

1 **Electronic Supplementary Material (ESI)**

2 **Engineering enzymatic cascades for efficient biotransformation of eugenol and**
3 **taxifolin to silybin and isosilybin**

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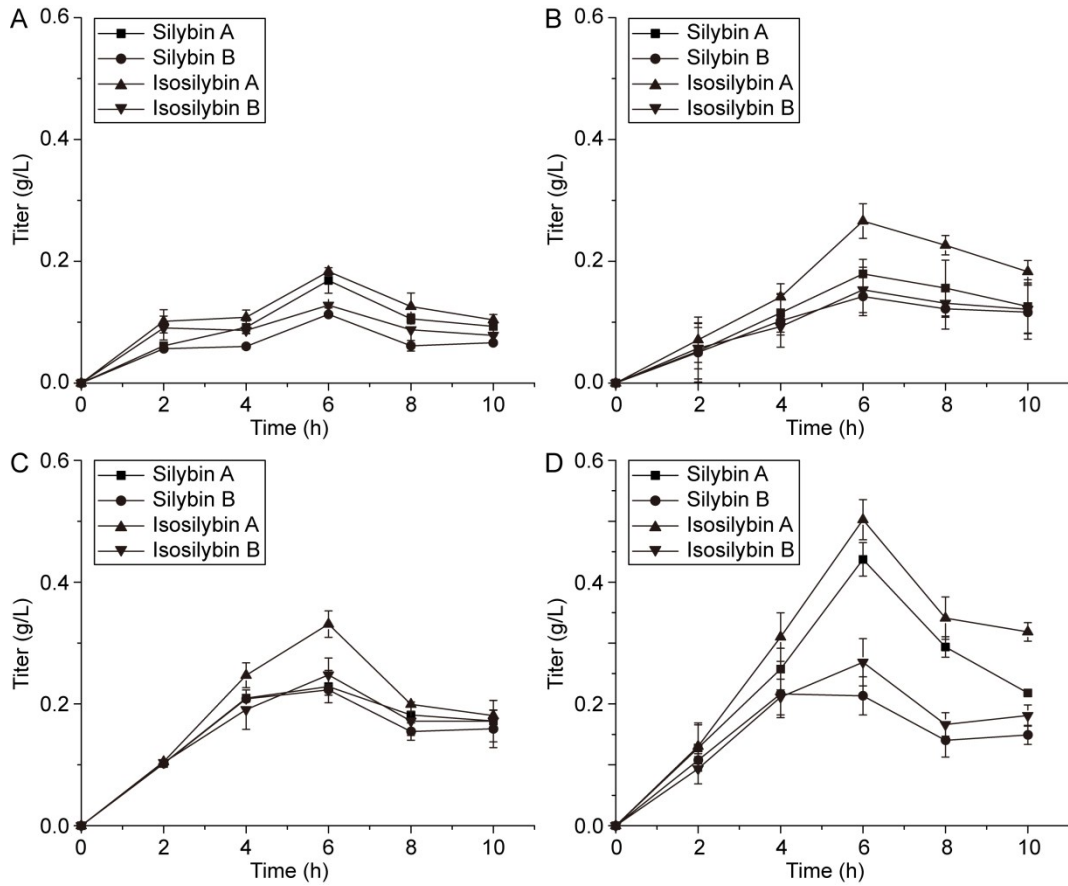
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22 **Figure S1** Silybin and isosilybin titers in bioconversions of different feeding rates.

