

Accepted Article

Title: Efficient Synthesis of 12-Oxochenodeoxycholic Acid Using a 12α-Hydroxysteroid Dehydrogenase from Rhodococcus ruber

Authors: Shou-Cheng Shi, Zhi-Neng You, Ke Zhou, Qi Chen, Jiang Pan, Xiao-Long Qian, Jian-He Xu, and Chun-Xiu Li

This manuscript has been accepted after peer review and appears as an Accepted Article online prior to editing, proofing, and formal publication of the final Version of Record (VoR). This work is currently citable by using the Digital Object Identifier (DOI) given below. The VoR will be published online in Early View as soon as possible and may be different to this Accepted Article as a result of editing. Readers should obtain the VoR from the journal website shown below when it is published to ensure accuracy of information. The authors are responsible for the content of this Accepted Article.

To be cited as: Adv. Synth. Catal. 10.1002/adsc.201900849

Link to VoR: http://dx.doi.org/10.1002/adsc.201900849

COMMUNICATION

DOI: 10.1002/adsc.201((will be filled in by the editorial staff))

Efficient Synthesis of 12-Oxochenodeoxycholic Acid Using a 12α-Hydroxysteroid Dehydrogenase from *Rhodococcus ruber*

Shou-Cheng Shi,^{a, #} Zhi-Neng You,^{a, #} Ke Zhou,^a Qi Chen,^{a, b} Jiang Pan,^{a, b} Xiao-Long Qian,^c Jian-He Xu,^{a, b, *} and Chun-Xiu Li ^{a, b, *}

- ^c Suzhou Bioforany EnzyTech Co. Ltd., No. 8 Yanjiuyuan Road, Economic Development Zone, Changshu, Jiangsu 215512, P. R. China
- [#] These authors contributed equally to this work.

Received: ((will be filled in by the editorial staff))

Supporting information for this article is available on the WWW under http://dx.doi.org/10.1002/adsc.201#######.((Please delete if not appropriate))

12α-Hydroxysteroid dehydrogenase $(12\alpha -$ Abstract: HSDH) has the potential to convert cheap and readily available cholic acid (CA) to 12-oxochenodeoxycholic acid (12-oxo-CDCA), a key precursor for chemoenzymatic synthesis of the therapeutic bile acid ursodeoxycholic acid (UDCA). In this work, a native nicotinamide adenine dinucleotide (NAD⁺) -dependent 12α-hydroxysteroid dehydrogenase (Rr12a-HSDH) from Rhodococcus ruber was identified using a structure-guided genome mining (SSGM) approach, which is based on the structure of cofactor pocket and the conserved nicotinamide cofactor binding motif alignment. Rr12a-HSDH was heterologously overexpressed in Escherichia coli BL21 (DE3), purified and characterized. The purified Rr12a-HSDH showed a high oxidative activity of 290 U mg⁻¹_{protein} toward CA, with a catalytic efficiency (k_{cat}/K_M) of 5.10 × 10³ mM⁻¹ s⁻¹. In a preparative biotransformation (100 mL), CA (200 mM, 80 g L^{-1}) was efficiently converted to 12-oxo-CDCA in 1 h, with a 85% isolated yield and a space-time yield (STY) of up to 1632 g L⁻¹ d⁻¹. Furthermore, $Rr12\alpha$ -HSDH was shown to be able to catalyze the oxidation of other 12α hydroxysteroids at high substrate loads (up to 200 mM), giving the corresponding 12-oxo-hydroxysteroids in 71%–85% yields, indicating the great potential of $Rr12\alpha$ -HSDH as a promising biocatalyst for the synthesis of various therapeutic bile acids.

Keywords: biocatalysis; 12α-hydroxysteroid dehydrogenase; NAD⁺-dependence; structure-guided genome mining; 12-oxochenodeoxycholic acid

Ursodeoxycholic acid (UDCA, 1e, Scheme 1) is an active pharmaceutical ingredient of bear bile powder,

which is a traditional Chinese medicine used for thousands of years.^[1] Clinically, **1e** is an effective drug for the treatment of cholesterol gallstones and cholestatic diseases.^[2] Traditionally, 1e is either obtained from bear bile powder or produced. chemically from cholic acid (CA, 1a, Scheme 1), which is the most abundant and cheapest bile acid.^[1,1] However, on the one hand, it is inhuman and unsustainable to extract 1e from the bile of live bears. On the other hand, chemical synthesis requires multiple protection and deprotection steps, leading to a low/moderate overall yield (about 30%-53%), and the inevitable use of toxic and hazardous reagents (e.g., pyridine and CrO₃) generates copious amounts of waste.^[4] Therefore, it is much more sustainable and economical enzymatic synthesis of 1e from 1a, given the availability of 1a as a cheap raw material and the eco-friendly nature of the enzymatic reaction conditions.^[3]

