Mutability-landscape guided enzyme engineering
van der Meer, Jan Ytzen

IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

Document Version
Publisher's PDF, also known as Version of record

Publication date:
2016

Link to publication in University of Groningen/UMCG research database

Citation for published version (APA):

Copyright
Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

Take-down policy
If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from the University of Groningen/UMCG research database (Pure): http://www.rug.nl/research/portal. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.
MUTATIONS CLOSER TO THE ACTIVE SITE IMPROVE THE PROMISCUOUS ALDOLASE ACTIVITY OF 4-OXALOCROTONATE TAUTOMERASE MORE EFFECTIVELY THAN DISTANT MUTATIONS

Mehran Rahimi,* Jan-Ytzen van der Meer,* Edzard M. Geertsema, Harshwardhan Poddar, Bert-Jan Baas, and Gerrit J. Poelarends

Department of Pharmaceutical Biology, Groningen Research Institute of pharmacy, University of Groningen, Antonius Deusinglaan 1, 9713 AV Groningen, The Netherlands
* These authors contributed equally to this work.

Published in ChemBioChem, 2016, 17(13), 1225-1228
ABSTRACT

The enzyme 4-oxalocrotonate tautomerase (4-OT), which in nature catalyzes an enol-keto tautomeration step as part of a degradative pathway for aromatic hydrocarbons, promiscuously catalyzes various carbon-carbon bond-forming reactions. This includes the aldol condensation of acetaldehyde with benzaldehyde to yield cinnamaldehyde. Here, we demonstrate that 4-OT can be engineered into a more efficient aldolase for this condensation reaction, with a >5000-fold improvement in catalytic efficiency (in terms of $k_{cat}/K_m$) and a $>10^7$-fold change in reaction specificity, by exploring small libraries in which only ‘hotspot’ positions are varied. These ‘hotspot’ positions were identified by a systematic mutagenesis strategy, covering each residue position, followed by an initial screen for single mutations that give a strong improvement in the desired aldolase activity. The beneficial mutations were all found to be near the active site of 4-OT, underpinning the general notion that new catalytic activities of a promiscuous enzyme are more effectively enhanced by mutations closer to the active site than by mutations at greater distance.
The homohexameric enzyme 4-oxalocrotonate tautomerase (4-OT) is a member of the tautomerase superfamily, a group of homologous proteins that share a β-α-β structural fold and a unique catalytic amino-terminal proline (Pro-1).\(^1\)\(^-\)\(^3\) 4-OT catalyzes the conversion of 2-hydroxy-2,4-hexadienedioate (1) to 2-oxo-3-hexenedioate (2) (Scheme 1) as part of a catabolic pathway for aromatic hydrocarbons in *Pseudomonas putida* mt-2.\(^4\)\(^,\)\(^5\) In this tautomerization reaction, residue Pro-1 functions as a general base that removes the 2-hydroxyl proton of 1 for delivery to the C-5 position to yield 2. Pro-1 can function as a general base because the prolyl nitrogen has a pK\(_a\) of ~6.4 and exists largely as the uncharged species at cellular pH.\(^6\)

**Scheme 1** – The proton-transfer reaction naturally catalyzed by 4-OT. In addition to its natural tautomerase activity, 4-OT promiscuously catalyzes several carbon-carbon bond-forming Michael-type addition and aldol condensation reactions.\(^7\)\(^-\)\(^16\) This includes the aldol condensation of acetaldehyde (3) with benzaldehyde (4) to yield cinnamaldehyde (6) (Scheme 2).\(^10\)\(^,\)\(^12\) where it catalyzes the conversion of 2-hydroxy-2,4-hexadienedioate (1) 4-OT catalyzes both the initial addition of 3 to 4 to yield 3-hydroxy-3-phenylpropanal (5) as well as the subsequent dehydration of 5 to give 6. 4-OT also catalyzes a retro-aldol reaction with 5 as the substrate, yielding 3 and 4.\(^12\) NaCNBH\(_3\) trapping, mass spectrometry, and X-ray crystallography experiments strongly suggest a mechanism in which Pro-1 functions as a nucleophile, rather than a base, and reacts with the carbonyl functionality of 3 to form a covalent enamine intermediate.\(^12\)\(^,\)\(^17\) This intermediate reacts with 4 in an aldol addition. After enzymatic dehydration of 5, the final product 6 is released from the active site upon hydrolysis. Notably, mechanism-inspired engineering provided an active site mutant (F50A) with enhanced aldol condensation activity (600-fold in terms of k\(_{\text{cat}}\)/K\(_{\text{m}}\)).\(^12\)

