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Supporting Information

Structural insights into the ene-reductase synthesis of Profens

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1. Supplementary Table

Table 1. Comparative steady state kinetics of ene-reductases with substrates 6-8.				
Substrate	Enzyme	Specific Activity (⊡mol/min/mg)	Literature values (⊡mol/min/mg)	Ref
0	PETNR OYE2 OYE3 XenA	$5.26 \pm 0.01 \\ 0.20 \pm 0.19 \\ 0.31 \pm 0.20 \\ 0.95 \pm 0.01$	5.51 <u>+</u> 0.10 N/A N/A 1.34	1
 o	GYE LeOPR1 TOYE	$2.77 \pm 0.02 \\ 0.67 \pm 0.06 \\ 1.37 \pm 0.04$	N/A N/A 2.29 <u>+</u> 0.01	3
	NerA NtDBR	0.31 <u>+</u> 0.01 1.69 <u>+</u> 0.13	N/A 1.48 <u>+</u> 0.05	4

Reactions (1 mL) were performed in in buffer (K_2HPO_4/KH_2PO_4 pH 7.5) containing the alkene (1 mM; stock in 100 % ethanol) and NADPH (100 μ M) at 25°C. [a] Reactions carried out at 50°C. [b] Reactions carried out with 200 μ M NADPH. [c] Reactions were performed in citrate buffer pH 5.4. N/A = published kinetic data not available for comparison. OYEs tested were PETNR = pentaerythritol tetranitrate reductase from *Enterobacter cloacae* PB2;¹ LeOPR1 = 12-oxophytodienoate reductase 1 from *Solanum lycopersicum*;⁵ NerA = GTN reductase from *Agrobacterium radiobacter*;⁶ OYE2 from *Saccharomyces cerevisiae*;⁷ OYE3 from *Saccharomyces cerevisiae*;⁷ GYE from *Gluconobacter oxydans*;⁸ XenA = xenobiotic reductase from *Pseudomonas putida*;² and TOYE = thermophilic Old Yellow Enzyme from *Thermoanaerobacter pseudethanolicus* E39.³

2. Supplementary Figures



Figure S1. Achiral GC analysis of methyl ester-derivatised **5a** and **1a** to **3a** and **4b**, respectively. Samples were run on an Agilent Technologies 7890A GC system with FID detector and a ZB-semi volatiles column (30 m; 0.25 mm; 0.25 μ m film thickness). Red (10.12 min) and black (10.5 min) peaks show the separation of **1a** and **5a**, respectively. The large peak at 3.55 min is the limonene internal standard.



Figure S2. Achiral preparative HPLC separation of **1a** and **5a**. Samples were run on an Agilent 1260 Infinity preparative HPLC system with a diode array detector, using a Phenomenex Luna C18 column (5 \square m x 21.2 mm x 250 mm). The flow rate was 15 mL/min with a gradient of acetonitrile:H₂O 10:90 to 50:50 over 15 minutes. Peaks at 9 and 13 minutes are **5a** and **1a**, respectively.



Figure S3. MS spectra of **1a** generated in the biotransformation of **5a** by A) XenA and B) GYE. Samples were run on an Agilent 1100 LC/MSD Ion Trap System.



Figure S4. Chiral HPLC analysis of enantiomers of **1a**. Samples were run on an Agilent 1100 HPLC system with a Chiralpak AS-RH reverse phase column (150 x 4.6 mm ID) using a diode array detector (220 nm). Mobile phase was composed of acetonitrile/H₂O 40:60 and with a flow rate of 0.8 mL/min at 20 °C. Black and red peaks show the racemic and (*S*)-**1a** products, respectively.



Figure S5. Chiral HPLC analysis of enantiomers of **1a** generated by reactions with GYE and XenA. Samples were run on an Agilent 1100 HPLC system with a Chiralpak AS-RH reverse phase column (150 x 4.6 mm ID) using a diode array detector (220 nm). Mobile phase was composed of acetonitrile/H₂O 40:60 and with a flow rate of 0.8 mL/min run at 20 °C. Black, red and green traces show the racemic standard and the GYE and XenA reaction products, respectively.



Figure S6. Chiral HPLC analysis of enantiomers of **4a**. Samples were run on an Agilent 1100 HPLC system with a Chiralpak AS-RH reverse phase column (150 x 4.6 mm ID) using a diode array detector (220 nm). Mobile phase was composed of acetonitrile/H₂O 40:60 and with a flow rate of 0.8 mL/min at 20 °C. Peaks at 15 and 17.5 minutes are (*R*)-**4a** and (*S*)-**4a**, respectively.



Figure S7. Achiral analysis and standard curves of A) **5b** and B) **1b** by GC. Samples were run on an Agilent Technologies 7890A GC system with FID detector and a ZB-semi volatiles column (30 m; 0.25 mm; 0.25 µm film thickness). The large peak at 3.55 min is the limonene internal standard. calibration curve; —10 mM; — 7.5 mM; — 5 mM; — 2.5 mM; — 1 mM.