The enzymatic synthesis of **1e** requires the use of a very important class of enzymes, hydroxysteroid dehydrogenases (HSDHs), which can perform oxidoreduction of the hydroxyl/carbonyl groups on the core structure of hydroxysteroids.^[5] These enzymes show very high regioselectivity toward the hydroxyl groups at different positions (e.g., C3, C7, and C12) of the steroid nucleus (Scheme 1).^[3] Furthermore, **HSDHs** display excellent stereoselectivity for each of these positions by oxidizing hydroxyl groups oriented either below (α -OH) or above (β -OH) the plane of the steroid molecule.^[6] To date, many HSDHs with known protein sequences have been reported. These include

^a Laboratory of Biocatalysis and Synthetic Biotechnology, State Key Laboratory of Bioreactor Engineering, East China University of Science and Technology, 130 Meilong Road, Shanghai 200237, P. R. China Fax: (+86)-21-6425 0840; e-mail: jianhexu@ecust.edu.cn or chunxiuli@ecust.edu.cn

^b Shanghai Collaborative Innovation Centre for Biomanufacturing, School of Biotechnology, East China University of Science and Technology, 130 Meilong Road, Shanghai 200237, P. R. China

3a-HSDHs from rat liver, Comamonas testosteroni, and Eggerthella lenta;^[7] 7α-HSDHs from Escherichia coli HB101, Eubacterium sp. VPI 12708, Clostridium sordelli, Bacteroides fragilis, Clostridium absonum (formerly Clostridium sardiniense), Clostridium difficile, Stenotrophomonas maltophilia, and Brevundimonas sp.;^[8] and 7β-HSDHs from Collinsella aerofaciens,^[9a] Clostridium absonum,^[8e] Ruminococcus gnavus,^[9b] Ruminococcus torques,^[9c] Lactobacillus spicheri,^[8g] and Clostridium sp. Marseille.^[8h] However, 12α-HSDHs with known gene sequences are rarely reported.^[10]

12α-Hydroxysteroid dehydrogenase (12α-HSDH; EC 1.1.1.176) is a key enzyme for chemoenzymatic synthesis of **1e** from **1a**.^[6] 12α-HSDHs catalyze the oxidation of the 12α-hydroxyl group of **1a**, forming 12-oxochenodeoxycholic acid (12-oxo-CDCA, **1b**), which can be subjected to a Wolff-Kishner-Huang reduction to remove the C12 carbonyl group. The 7αhydroxylated chenodeoxycholic acid (CDCA, **1c**) is then epimerized to 7β-hydroxylated **1e** through the stable intermediate 7-oxo-lithocholic acid (7-oxo-LCA, **1d**) using two stereo-complementary enzymes, 7α-HSDH and 7β-HSDH (Scheme 1).^[6,11] Up to now, the nicotinamide adenine dinucleotide phosphate (NADP⁺)-dependent 12 α -HSDH with published sequence was identified from *Clostridium* sp. strain ATCC 29733/VPI C48-50 and showed low catalytic activity.^[7c,12] Ridlon *et al.* discovered several new 12 α -HSDHs from *Eggerthella* sp. CAG:298, *Clostridium hylemonae*, *Clostridium scindens*, and *Clostridium hiranonis*, respectively.^[7c,10]

Nevertheless, all of these documented 12α -NADP⁺-dependent **HSDHs** are stringently oxidoreductases (Table 1, entries 3-7). When compared with NADP+, nicotinamide adenine dinucleotide (NAD⁺) is much less costly and more stable under industrial conditions, making it the preferred cofactor for practical application of dehydrogenases.^[13] Most recently, a new NAD⁺dependent 12a-HSDH from Eggerthella lenta (El12a-HSDH) was reported by the group of Ulf Hanefeld. However, $El12\alpha$ -HSDH showed а productivity of only 4 g $L^{-1} d^{-1}$ as a biocatalyst for application.^[14] Therefore, the synthetic the identification of novel NAD+-dependent 12a-HSDHs with high enzymatic activity for efficient and economical synthesis of 1e precursor will promote sustainable and cost-efficient production of therapeutic bile acids.



Scheme 1. 12α -HSDH mediated oxidation of 1a as the first step of chemoenzymatic synthesis of 1e.

Entry	Enzyme	NCBI accession no.	Sequence identity [%]	Cofactor dependence	Specific activity [U mg ⁻¹]
1	Rr12α-HSDH	WP_026137560.1	100	NAD^+	289 ± 13
2	<i>El</i> 12α-HSDH	WP_114518444.1	43	\mathbf{NAD}^+	76 ± 2.1
3	<i>Cl</i> 12α-HSDH	ERJ00208.1	42	NADP ⁺	40 ± 0.8
4	<i>Eg</i> 12α-HSDH	CDD59475.1	39	NADP ⁺	59 ± 0.3
5	rCHYL	EEG75500.1	42	NADP ⁺	103 ± 3
6	rCSCI	EDS06338.1	41	\mathbf{NADP}^{+}	84 ± 2
7	rCHIR	EEA85268.1	38	$NADP^+$	197 ± 4

Table 1. Specific activity of 12α-HSDHs toward 1a.^[a]

^[a] Specific activity of 12 α -HSDHs was measured in 100 mM potassium phosphate, pH 8.0, containing 1.0 mM NAD⁺ or NADP⁺, and 2 mM substrate **1a** at 30°C using purified enzyme.