**Scheme 2** – The aldol condensation reaction promiscuously catalyzed by 4-OT.

The aldol reaction is one of the most important reactions in synthetic chemistry and has been widely used for the production of valuable compounds.\(^18\)\(^-\)\(^22\) Therefore, there is great interest in the development of novel aldolases for biocatalytic applications. In this study, we investigated whether 4-OT can be engineered into a more efficient aldolase by exploring small libraries in which only ‘hotspot’ positions are varied. Since
residues that affect activity can be found anywhere in proteins, we first applied a systematic mutagenesis strategy to identify residue positions at which mutations give a marked improvement in the aldolase activity of 4-OT. For this, a previously constructed collection of 1040 single mutants of 4-OT, covering at least 15 of the 19 possible variants at each residue position, from Ile-2 to Arg-62 (the 4-OT monomer consists of 62 amino acid residues), was used. A heat map for the aldolase activity of 4-OT was generated by determining the effect of each mutation on the ability of the enzyme to catalyze the aldol condensation of 3 with 4 to yield 6 (Fig. 1). Given the low-level aldolase activity of wild-type 4-OT, the activity measurements were performed under screening conditions that allowed only for the detection of variants with strongly improved aldolase activity.

Using this systematic mutagenesis approach, three ‘hotspot’ positions at which single mutations greatly improve the aldolase activity of 4-OT were identified (Fig. 1). These include mutations at positions His-6 (Val, Ile, Leu), Met-45 (His) and Phe-50 (Ala, Val, and Ile). Residues His-6, Met-45 and Phe-50 are lining the Pro-1
pocket, illustrating that single mutations close to the active site can strongly improve
the promiscuous aldolase activity of 4-OT. The single mutants with the best aldolase
activity at each of these residue positions (H6I, M45H, and F50V; see Supplementary
Figure 1) were purified, and their catalytic performance was compared to that of
wild-type 4-OT by transformations using 150 μM enzyme and a 25-fold excess of 3
(50 mM) over 4 (2 mM). Analysis of the progress curves of these reactions showed that
the single mutants H6I, M45H and F50V have strongly enhanced aldolase activity for
the condensation of 3 with 4 when compared to wild-type 4-OT, with mutant F50V
displaying the highest aldolase activity (Fig. 2 and Supplementary Figure 2). Notably,
no mutations which significantly enhance the aldolase activity of 4-OT were found at
distant residue positions.

![Figure 2 – UV traces monitoring the formation of cinnamaldehyde (6) (λ_{max} = 290 nm) from acetaldehyde (3) and benzaldehyde (4) in the absence of enzyme (blank) or in the presence of purified wild-type 4-OT, 4-OT H6I, 4-OT M45H or 4-OT F50V.]

To investigate whether the three ‘hotspot’ positions (His-6, Met-45 and Phe-50) are
good targets to further enhance 4-OT’s promiscuous aldolase activity, these positions
were subjected to combinatorial mutagenesis. The NNK-codon degeneracy, covering
all 20 possible amino acids, was used for randomization of positions His-6 and Met-45,
whereas Phe-50 was varied using NYK-codon degeneracy.28-31 The NYK-codon
degeneracy was chosen for position Phe-50 because it reduces the library size by
covering only the codons of nine different aliphatic and polar amino acid residues,
including those residues which result in an enhanced aldolase activity (Ala, Val and Ile),
as well as the wild-type residue (Phe). In addition to this triple-site library, a double-
site library was constructed by varying positions Met-45 and Phe-50 simultaneously
using NNK-codon degeneracy for both positions. Positions Met-45 and Phe-50 were
chosen for this double-site library as single mutations at these positions resulted
in higher aldolase activity as compared to the activity of single mutants at position
His-6 (Fig. 2).
The two libraries were used to transform *Escherichia coli* cells. The double-site library was screened by evaluating ~500 transformants, whereas ~3500 transformants of the triple-site library were screened for the aldol condensation of 3 and 4. Activity screening of the two libraries resulted in the identification of two mutants (M45T/F50A from the double-site library and H6F/M45T/F50A from the triple-site library) that showed a significant improvement in aldolase activity compared to that of the best single mutant F50V (which was used as a control in the screening assays). The progress curves of the aldol condensation of 3 (50 mM) with 4 (2 mM) catalyzed by the purified enzymes confirmed the enhanced activities of mutants M45T/F50A and H6F/M45T/F50A when compared to wild-type 4-OT and mutant F50V (Fig. 3). 1H NMR spectroscopic analysis confirmed that product 6 is formed in the aldol condensation of 3 with 4 catalyzed by mutant F50V, M45T/F50A or H6F/M45T/F50A (Supplementary Figure 3).