23 The starting concentration was 5 mM eugenol and 1 mM taxifolin. The feeding rate

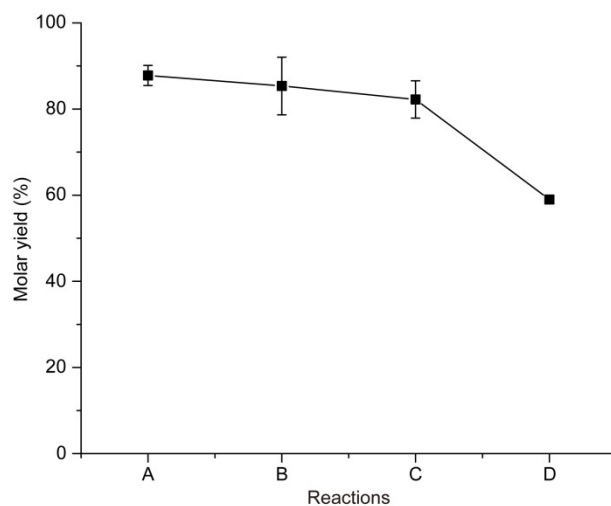
24 was **(A)** 6.25 μ L/h, equal to 0.25 mM/h eugenol and 0.05 mM/h taxifolin, **(B)** 12.5

25 μ L/h, equal to 0.5 mM/h eugenol and 0.1 mM/h taxifolin, **(C)** 25 μ L/h, equal to 1

26 mM/h eugenol and 0.2 mM/h taxifolin, and **(D)** 62.5 μ L/h, equal to 2.5 mM/h eugenol

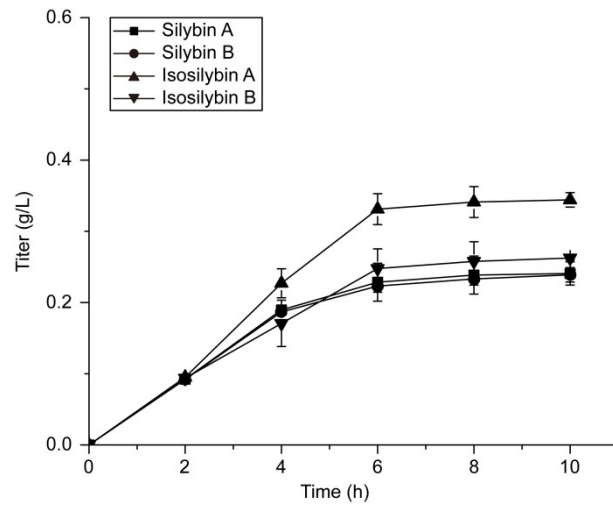
27 and 0.5 mM/h taxifolin.

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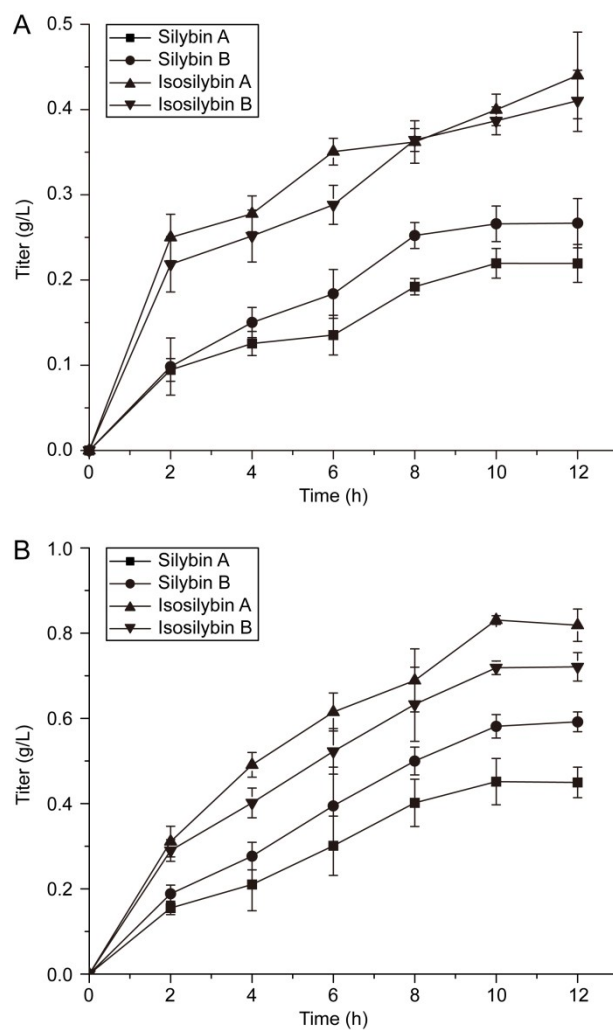
30 **Figure S2** Molar yields of silybin and isosilybin in bioconversions of different
31 feeding rates. The starting concentration was 5 mM eugenol and 1 mM taxifolin. The
32 feeding rate was **(A)** 6.25 $\mu\text{L}/\text{h}$, equal to 0.25 mM/h eugenol and 0.05 mM/h taxifolin,
33 **(B)** 12.5 $\mu\text{L}/\text{h}$, equal to 0.5 mM/h eugenol and 0.1 mM/h taxifolin, **(C)** 25 $\mu\text{L}/\text{h}$, equal
34 to 1 mM/h eugenol and 0.2 mM/h taxifolin, and **(D)** 62.5 $\mu\text{L}/\text{h}$, equal to 2.5 mM/h
35 eugenol and 0.5 mM/h taxifolin. The molar yield was calculated based on taxifolin.
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38 **Figure S3** Bioconversion under pH6.0. The starting concentration was 5 mM eugenol
39 and 1 mM taxifolin. The feeding rate was 25 μ L/h. The bioconversion was carried out
40 in the fermented broth, and the pH was adjusted to 6.0 using 1 M HCl.