Figure 1. Structural models of (A) $Cl12\alpha$ -HSDH with NADPH, (B) $El12\alpha$ -HSDH with NADH, and (C) $Rr12\alpha$ -HSDH with NADH.

Herein, we discovered a new NAD+-dependent Rr12a-HSDH accession (NCBI no. WP 026137560.1), which was identified from Rhodococcus ruber using a structure-guided genome mining (SGGM) approach based on the 3D structure of the enzyme's cofactor pocket and the alignment of a conserved nicotinamide cofactor-binding motif. Rr12α-HSDH possesses the highest specific activity toward **1a** when compared with other 12α -HSDHs (Table 1). Up to 200 mM (80 g L^{-1}) of **1a** was efficiently converted by $Rr12\alpha$ -HSDH to **1b** with a space-time yield (STY) of as high as 1632 g $L^{-1} d^{-1}$ (Table 5, entry 7). Moreover, $Rr12\alpha$ -HSDH can biooxidize other 12α -bile acids and their glyco and tauro conjugates with 99% conversion, forming the corresponding 12-oxo-hydroxysteroids (Table 4), which are important precursors for the synthesis of pharmaceutically relevant bile acids.

To discover novel and native NAD+-dependent 12α-HSDHs, a structure-guided genome mining (SGGM) strategy was proposed. Firstly, we structurally analyzed the phosphate- and hydroxylbinding pockets of Cl12α-HSDH and El12α-HSDH, respectively. The phosphate-binding motif (GRN) in NADP⁺-dependent $Cl12\alpha$ -HSDH (Figure 1A) was found to be replaced by a hydroxyl-binding motif (DLF) in the NAD⁺-dependent *El*12α-HSDH (Figure 1B). This change in the amino acid residues located on the phosphate/hydroxyl-binding loops would be responsible for NAD(H)/NADP(H) cofactor recognition.^[8g,14,15] In general, NADP⁺-dependent enzymes have larger phosphate-binding pockets with positively charged residues (such as Arg51 in Cl12a-HSDH, Figure 1A) that interact with the negatively charged 2'-phosphate group of NADPH (phospho-) adenosine ribose, while NAD+-dependent enzymes prefer negatively charged residues (such as Asp38 in *El*12α-HSDH, Figure 1B).^[13c,15,16] Therefore, NAD⁺dependent enzymes could be rationally discovered by discriminating the residues on the cofactor pocket.

Subsequently, we performed a pBLAST search of the NCBI nonredundant database using the protein sequence of $El12\alpha$ -HSDH (NCBI accession no.

WP_114518444.1) as the template, and carried out an alignment of the conserved cofactor-binding motifs. Twenty eight enzyme genes with negatively charged residues (Asp) on the *N*-terminal of hydroxyl-binding loop were selected from 1000 sequences (Figure S1), cloned into pET28a vector, and heterologously overexpressed in Escherichia coli BL21 (DE3) (Table S1). The activity of each enzyme (using crude enzyme extracts as the catalysts) toward 1a was tested using NAD⁺ as a cofactor. One of the tested enzymes. Rr12a-HSDH originating from Rhodococcus ruber, showed a significant activity on 1a and was thus chosen for further studies. No activity was detected when using NADP⁺ as a cofactor, indicating that Rr12a-HSDH is a native NAD⁺-dependent enzyme. As shown in Figure 1C, a DVD motif was present on the hydroxyl-binding loop *Rr*12α-HSDH. of the NAD⁺-dependent The negatively charged Asp36 residue may form hydrogen bonds with the 2'-hydroxyl group of the adenosine ribose in NADH, which facilitates the tight binding of NADH with the enzyme. However, this position in all the NADP⁺-dependent 12α -HSDHs was replaced by a phosphate-binding motif (GRN) (Figure S6). The results demonstrated that SGGM strategy could enable effective and target-focused identification of the unknown but naturally occurring NAD⁺-dependent dehydrogenases.

 $Rr12\alpha$ -HSDH is shown to be a new 12α -HSDH because it shares only 38%–43% of its identity with the reported $El12\alpha$ -HSDH (Eggerthella lenta), $Cl_{12\alpha}$ -HSDH (Clostridium sp. strain ATCC 29733/VPI C48-50), Eg12α-HSDH (Eggerthella sp. CAG: 298), rCHYL (Clostridium hylemonae DSM 15053), rCSCI (Clostridium scindens ATCC 35704), and rCHIR (Clostridium hiranonis DSM 13275) (Table 1). To characterize the enzymatic properties of *Rr*12α-HSDH, the *N*-terminal His-tagged recombinant enzyme was purified by nickel affinity chromatography and analyzed by sodium dodecyl sulfate polyacrylamide gel electrophoresis (Figure S2). As shown in Table 1, the oxidation activity of purified $Rr12\alpha$ -HSDH was 290 U mg⁻¹_{protein} (under