Having established that mutants F50V, M45T/F50A and H6F/M45T/F50A have greatly improved aldolase activity, apparent kinetic parameters were determined using a fixed concentration of 3 (50 mM) and varying concentrations of 4 (0.1 - 15 mM). As shown in Table 1, the catalytic efficiency (in terms of $k_{cat}/K_m$) of the single mutant F50V is ~640-fold higher than that of the wild-type 4-OT. Strikingly, the catalytic efficiencies of the double mutant M45T/F50A and the triple mutant H6F/M45T/F50A are 3300-fold and ~5300-fold higher than that of wild-type 4-OT, respectively. The improved catalytic efficiencies of the double and triple mutants, when compared to the single mutant F50V, are due to a lowered $K_m$ value for substrate 4.

Next, we chemically synthesized compound 5\(^{12,32}\) and assessed the ability of mutants F50V, M45T/F50A and H6F/M45T/F50A to catalyze dehydration and retro-aldo reactions with this substrate. UV spectroscopic analysis revealed increases

---

**Figure 3** – UV traces monitoring the formation of cinnamaldehyde (6) ($\lambda_{max} = 290$ nm) from acetaldehyde (3) and benzaldehyde (4) in the presence of purified wild-type 4-OT, 4-OT F50V, 4-OT M45T/F50A or 4-OT H6F/M45T/F50A.
in absorbance at 250 nm and 290 nm (Supplementary Figure 4). The increase in absorbance at 290 nm corresponds to the formation of 6, which results from the dehydration of 5. The increase in absorbance at 250 nm corresponds to the formation of 4, which results from the retro-aldol cleavage of 5. Interestingly, while mutants M45T/F50A and H6F/M45T/F50A catalyze both retro-aldol and dehydration reactions using 5 as the substrate, mutant F50V appears to mainly catalyze the dehydration reaction (Supplementary Figure 4). All three mutants showed a strongly improved activity with substrate 5 as compared to wild-type 4-OT. Notably, additional increases in absorbance at 227 nm, which corresponds to the formation of but-2-enal (i.e., the product of the self-condensation of 3),10 were observed in samples containing the mutant enzymes, indicating the formation of 3 during the course of the retro-aldol reactions.

\(^1\)H NMR spectroscopic analysis confirmed the enhanced activity of the three mutant enzymes for substrate 5 when compared to wild-type 4-OT (Supplementary Figure 5). After 18 h of incubation, compound 5 was fully converted by the three mutant enzymes, while only 34% conversion (26% conversion of 5 into 6 and 8% conversion of 5 into 3 and 4) was observed in the reaction mixture with wild-type 4-OT. The \(^1\)H NMR data confirmed that mutant F50V mainly catalyzes the dehydration reaction (65% dehydration versus 35% retro-aldol reaction), and demonstrated that mutants M45T/F50A (28% dehydration versus 72% retro-aldol reaction) and H6F/M45T/F50A (21% dehydration versus 79% retro-aldol reaction) mainly catalyze the retroaldol cleavage of 5. These results surprisingly demonstrate that the double and triple mutants have an inverted reaction specificity as compared to wild-type 4-OT and the single mutant F50V.

Finally, we examined whether the engineered 4-OT variants (F50V, M45T/F50A, and H6F/M45T/F50A) still possess native tautomerase activity. Accordingly, kinetic parameters were determined using varying concentrations of the natural substrate 1 (Table 2).\(^5\) With 87-, 5750- and 4893-fold decreases in \(k_{cat}/K_m\) for the F50V-, M45T/F50A- and H6F/M45T/F50A-catalyzed tautomerization reactions, respectively, these mutants have a largely decreased catalytic efficiency compared to that of the wild-type 4-OT. Notably, the mutations M45T/F50A and H6F/M45T/F50A resulted

---

**Table 1 – Apparent kinetic parameters for the aldol condensation of 3 and 4, to yield 6, catalyzed by wild-type 4-OT and 4-OT variants**

