L reaction volume: 100 mM MOPS buffer (pH 7.5), 6.25 mM  $MgCl_2$ , 50 mM glucose, 5 mM sodium benzoate, 4 mg  $mL^{-1}$  sodium polyphosphate, 1 mM ATP, 0.5 mM NADPH, *NoCAR/EcPPTase*, 100  $\mu g mL^{-1}$  *MrPPK*, 40  $\mu g mL^{-1}$  *SmPPK*, 25  $\mu g mL^{-1}$  *EcPPase*, 50  $\mu g mL^{-1}$  *GDH*, 30°C, 750 rpm. Sampling after 1 h of reaction with subsequently HPLC analysis. Values shown are mean values of technical triplicates ( $n_{biological} = 1$ ). Error bars for the technical replicates were too small to indicate.<sup>[17][18]</sup>

## 6. Analytics

### 6.1. Calibration curves

The calibration curves constructed to determine the conversions of sodium benzoate (NaBZ), benzaldehyde (BA) and benzyl alcohol (BZ alcohol) are shown below. The internal standard used was ethyl *para*-hydroxybenzoate.



**Figure S10.** Calibration curves for sodium benzoate (NaBZ), benzaldehyde (BA), and benzyl alcohol (BZ alcohol). The y-axis corresponds to the ration of the area of one of these compounds (A1) and the area of the internal standard (A2).

## 6.2. Chromatogram

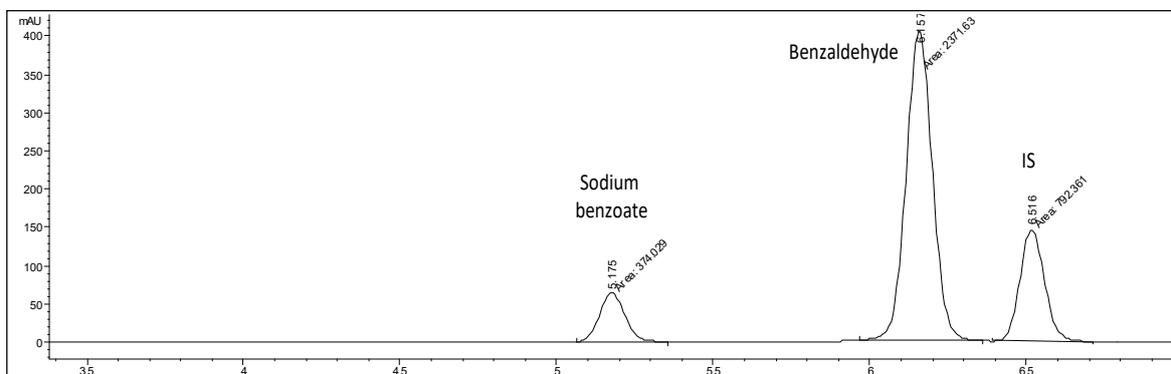


Figure S11. Exemplary chromatogram for an *in vitro* reaction.

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