standard conditions), which is the highest specific activity toward **1a** for 12α-HSDHs reported to date. $Rr12\alpha$ -HSDH showed higher catalytic activity at a temperature range of 35-45°C, and exhibited the highest activity at 40°C, retaining 70% activity at 30°C (Figure S3). The pH properties of the purified $Rr12\alpha$ -HSDH in both the reductive and oxidative reactions are shown in Figure S4. Rr12a-HSDH displayed a maximum activity at pH 10.0 for 1a dehydrogenation with NAD⁺ as a cofactor and an optimum at pH 6.0 for 1b reduction with NADH as a cofactor. The thermostability of Rr12a-HSDH was also examined, giving half-lives $(t_{1/2})$ of 72, 20, and 0.25 h, respectively, at 30, 40, and 50°C (Figure S5), implying that the enzyme was quite stable at 30°C but deactivated at higher temperatures. Hence, the enzymatic synthesis reactions were performed at 30°C so as to avoid the negative influences of the poor thermostability.

The kinetic parameters of 12α-HSDHs toward 1a and cofactor were determined. As shown in Table 2 (entries 1–2), the Michaelis–Menten constant (K_m) of Rr12α-HSDH for 1a was 0.025 mM, displaying a 25fold higher affinity than *El*12α-HSDH (0.64 mM). The turnover frequency (k_{cat}) of $Rr12\alpha$ -HSDH for **1a** was 128 s⁻¹, affording the catalytic efficiency (k_{cat}/K_m) of 5.10×10^3 mM⁻¹ s⁻¹, which is 88-fold greater than that of El12a-HSDH. In addition, compared with El12a-HSDH, Rr12a-HSDH showed a much better affinity to cofactor NAD⁺ with a K_m of 0.063 mM (Table 2, entry 3), which is 15 times lower than $El12\alpha$ -HSDH (0.92 mM) (Table 2, entry 4), indicating that $Rr12\alpha$ -HSDH has a greater application prospect in enzymatic synthesis. The kinetic parameters of $Rr12\alpha$ -HSDH toward other 12α hydroxysteroids were also measured, as summarized in Table 2 (entries 5-11). Rr12a-HSDH exhibited relatively high k_{cat} values for all the 12 α hydroxysteroids tested (78.3–141 s^{-1}) and the highest k_{cat} was observed when using glycocholic acid (GCA, **6a**) as substrate. The K_m values of $Rr12\alpha$ -HSDH for majority of the 12α -hydroxysteroids ranged from 0.025 to 0.046 mM, indicating that the enzyme has excellent affinity to these substrates except for deoxycholic acid (DCA, 4a, $K_{\rm m} = 0.138$ mM). The results demonstrated that $Rr12\alpha$ -HSDH can be used as a potential biocatalyst for the production of various health-promoting bile acids.

Table 2.	Kinetic parameters	s of recombinant	$Rr12\alpha$ -HSDH and	$El12\alpha$ -HSDH. ^[a]
----------	--------------------	------------------	------------------------	------------------------------------

fold higher affinity than $El_{12\alpha}$ -HSDH (0.64 mM). health-promoting bile acids.								
Table 2. Kinetic parameters of recombinant $Rr_{12\alpha}$ -HSDH and $E/_{12\alpha}$ -HSDH. ^[a]								
Frade 2. Knette parameters of recombinant K/120-HSDH and E/120-HSDH. ⁽²⁾ $\downarrow \downarrow $								
Entry	Substrate $(R^1 =, R^2 =)$	V _{max} [µmol∙min ⁻¹ ∙mg ⁻¹]	K _m [mM]	$k_{ m cat}$ $[{ m s}^{-1}]$	$k_{\text{cat}}/K_{\text{m}}$ [mM ⁻¹ s ⁻¹]	0		
1	1a (α-OH, H)	290 ± 13	0.025 ± 0.005	128 ± 6	$5.10 imes 10^3$	-0		
2	1a (α -OH, H) ^[b]	78 ± 2.1	0.640 ± 0.060	36.5 ± 1.0	57.0	+		
3	$NAD^{+[c]}$	292 ± 5	0.063 ± 0.005	129 ± 2	$2.03 imes 10^3$	\mathbf{O}		
4	$NAD^{+[d]}$	65 ± 6	0.920 ± 0.160	30.6 ± 2.6	33.3	()		
5	2a (Ketone, H)	178 ± 4	0.041 ± 0.003	78.3 ± 1.8	$1.91 imes 10^3$	0		
6	3a (β-OH, H)	240 ± 13	0.046 ± 0.008	106 ± 6	$2.30 imes 10^3$	X		
7	4a (H, H)	276 ± 21	0.138 ± 0.003	121 ± 9	$8.80 imes 10^2$			
8	5a (α-OH, Taurine)	319 ± 15	0.035 ± 0.007	140 ± 7	$4.01 imes 10^3$			
9	6a (α-OH, Glycine)	320 ± 15	0.042 ± 0.008	141 ± 7	3.35×10^3			
10	7a (H, Taurine)	295 ± 8	0.038 ± 0.004	130 ± 4	3.40×10^3			
11	8a (H, Glycine)	293 ± 4	0.042 ± 0.002	129 ± 2	$3.10 imes 10^3$			

^[a] Kinetic parameters were determined at different substrate concentrations (0-10 mM) in the presence of 1 mM NAD⁺ using purified Rr12a-HSDH, and ^[b] El12a-HSDH, respectively. ^[c] Kinetic parameters were determined at different NAD⁺ concentrations (0–1.0 mM) in the presence of 2 mM 1a using purified Rr12a-HSDH, and ^[d] El12a-HSDH, respectively. The k_{cat} values were calculated considering a subunit size of 28.0 and 28.3 kDa for $Rr12\alpha$ -HSDH and $El12\alpha$ -HSDH, respectively.