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>(k_{cat}) (\text{min}^{-1})</th>
<th>(K_m) for 4 (\text{mM})</th>
<th>(k_{cat}/K_m) (\text{M}^{-1} \text{min}^{-1})</th>
<th>Relative (k_{cat}/K_m)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wild-type</td>
<td>n.d.(^a)</td>
<td>n.d.(^a)</td>
<td>5.08 × 10(^{-2})</td>
<td>1</td>
</tr>
<tr>
<td>F50V</td>
<td>0.27 ± 0.01</td>
<td>8.4 ± 0.8</td>
<td>32</td>
<td>636</td>
</tr>
<tr>
<td>M45T/F50A</td>
<td>0.28 ± 0.008</td>
<td>1.7 ± 0.1</td>
<td>168</td>
<td>3300</td>
</tr>
<tr>
<td>H6F/M45T/F50A</td>
<td>0.19 ± 0.005</td>
<td>0.7 ± 0.06</td>
<td>268</td>
<td>5276</td>
</tr>
</tbody>
</table>

\(^a\) n.d., not determined.
in enzymes with a $>10^7$-fold change in reaction specificity. Hence, the large increase in promiscuous aldolase activity for these mutants is accompanied by a large decrease in natural tautomerase activity, indicating a strong negative tradeoff between evolving and existing activity.\textsuperscript{33-37}

In summary, we demonstrated that the promiscuous enzyme 4-OT can be engineered into a more efficient aldolase by exploring small libraries in which only ‘hotspot’ positions are varied. The ‘hotspot’ positions were identified by a systematic mutagenesis strategy, covering each residue position, followed by a screen for single mutations that give a marked improvement in the desired aldolase activity. These mutations were all found to be near the active site, providing direct support for the notion that for new catalytic activities in a promiscuous enzyme, mutations closer to the active site improve the enzyme more effectively than distant ones.\textsuperscript{23} In future work, we aim to explore the substrate scope of the engineered 4-OT variants, focusing on challenging aldol reactions between two aldehydes, and design new 4-OT variants that lack dehydration activity but do possess further enhanced aldolase activity. To support the latter goal and to place our engineering efforts into a structural context, work is in progress to determine the crystal structures of 4-OT and the best 4-OT variants in complex with the unnatural substrate 5 or product 6.

Table 2 – Kinetic parameters for the ketonization of 1, to yield 2, catalyzed by wild-type 4-OT and 4-OT variants

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>$k_{\text{cat}}$ (s$^{-1}$)</th>
<th>$K_m$ (µM)</th>
<th>$k_{\text{cat}}/K_m$ (M$^{-1}$ s$^{-1}$)</th>
<th>Relative $(k_{\text{cat}}/K_m)$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wild-type</td>
<td>1433 ± 35</td>
<td>31 ± 2</td>
<td>$4.6 \times 10^7$</td>
<td>1</td>
</tr>
<tr>
<td>F50V</td>
<td>134 ± 1</td>
<td>253 ± 6</td>
<td>$5.3 \times 10^5$</td>
<td>(87)$^{-1}$</td>
</tr>
<tr>
<td>M45T/F50A</td>
<td>n.d.$^a$</td>
<td>n.d.$^a$</td>
<td>$8.0 \times 10^3$</td>
<td>(5750)$^{-1}$</td>
</tr>
<tr>
<td>H6F/M45T/F50A</td>
<td>n.d.$^a$</td>
<td>n.d.$^a$</td>
<td>$9.4 \times 10^3$</td>
<td>(4893)$^{-1}$</td>
</tr>
</tbody>
</table>

$^a$n.d., not determined.
REFERENCES


SUPPLEMENTARY INFORMATION

Supplementary Materials and Methods

Materials
The sources for the buffers, solvents, components of Luria-Bertani (LB) media, as well as the materials, enzymes and reagents exploited in molecular biology procedures are reported elsewhere.¹

General methods
Standard molecular biology techniques were performed based on methods described elsewhere.² Protein was analyzed by polyacrylamide gel electrophoresis (PAGE) using pre-casted 10% polyacrylamide gels (NuPAGE® Novex® 10% Bis-Tris). Coomassie brilliant blue was used to stain the gels. Protein concentrations were determined using the Waddell method.³ Enzymatic assays were performed either on a V-650 or V-660 spectrophotometer from Jasco (IJsselstein, The Netherlands) or on a SPECTROstar Omega plate reader (BMG LABTECH, Isogen Life Science, de Meern, NL). ¹H NMR spectra were recorded on a Varian Inova 500 (500 MHz) spectrometer using a pulse sequence for selective presaturation of the water signal. Chemical shifts for protons are reported in parts per million scale and are referenced to H₂O (δ = 4.80).