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43 **Figure S4** Scale-up of the bioconversion. The bioconversions were carried out in 1.5-

44 L in a 3.0-L fermenter. The starting concentration was 5 mM eugenol and 1 mM

45 taxifolin. The feeding rates were 1.5 mL/h (**A**) and 3.75 mL/h (**B**), respectively.

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47 **Table S1** Ratio of isomers produced by different peroxidases

Peroxidase	Silybin A (%)	Silybin B (%)	Isosilybin A (%)	Isosilybin B (%)
EcoDyPrx02_536	16.39±3.02	15.55±2.66	43.30±3.63	24.75±7.07
EcoDyPrx01_K12	11.78±2.93	ND ¹	88.22±2.73	ND
SceCcP01	17.28±0.64	20.33±1.12	36.31±1.61	26.09±1.26
PpasCcP01	17.98±4.39	20.19±5.14	36.22±6.74	25.61±3.86
APX1	17.79±0.71	21.66±0.67	35.51±0.76	25.03±0.38

48 1. ND refers to not detected.

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50 **Table S2** Primers used in this study

Primers	Sequence (5' to 3')
SceCcP01 F	<u>GGAATTC</u> ATGACTACTGCTGTTAGGCTTTTAC ¹
SceCcP01 R	CCGCTCGAGTAAACCTTGTTCCCTCTAAAGTC
PpasCcP01 F	<u>GGAATTC</u> ATGTCGTCCATTGCATTCCATACAT
PpasCcP01 R	CCAAGCTTACTCTGCTCGTCTAGTGTCCTG
APX1-PsVAO F1	<u>GGAATTC</u> ATGCCGGTGGTTGATAACCGA
APX1-PsVAO R1	CGAAATTCCTGGGTTTTGCTCAT <u>AGAACCACCAC</u> <u>CCATTTTCTTACGGGCTTCG</u>
APX1-PsVAO F2	CTACGAAGCCCGTAAGAAAATGGGTGGTGGTTCT ATGAGCAAAACCCAGGAATTTC
APX1-PsVAO R2	CCAAGCTTACAGTTTCCAGGTGACGTGGC
PsVAO-APX1 F1	<u>GGAATTC</u> ATGAGCAAAACCCAGGAATTTC
PsVAO-APX1 R1	ATTCGGTATCAACCACCGGCAT <u>AGAACCACCACC</u> CAGTTTCCAGGTGACGTGGC
PsVAO-APX1 F2	GCCACGTCACCTGGAAACTGGGTGGTGGTTCTAT GCCGGTGGTTGATAACCGAATATC
PsVAO-APX1 R2	CCAAGCTTACATTTTCTTACGGGCTTCG

51 1. Underlined letters refer to restriction enzymes or overlapping sequences.

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