		COOH $Rr12\alpha$ -HSDH NAD ⁺ Lactate LdLDH Pyruvate	HOW	р Соон Соон Соон в		
Entry	1a [mM]	$Rr12\alpha$ -HSDH [g L ⁻¹]	NAD ⁺ [mM]	Time [h]	Conv. [%] ^[b]	
1	50	1	0.2	0.5	>99	
2	100	1	0.2	24	82	
3	100	1	0.4	1	>99	
4	200	2	0.4	12	50	
5	200	2	0.6	1.5	>99	
6	200	5	0.5	0.5	>99	

Table 3. Optimization of reaction conditions for the oxidation of **1a** catalyzed by $Rr12\alpha$ -HSDH.^[a]

^[a] Reaction conditions: 10 mL reaction mixture, containing 50–200 mM substrate **1a**, 1.5-fold equivalent pyruvate, 1–5 g L^{-1} each of lyophilized *E. coli* cells harboring *Rr*12 α -HSDH and *Ld*LDH genes respectively, 0.2–0.6 mM NAD⁺, and potassium phosphate buffer (100 mM, pH 8.0), was incubated at 30°C and 220 rpm. ^[b] Conversion was determined by reversed-phase high-performance liquid chromatography (RP-HPLC).

To evaluate the feasibility of utilizing $Rr12\alpha$ -HSDH for the biocatalytic process, the pyruvate/LDH system was chosen for the regeneration of cofactor NAD⁺. Compared with other NAD⁺ regeneration such O₂/NOX and□ systems as αketoglutarate/glutamate dehydrogenase system, the lactate dehydrogenase (LdLDH) identified from Lactobacillus delbrueckii subsp. bulgaricus LdLDH possesses higher specific activity (331 U mg⁻¹_{protein}).^[11a,17a] In practical industrial applications, the supply of O_2 could be very problematic,^[17b] and α -ketoglutarate is very expensive since it is used for medical treatments and as a chemical building block.^[17c] The pyruvate/LDH system utilized to regenerate cofactor NAD⁺ is more efficient and economical. Initial experiments were performed in a 10 mL reaction system with 50 mM 1a, 0.2 mM NAD⁺, 75 mM pyruvate, and 1 g L^{-1} each of lyophilized E. coli cells harboring Rr12a-HSDH and LdLDH genes, respectively. As a result, 1a was completely converted to 1b within 0.5 h (Table 3, entry 1). An increase of substrate loading to 100 mM without changing other conditions led to 82% conversion in 24 h (Table 3, entry 2). When 0.4 mM NAD⁺ was added to the reaction mixture, $Rr12\alpha$ -HSDH completely oxidized 100 mM 1a within 1 h (Table 3, entry 3). The substrate loading could be further raised to 200 mM, but the conversion was only 50% after 12 h (Table 3, entry 4). It was found that 99% conversion could be achieved in 1.5 h with

a load of 0.6 mM cofactor (Table 3, entry 5). For cost effectiveness, taking into account the internal cofactor content of lyophilized E. coli cells,^[18] the reaction was carried out using 5 g L⁻¹ biocatalyst and 0.5 mM of external NAD⁺. Accordingly, 200 mM substrate was transformed completely with 99% conversion within 0.5 h (Table 3, entry 6), indicating the great potential of $Rr12\alpha$ -HSDH as a biocatalyst for practical applications. In the 10-mL scale biotransformation, 50 mM CA could be rapidly converted to 12-oxo-CDCA. But when the substrate loading was gradually increased to 200 mM, both the concentrations of biocatalyst and cofactor had to be increased simultaneously to achieve complete oxidation of CA, indicating that the enzymes and cofactor might have been partially inactivated during the reaction. Further work will be required to elucidate the mechanisms that lead to the loss of enzyme activity and/or degradation of the cofactor.