Expression and purification of 4-OT wild-type and mutants
All 4-OT enzymes were produced in E. coli BL21 (DE3), as native proteins without any affinity tag, using the pET20b(+) expression system as described before.⁴ The construction of the expression vector for the production of 4-OT and the purification procedure for this enzyme have been reported previously.⁴ To confirm that the proteins had been processed correctly and the initiating methionine had been removed, the masses of purified 4-OT wild-type and mutants were determined by ESI-MS.

Preparation of 1040 single 4-OT mutants
A defined collection of 1040 single mutant 4-OT genes, each cloned individually into a pJexpress 414 vector, was purchased from DNA2.0 (Menlo Park, CA).³ This collection covered at least 15 of the 19 possible variants on each residue position, ranging from Ile-2 to the carboxy-terminal Arg-62. Single mutants of the amino-terminal proline residue (Pro-1) were not included in the collection, because Pro-1 is a key catalytic residue and mutations at this position lead to incorrect demethionylation of the protein.⁵ In total 90% of all possible single 4-OT mutants is present in this collection. An aliquot of each pJexpress 414 vector with a unique mutant 4-OT gene was transformed individually into E. coli BL21 (DE3), as described elsewhere.⁵ Each E. coli BL21(DE3) transformant harboring a pJexpress 414 vector with a unique mutant 4-OT gene was stored at -80°C until further use.
Cell-free extract preparation and 4-OT concentration assessment

The expression levels and activities of all members of the 4-OT mutant collection were determined using cell-free extracts (CFEs) of cultures each expressing a different 4-OT mutant. Aliquots of the -80°C stock of the transformed E. coli BL21 (DE3) cells were placed into wells of 96-deep-well plates (Greiner Bio-one, 96 well Masterblock®). Each mutant was placed into two wells as a duplicate. Each well contained 1.25 mL LB, supplemented with 100 µg/mL ampicillin and 100 µM isopropyl-β-D-1-thiogalactopyranoside (IPTG) as inducer. The deep-well plates with inoculated LB medium were sealed with sterile, gas-permeable seals (Greiner Bio-one, BREATHseal™) and incubated overnight at 37°C with shaking at 250 rpm. After the incubation, the cultures were pelleted at 3500 RPM for 30 min at 4°C. The pellets of the duplicates were pooled and lysed with 375 µl BugBuster™ (Novagen), which was supplemented with 25 U/mL benzonase nuclease. The cells were lysed at room temperature for 20 minutes with vigorous shaking. The cell lysates were cleared by centrifugation at 4000 RPM for 20 minutes at 4°C, after which the CFE was obtained as the supernatant. The 4-OT concentration in each CFE was determined using a quantitative densitometric analysis as described before. 5

Determination of the aldolase activity of the single 4-OT mutants

The produced CFEs were used to determine the aldolase activity of the single mutants of 4-OT using UV-spectroscopy. The UV-spectroscopic measurements were performed in 96-wells micro titer plates (MTPs) (UV-star µclear, Greiner Bio-one). The reaction mixtures consisted of CFE (30% v/v), acetaldehyde (3, 50 mM) and benzaldehyde (4, 2 mM) in 10 mM NaH₂PO₄ buffer (pH 7.3). The volume of these reaction mixtures was 100 µL and the MTPs were sealed with UV-transparent plate seals (VIEWseal™, Greiner Bio-one) to eliminate evaporation. The MTPs were incubated for 16 h at 25°C during which the reaction progress was monitored by UV-spectroscopy (220-500 nm). Formation of product 6 ($\lambda_{\text{max}} = 290$ nm) was quantified based on the increase in absorbance at 290 nm after 16 h. To eliminate false positives in which the increase in absorbance at 290 nm was a result of protein precipitation (in these cases there is an increase in absorbance over the whole range of the UV-spectrum), the $\Delta A_{290}$ values are corrected for absorbance changes at 350 nm. At this wavelength product 6 has no UV-absorbance. Reaction mixtures in which there was a high increase of absorbance at 350 nm ($\Delta A_{350} > 0.5$) were assigned as “precipitation” (Fig. 1). The low-level aldolase activity of wild-type 4-OT was below the detection limit of this assay. Therefore, only single mutants with a strongly improved aldolase activity were identified. Using Microsoft excel 2010, the activity data were represented as colors in the data matrix to create a visually interpretable heat map (Fig. 1).