Figure S8. Chiral HPLC analysis of enantiomers of **1b**. Samples were run on an Agilent 1100 HPLC system with a Chiralpak AD-H column (150 x 4.6 mm ID) using a diode array detector (220 nm). Mobile phase was composed of hexane:isopropanol (95:5) at 20 °C with a flow rate of 1 mL/min at 20 °C. Black and red peaks show the (*R*)-**1b** and (*S*)-**1b** products, respectively.



Figure S9. Chiral HPLC analysis of enantiomers of **1b** generated by the reaction of **5b** with XenA. Samples were run on an Agilent 1100 HPLC system with a Chiralpak AS-RH reverse phase column (150 x 4.6 mm ID) using a diode array detector (220 nm). Mobile phase was composed of acetonitrile/H₂O 40:60 and with a flow rate of 0.8 mL/min run at 20 °C. Black, red and green traces show the (*R*)-**1b** and (*S*)-**1b** standards and XenA reaction products, respectively.

3. LCMS Identification of products of the biotransformation of 5b to 1b



Figure S10. UHPLC-MS analysis of the XenA and NerA reactions. Red boxes indicate extracted ion chromatogram (EIC) mass target, green box indicates ion count. i) **Top** - EIC at 149m/z from the atropic acid standard indicating the presence of a peak at 7.8 mins. **Bottom** - Subsequent summation of all mass spectra within peak at 7.8 indicates a parent-daughter pairing that represent the [Atropic Acid]^{H+} and [decarboxylated form]^{H+} as a result of fragmentation. **ii) Top** - Extracted ion chromatogram at 151m/z indicating the presence of a peak at 7.8 mins. **Bottom** - Subsequent summation of all mass spectra within peak at 7.8 indicates a parent-daughter pairing that represent the [Atropic Acid]^{H+} and [decarboxylated form]^{H+} as a result of fragmentation. **iii)** Top - Extracted ion chromatogram at 151m/z indicating the [Atropic Acid]^{H+} and [decarboxylated form]^{H+} as a result of fragmentation. **iii)** Extracted ion chromatogram of mass 151 indicating the lack of any major peak at 7.8 mins. Intensity of 9.53x10⁶ indicating a background signal (green box) **iv)** Top - Extracted ion chromatogram of mass 149 indicating the presence of a peak at 7.8 mins. **Bottom** - Subsequent summation of all mass spectra within peak at 7.8 mins. **Bottom** - Subsequent summation of all mass spectra within peak at 7.8 mins. **Bottom** - Subsequent summation of mass 149 indicating the presence of a peak at 7.8 mins. **Bottom** - Subsequent summation of all mass spectra within peak at 7.8 mins. **Bottom** - Subsequent summation of all mass spectra within peak at 7.8 mins. **Bottom** - Subsequent summation of all mass spectra within peak at 7.8 mins. **Bottom** - Subsequent summation of all mass spectra within peak at 7.8 mins. **Bottom** - Subsequent summation of all mass spectra within peak at 7.8 mins. **Bottom** - Subsequent summation of all mass spectra within peak at 7.8 mins. **Bottom** - Subsequent summation of all mass spectra within peak at 7.8 mins. **Bottom** - Subsequent summation of all mass spectra within peak at 7.8 mins. **Bottom**

An initial full scan MS over 50-750m/z of a pure standard of 2-phenylacrylic acid **5b** revealed a parent ion peak centred at 7.80 min with a primary mass of 149.05977 m/z. MS² analysis indicates a decarboxylated daughter fragment. An identical analysis on the XenA enzyme system indicates the presence of a peak at 7.8 mins with a primary mass of 151.0754 m/z. MS² analysis indicates a decarboxylated daughter fragment. The extra 2Da increase in product of the XenA system is representative of a mass gain from two protons by the reduction of the methylene carbons. Figure S10 iii/iv indicate the lack of the reduced 151m/z form but the presence of the unreacted 2-phenylacrylic acid **5b**.

4. NMR Traces



Figure S10. ¹H NMR spectrum of compound **1a** generated by large-scale biotransformation of **5a** by GYE. Spectrum was recorded on a 400 MHz spectrometer in CDCl₃.



Figure S11. ¹H NMR spectrum of compound **1a** generated by preparative biotransformation of **5a** by XenA. Spectrum was recorded on a 400 MHz spectrometer in CDCl₃.



Figure S12. ¹H NMR spectrum of compound **1a** generated by large-scale biotransformation of **5a** by XenA after 72 hours. Spectrum was recorded on a 400 MHz spectrometer in CDCl₃.



Figure S13. ¹H NMR spectrum of compound **7b** generated by large-scale biotransformation of **7a** by XenA. Spectrum was recorded on a 400 MHz spectrometer in CDCl₃.



Figure S14. A)¹H NMR and B)¹³C NMR spectra of compound **3a**. Spectra were recorded on a 400 MHz spectrometer in CDCl₃. The inset in A shows the aromatic region in more detail.



Figure S15. A)¹H NMR and B)¹³C NMR spectra of compound **5a**. Inset: COSY spectrum of compound **5a**. Spectra were recorded on a 400 MHz spectrometer in d_6 -DMSO.

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