Finally, in order to demonstrate the practical capability of $Rr12\alpha$ -HSDH for synthetic reactions, the oxidation of various 12α -hydroxysteroids were performed on a preparative scale (100 mL) under the optimized conditions. Consequently, 200 mM **1a** was completely oxidized (>99% conversion) into **1b** by $Rr12\alpha$ -HSDH within 1 h. After extraction and purification, **1b** was isolated in 85% yield (Table 4, entry 1), giving a STY of up to 1632 g L⁻¹ d⁻¹, which represents the highest reported productivity to the best of our knowledge (Table 5). For substrates 7-

oxo-deoxycholic acid (7-oxo-DCA, **2a**), ursocholic acid (UCA, **3a**), and **4a**, the corresponding products 7,12-dioxo-lithocholic acid (7,12-dioxo-LCA, **2b**), 12-oxoursodeoxycholic acid (12-oxo-UDCA, **3b**), and 12-oxo-lithocholic acid (12-oxo-LCA, **4b**) were isolated after 3.5–4.5 h of reaction in 75%, 81%, and 82% yields, respectively, albeit at a slightly lower substrate loading (150 mM) (Table 4, entries 2–4). Their respective STYs, 240, 333, and 295 g L⁻¹ d⁻¹, were obviously lower than that of **1b**. This might be attributed to the slightly lower k_{cat} of $Rr12\alpha$ -HSDH toward **2a** and **3a** and higher K_m toward **4a** than **1a**

(Table 2, entries 5–7). Following the same protocol, 200 mM substrates of taurocholic acid (TCA, 5a), glycocholic acid (GCA, 6a), taurodeoxycholic acid (TDCA, 7a), and glycodeoxycholic acid (GDCA, 8a) were totally converted within 1-2 h, affording the corresponding 12-oxo-hydroxysteroids with 99% conversion (Table 4, entries 5-8). These results demonstrated that Rr12a-HSDH is an efficient biocatalyst for the technically competitive and viable bioproduction of economically 12-oxohydroxysteroids, all acting as precursors for manufactory of therapeutic bile acids.

Table 4. Oxidation of hydroxysteroids catalyzed by *Rr*12α-HSDH.^[a]



^[a] Reaction conditions: 100 mL reaction mixture, containing 150–200 mM substrate, 1.5-fold equivalent pyruvate, 5 g L⁻¹ lyophilized *E. coli* cell harboring *Rr*12 α -HSDH gene, 5 g L⁻¹ lyophilized *E. coli* cell harboring *Ld*LDH gene, 0.5 mM NAD⁺, and potassium phosphate buffer (100 mM, pH 8.0), was incubated at 30°C and 220 rpm. ^[b] Conversion was determined by RP-HPLC. ^[c] Isolated yields.

Entry	Catalyst	1a [mM]	Time [h]	Conv. /Yield [%]	<i>E</i> factor ^[a]	Atom efficiency [%] ^[b]	STY $[g L^{-1} d^{-1}]$	Ref.
1	Chemical catalysts ^[c]	312.5	21	47.5	55.4	48.5	68	Hofmann ^[4]
2	12α -HSDH ^[d]	100	4	>99/88	1.8	64.3	240	Carrea et al. ^[19]
3	12a-HSDH ^[e]	100	24	92	6.1	87.1	37	Fossati et al. ^[20]
4	12a-HSDH ^[f]	12	12	98	3.3	81.9	9	Giovannini et al. ^[21]
5	$El12\alpha$ -HSDH ^[g]	10	24	>99	2.5	95.8	4	Tonin et al. ^[14]
6	$El12\alpha$ -HSDH ^[h]	10	4	>99	4.4	75.2	24	Tonin et al. ^[14]
7	Rr12a-HSDH ^[i]	200	1	>99/85	1.08	81.9	1632	This work

Table 5. Comparison of $Rr12\alpha$ -HSDH with other reported catalysts in synthesis of 1b from 1a.

^[a] The calculations did not take into account the waste generated for the preparation of the catalysts and the downstream processes. The detailed calculations of *E* factor and ^[b] atom efficiency are listed in Supporting Information. ^[c] The 400 mL reaction mixture contained 50 g **1a** (312.5 mM). ^[d] 12 α -HSDH was extracted from *Clostridium* group P. 70 mL reaction mixture contained 0.37 U/mL 12 α -HSDH and 0.06 mM NADP⁺. ^[e] Purified 12 α -HSDH from *Clostridium* sp. 10 mL reaction mixture contained 20 U/mL 12 α -HSDH and 0.1 mM NADP⁺. ^[f] Partially purified 12 α -HSDH from *calcoaceticus lwoffii*. 100 mL reaction mixture contained 0.028 U/mL 12 α -HSDH and 0.2 mM NAD⁺. ^[g] Purified *El*12 α -HSDH (recombinant *E. coli*/pET28 α -*El*12 α -HSDH) combined with NOX (75 mL reaction mixture contained 0.1 U/mL *El*12 α -HSDH and 0.5 mM NAD⁺), and ^[h] MDH (50 mL reaction mixture contained 0.1 U/mL *El*12 α -HSDH and 0.5 mM NAD⁺), respectively. ^[i] Lyophilized cells of recombinant *E. coli*/pET28 α -*Rr*12 α -HSDH. 100 mL reaction mixture contained 10 U/mL *Rr*12 α -HSDH and 0.5 mM NAD⁺.