Construction of double- and triple-site mutant libraries

4-OT mutant libraries were constructed by PCR, using the coding sequence for 4-OT in plasmid pET20b (4-OT) as the template. For the Met45NNK/Phe50NNK library
the following primers were used: F5’-A TAG CAG GTA CAT ATG CCT ATT GCC CAG ATC CAC ATC-3’ and R5’-A TGT TAT GGA TCC TCA GCG TCT GAC CTT GCT GGC CAG TTC GCC GCC GAT GCC MNN GTG GCC CTT GGC MNN CTC CGT-3’. For the H6NNK/Met45NNK/Phe50NYK library the following primers were used: F5’-A TAG CAG GTA CAT ATG CCT ATT GCC CAG ATC NNK ATC-3’ and R5’-A TGT TAT GGA TCC TCA GCG TCT GAC CTT GCT GGC CAG TTC GCC GCC GAT GCC MRN GTG GCC CTT GGC MNN CTC CGT-3’. Mutated codons are in bold and restriction sites are underlined. The following PCR program was used: 95°C (denaturation, 2 min), 55°C (annealing, 1 min), 72°C ( elongation, 1 min) for 35 cycles, followed by a final elongation step (72°C, 10 min). The resulting PCR products were gel purified, digested, and cloned in frame with the ATG start codon of the pET20b(+) vector. The ligation mixtures were used to transform competent E. coli DH10B cells using electroporation. The transformants were selected overnight at 37°C on LB-agar plates supplemented with 100 μg/mL ampicillin. Plasmid DNA was extracted from randomly picked colonies and the 4-OT gene was fully sequenced to assure that the desired mutations were introduced. After having established that the libraries were of good quality, all colonies were collected into 10 mL LB and cells were harvested by centrifugation (13000g, 10 min). From these cells, plasmid DNA was isolated and subsequently transformed into E. coli BL21(DE3) cells to express the mutant 4-OT genes.

Activity screening of double- and triple-site mutant libraries
Colonies of E. coli BL21(DE3) expressing the mutant 4-OT genes were picked individually and grown overnight at 37°C in 96-deep-well plates containing 1.25 mL LB medium supplemented with 100 μg/mL ampicillin. Colonies expressing F50V (positive control) or wild-type 4-OT and colonies containing empty plasmids (negative control) were also picked and grown overnight in each 96-deep well plate. The cells were collected by centrifugation (3500 rpm, 30 min, 4°C) and lysed with BugBuster™ (200 μL per well, 20 min incubation with vigorous shaking) containing benzonase nuclease (25 U/mL). The cell lysate was cleared by centrifugation (4000 rpm, 30 min, 4°C), after which the CFE was obtained as the supernatant. An aliquot of each CFE (30 μL) was transferred into a well of a MTP and incubated with 50 mM 3 and 2 mM 4 in 20 mM NaH₂PO₄ buffer (pH 7.3; 0.3 mL final volume). Absorbance spectra were recorded from 200 to 400 nm (Supplementary Figure 2).

UV-spectroscopic assay for the aldolase activity of purified enzymes
The aldolase activity of purified wild-type 4-OT and 4-OT mutants was monitored by following the increase in absorbance at 290 nm, which corresponds to the formation of cinnamaldehyde (6) (ε = 26.7 mM⁻¹ cm⁻¹). Purified enzyme (300 μg, 149 μM) was incubated in a 1 mm cuvette with 3 (50 mM) and 4 (2 mM) in 20 mM NaH₂PO₄ buffer (pH 7.3; 0.3 mL final volume). Absorbance spectra were recorded from 200 to 400 nm (Supplementary Figure 2).
Procedure for progress curve analysis: The reaction progress of the aldol condensation of 3 with 4 catalyzed by purified wild-type 4-OT or 4-OT mutants was monitored by following the increase in absorbance at 290 nm, which corresponds to the formation of 6. An aliquot of purified enzyme was added to NaH$_2$PO$_4$ buffer (0.3 mL, 20 mM; pH 7.3) in a 1 mm cuvette, yielding a final enzyme concentration of 1 mg/mL. The final concentrations of 3 and 4 were 50 and 2 mM, respectively. To obtain the progress curves, the increase in absorbance was plotted against time (Figs. 2 and 3).