The enzymatic synthesis of **1b** from **1a** mediated by the combination of Rr12a-HSDH and LDH showed an atom efficiency of 81.9% (Table 5), slightly lower than that obtained by the El12a-HSDH combined with NOX, but still acceptable compared with the chemical route. More importantly, as shown in Table 5, the *E* factor (environmental factor) for the production of **1b** catalyzed by Rr12a-HSDH was estimated to be 1.08, in contrast to those for other reported biocatalysts and 55.4 for the chemical route, indicating the significant environmental benefit of biocatalysts, especially Rr12a-HSDH.

In summary, a new and native NAD⁺-dependent Rr12a-HSDH with high catalytic efficiency was discovered from *Rhodococcus ruber* by the proposed structure-guided genome mining approach (SGGM). $Rr12\alpha$ -HSDH showed higher specific activity toward **1a** than other reported 12α -HSDHs. By stepwise optimization of reaction conditions, as much as 80 g L^{-1} (200 mM) of **1a** could be completely oxidized within 1 h, and efficiently converted to 1b, with an isolated yield of 85% and a STY of up to 1632 g L^{-1} d⁻¹. The biocatalytic process gave an atom efficiency of 81.9% and an E factor of 1.08. Furthermore, various 12a-hydroxysteroids were bio-oxidized to the corresponding 12-oxo-hydroxysteroids by $Rr12\alpha$ -HSDH at high substrate loads (up to 200 mM) and in good yields (up to 85%), indicating that E. coli/pET28a-Rr12a-HSDH can serve as an attractive biocatalyst for highly efficient and environmental scaffolds benign production of important of pharmaceutical bile acids. Further reactio pilot-scale engineering for and large-scale applications is ongoing in our laboratory.

Experimental Section

Structure-Guided Genome Mining of New 12α-HSDHs

To discover novel and native NAD⁺-dependent 12α -HSDHs, a structure-guided genome mining (SGGM) strategy was adopted. We performed a pBLAST search of the NCBI nonredundant database (http://www.ncbi.nlm.nih.gov) using the protein sequence of *El*12α-HSDH (NCBI accession no. WP 114518444.1) as the template, and carried out an alignment of the conserved cofactor-binding motifs. To ensure the diversity of sequences, 1000 candidate sequences with 20-60% similarities to the template sequence were selected. Based on the fact that the residues located on the phosphate/hydroxyl-binding loops would be responsible for NAD(H)/NADP(H) cofactor recognition, 28 putative 12α-HSDH sequences encoding a negatively charged amino acid residue (Asp) on the N-terminal of hydroxylbinding loop were chosen among the 1000 candidate genes and used for cloning, expression, and activity detection (Supporting Information).

Activity Assays and Kinetic Parameters

Enzyme activity was determined by spectrophotometric assay at 30°C measuring the oxidation of NAD(P)H or reduction of NAD(P)⁺ at 340 nm ($\varepsilon = 6.22 \text{ mM}^{-1} \text{ cm}^{-1}$). The reaction mixture (1 mL) was composed of 970 µL potassium phosphate buffer (KPi, 100 mM, pH 8.0), 10 µL of substrate stock solution (200 mM), 10 µL NAD(H) or NADP(H) solution (100 mM), and 10 µL purified enzyme with an appropriate concentration. One unit of the enzyme activity is defined as the amount of enzyme that catalyzes the reduction (or oxidation) of 1 µmol NAD(P)(H) per minute under the assay conditions. Kinetic parameters were determined at different substrate concentrations (0– 10 mM) and cofactor (NAD⁺ or NADP⁺) concentrations (0–1.0 mM). The resultant data were adjusted to a Michaelis-Menten model using Origin 8.6.

Preparative Synthesis of 12-Oxo-hydroxysteroids

The biotransformation was conducted at 30°C and 220 rpm for 24 h in a 100 mL solution containing 150-200 mM 12α -hydroxysteroids, 1.5-fold equivalent pyruvate, 5 g L⁻¹ each of lyophilized E. coli cells harboring Rr12a-HSDH and LdLDH genes respectively, 0.5 mM NAD⁺, and potassium phosphate buffer (KPi, 100 mM, pH 8.0). The conversion of substrates was determined by RP-HPLC (Supporting Information). After complete conversion, the solution was acidified with 1 M HCl till pH 3.0, and the precipitated product was filtered and washed with 50-100 mL of ethanol. Subsequently, the ethanol is evaporated, and the powder was dried, and purified by silica gel column chromatography eluting with a mixture of dichloromethane and methanol (20/1-10/1) to yield pure 12-oxo-hydroxysteroids. The product was characterized by NMR spectroscopy and high-resolution mass spectrometry (HRMS) (Supporting Information).

Acknowledgements

This work was financially supported by The National Key Research and Development Program of China (No. 2018YFC1706200), The National Natural Science Foundation of China (Nos. 21536004, 21871085, and 31500592), and the Fundamental Research Funds for the Central Universities (No. 22221818014). We are grateful to Dr. Yu-Cong Zheng and Dr. Chao Shou, both from East China University of Science and Technology, for their experimental assistance.