$^1$H NMR spectroscopic assay for aldolase activity

In separate experiments, wild-type 4-OT and the 4-OT mutants F50V, M45T/F50A and H6F/M45T/F50A (1 mg/mL, 150 μM in 20 mM NaH$_2$PO$_4$, pH 7.3) were incubated with 3 (30 mM in 20 mM NaD$_2$PO$_4$, pD 7.5), 4 (15 mM in 20 mM NaD$_2$PO$_4$, pD 7.5) and 18-crown-6 (internal standard; 3.75 mM), and the reaction progress was monitored by $^1$H NMR spectroscopy. In addition, a control sample was prepared with all the components except for the enzyme. The first $^1$H NMR spectrum was recorded immediately after mixing, and then after 1 and 4 d (Supplementary Figure 3). The $^1$H NMR signals for 3 (and its hydrate), 4, 6 and internal standard are reported below.

**Compound 3 and its hydrate (3’):** $^1$H NMR (500 MHz, D$_2$O, 25°C): $\delta$ = 9.67 (q, $J$ = 3.0 Hz, 1H, 3), 5.24 (q, $J$ = 4.8 Hz, 1H, 3’), 2.23 (d, $J$ = 3.0 Hz, 3H, 3), 1.32 (d, $J$ = 4.8 Hz, 3H, 3’).

**Compound 4:** $^1$H NMR (500 MHz, D$_2$O, 25°C): $\delta$ = 9.94 (s, 1H), 7.96 (d, $J$ = 8.0 Hz, 2H), 7.76 (t, $J$ = 7.5 Hz, 1H), 7.63 (t, $J$ = 7.5 Hz, 2H).

**Compound 6:** $^1$H NMR (500 MHz, D$_2$O, 25°C): $\delta$ = 9.57 (d, $J$ = 8.0 Hz, 1H), 7.80 (d, $J$ = 15.5 Hz, 1H), 7.74 (d, $J$ = 8.0 Hz, 2H), 7.52 (m, 3H), 6.84 (dd, $J$ = 8.0, 8.0 Hz, 1H).

**Internal standard 18-crown-6 (1,4,7,10,13,16-hexaoxacyclooctadecane):** $^1$H NMR (500 MHz, 20 mM NaD$_2$PO$_4$; pD 7.6): $\delta$ = 3.68 (s, 24H)

Chemical synthesis of compound 5

The chemical synthesis of 3-hydroxy-3-phenylpropanal (5) has been described elsewhere, but also the subsequent dehydration of this aldol compound to yield cinnamaldehyde as the final product. Mechanism-inspired engineering provided an active site mutant (F50A).

UV-spectroscopic assay for monitoring dehydration and retro-aldol cleavage of 5

The retro-aldol and dehydration activities of wild-type 4-OT and 4-OT mutants were monitored by following the formation of 6 and 4 by UV-spectroscopy. In separate
experiments, wild-type 4-OT and 4-OT mutants F50V, M45T/F50A and H6F/M45T/F50A (1 mg/mL, 150 μM) were incubated with 5 (2 mM) in 20 mM NaH₂PO₄ buffer (pH 7.3; 0.3 mL final volume in a 1 mm cuvette). Absorbance spectra of the reaction mixtures were recorded from 200-400 nm every three minutes (Supplementary Figure 4).

¹H NMR spectroscopic assay for monitoring dehydration and retro-aldol cleavage of 5

¹H NMR spectra monitoring the conversion of 5 into 3 and 4 (retro-aldolase activity) and 6 (dehydration activity) catalyzed by wild-type 4-OT and 4-OT mutants were recorded as follows. In separate experiments, wild-type 4-OT and 4-OT mutants F50V, M45T/F50A and H6F/M45T/F50A (1 mg/mL, 150 μM) were incubated with 5 (8.8 mM) and 18-crown-6 ether (internal standard, 1.1 mM) in 20 mM NaD₂PO₄, pH 7.5 (total volume of 650 μL). In addition, a control experiment without enzyme but with otherwise identical conditions was performed as well. The first ¹H NMR spectrum was recorded after 2 h, and then after 18 h (Supplementary Figure 5). The ¹H NMR signals observed for 3, 4, and 6 were in accordance with those of the corresponding standards. The ¹H NMR signals for 5 and its hydrated form are given below.

²H NMR (300 MHz, D₂O, 25°C): 3-hydroxy-3-phenylpropanal (5);  δ = 9.72 (dd,  J = 1.9, 1.9 Hz, 1H), 7.49 – 7.34 (m, 5H), 5.32 (dd,  J = 7.8, 5.4Hz, 1H), 3.04 (ddd,  J = 17.1, 7.8, 1.9 Hz, 1H), 2.96 (ddd,  J = 17.1, 5.4, 1.9 Hz, 1H)

3-phenylpropane-1,1,3-triol (5’, hydrated form of 5);  δ = 7.49 – 7.34 (m, 5H), 5.03 (dd,  J = 6.0, 5.4 Hz, 1H), 4.85 (dd,  J =8.4, 5.8 Hz, 1H), 2.15 (ddd,  J = 13.9, 8.4, 5.4 Hz, 1H, 1H), 2.00 (ddd,  J = 13.9, 6.0, 5.8 Hz, 1H).

Kinetics assays for aldolase activity

The apparent kinetic parameters for the aldolase activity of wild-type 4-OT and 4-OT mutants were determined at 22°C by incubating the purified enzyme (150 μM) with a fixed concentration of 3 (50 mM) and varying concentrations of 4 (0.5 - 15 mM) in 20 mM NaH₂PO₄ buffer, pH 7.3 (final volume of 0.3 mL in a 1 mm cuvette). The reaction was monitored by following the increase in absorbance at 290 nm, which corresponds to the formation of 6. The initial rates (mM/min) were plotted versus the concentration of 4 (mM). SigmaPlot was used to fit the data to Michaelis-Menten kinetics and to calculate the apparent kinetic parameters kₗ and Kₘ (for 4).

Kinetic assays for tautomerase activity

The tautomerase activity of wild-type 4-OT and 4-OT mutants was measured by monitoring the ketonization of 2-hydroxyhexa-2,4-dienedioate (1) to 2-oxohexa-3-enedioate (2) in 20 mM NaH₂PO₄ buffer (pH 7.3) at 22 °C. Stock solutions of 1 were generated by dissolving the appropriate amount of 1 in absolute ethanol. The ketonization of 1 to 2 was monitored by following the increase in absorbance at
236 nm, which corresponds to the formation of 2 (ε = 6.58 × 10³ M⁻¹ cm⁻¹). The assay was initiated by the addition of a small aliquot of 1 (2–15 μL) to 1 mL of the assay buffer containing an appropriate amount of enzyme. The initial rates (μM/s) were plotted versus the concentration of 1 (μM). SigmaPlot was used to fit the data to Michaelis-Menten kinetics and to calculate the kinetic parameters $k_{cat}$ and $K_m$. 
Supplementary Figure 1 – UV spectra recorded after incubation of 3 and 4 ($\lambda_{\text{max}} = 250$ nm) with cell free extracts prepared from *E. coli* BL21 (DE3) cultures expressing: A) wild type 4-OT; B) H6I; C) M45H and D) F50V. Formation of cinnamaldehyde (6) ($\lambda_{\text{max}} = 290$ nm) was monitored in the course of the reactions.
Supplementary Figure 2 – UV spectra recorded after incubation of acetaldehyde (3) and benzaldehyde (4) ($\lambda_{\text{max}} = 250 \text{ nm}$) with A) no enzyme (control sample); B) purified wild-type 4-OT; C) purified H6I; D) purified M45H; and E) purified F50V. Formation of cinnamaldehyde (6) ($\lambda_{\text{max}} = 290 \text{ nm}$) was monitored in the course of the reactions.
Supplementary Figure 3 – Stack plot of $^1$H NMR spectra recorded after 1 d of incubation of $3$ and $4$ with A) no enzyme; B) wild-type 4-OT; C) 4-OT F50V; D) 4-OT M45T/F50A; and E) 4-OT H6F/M45T/F50A. Signals corresponding to $3$ and its hydrate ($3'$), $4$ and $6$ are marked.
Supplementary Figure 4 – UV spectra recorded after incubation of 5 (2 mM in 20 mM NaH$_2$PO$_4$ buffer at pH 7.3) with A) no enzyme (control sample); B) wild-type 4-OT; C) 4-OT F50V; D) 4-OT M45T/F50A; and E) 4-OT H6F/M45T/F50A.
Supplementary Figure 5 – Stack plot of $^1$H NMR spectra recorded after 18 h of incubation of 5 with A) no enzyme; B) wild-type 4-OT; C) 4-OT F50V; D) 4-OT M45T/F50A; and E) 4-OT H6F/M45T/F50A. Signals corresponding to 3 and its hydrated (3’), 4, 5 and its hydrate (5’), and 6 are marked.
SUPPLEMENTARY REFERENCES