References

- [1] Y. Feng, K. Siu, N. Wang, K. M. Ng, S. W. Tsao, T. Nagamatsu, Y. Tong, J. Ethnobiol. Ethnomed. 2009, 5, 2.
- [2] T. Ikegami, Y. Matsuzaki, *Hepatol. Res.* 2008, 38, 123–131.
- [3] a) F. Tonin, I. W. C. E. Arends, *Beilstein J. Org. Chem.* **2018**, *14*, 470–483; b) T. Eggert, D. Bakonyi, W. Hummel, *J. Biotechnol.* **2014**, *191*, 11–21.
- [4] a) A. F. Hofmann, *Acta Chem. Scand.* 1963, *17*, 173–186; b) P. S. Dangate, C. L. Salunke, K. G. Akamanchi, *Steroids* 2011, *76*, 1397–1399.
- [5] a) S. Savino, E. E. Ferrandi, F. Forneris, S. Rovida, S. Riva, D. Monti, A. Mattevi, *Proteins Struct. Funct. Bioinf.* 2016, 84, 859–865. b) R. Wang, J. Wu, D. K. Jin, Y. Chen, Z. Lv, Q. Chen, Q. Miao, X. Huo, F.

Wang, Acta Crystallogr., Sect. F: Struct. Biol. Cryst. Commun. 2017, 73, 246–252.

- [6] D. Monti, E. E. Ferrandi, I. Zanellato, L. Hua, F. Polentini, G. Carrea, S. Riva, Adv. Synth. Catal. 2009, 351, 1303–1311.
- [7] a) J. E. Pawlowski, M. Huizinga, T. M. Penning, J. Biol. Chem. 1991, 266, 8820–8825; b) C. Grimm, E. Maser, E. Möbus, G. Klebe, K. Reuter, R. Ficner, J. Biol. Chem. 2000, 275, 41333–41339; c) S. M. Mythen, S. Devendran, C. Méndez-García, I. Cann, J. M. Ridlon, Appl. Environ. Microbiol. 2018, 84, e02475-17.
- [8] a) T. Yoshimoto, H. Higashi, A. Kanatani, X. S. Lin, H. Nagai, H. Oyama, K. Kurazono, D. Tsuru, J. Bacteriol. 1991, 173, 2173–2179; b) S. F. Baron, C. V. Franklund, P. B. Hylemon, J. Bacteriol. 1991, 173, 4558–4569; c) J. P. Coleman, L. L. Hudson, M. J. Adams, J. Bacteriol. 1994, 176, 4865–4874; d) M. J. Bennett, S. L. McKnight, J. P. Coleman, Curr. Microbiol. 2003, 47, 475–484; e) E. E. Ferrandi, G. M. Bertolesi, F. Polentini, A. Negri, S. Riva, D. Monti, Appl. Microbiol. Biotechnol. 2012, 95, 1221–1233; f) D. Bakonyi, W. Hummel, Enzyme Microb. Technol. 2017, 99, 16–24; g) F. Tonin, L. G. Otten, I. W. C. E. Arends, ChemSusChem 2019, 12, 3192–3203; h) X. Chen, Y. Cui, J. Feng, Y. Wang, X. Liu, Q. Wu, D. Zhu, Y. Ma, Adv. Synth. Catal. 2019, 361, 2497–2504.
- [9] a) L. Liu, A. Aigner, R. D. Schmid, *Appl. Microbiol. Biotechnol.* 2011, 90, 127–135; b) J. Y. Lee, H. Arai, Y. Nakamura, S. Fukiya, M. Wada, A. Yokota, *J. Lipid Res.* 2013, 54, 3062–3069; c) M. M. Zheng, R. F. Wang, C. X. Li, J. H. Xu, *Process Biochem.* 2015, 56, 598–604.
- [10] H. Doden, L. A. Sallarn, S. Devendran, L. Ly, G. Doden, S. L. Daniel, J. M. P. Alves, J. M. Ridlon, *Appl. Environ. Microbiol.* 2018, 84, e00235-18.
- [11] a) M. M. Zheng, K. C. Chen, R. F. Wang, H. Li, C. X. Li, J. H. Xu, J. Agric. Food. Chem. 2017, 65, 1178–1185; b) M. Braun, B. Sun, B. Anselment, D. Weuster-Botz, Appl. Microbiol. Biotechnol. 2012, 95, 1457–1468; c) D. Bakonyi, A. Wirtz, W. Hummel, Z. Naturforsch. 2012, 67, 1037–1044; d) L. Liu, M. Braun, G. Gebhardt, D. Weuster-Botz, R. Gross, R. D. Schmid, Appl. Microbiol. Biotechnol. 2013, 97, 633–639; e) B. Sun, C. Kantzow, S. Bresch, K. Castiglione, D. Weuster-Botz, Biotechnol. Bioeng. 2013, 110, 68–77; f) B. Sun, F. Hartl, K. Castiglione, D. Weuster-Botz, Progr. 2015, 31, 375–386.
- [12] M. Braun, H. Link, L. Liu, R. D. Schmid Weuster- Botz, D. *Biotechnol. Bioeng.* 2011, 108, 1307–1317.
- [13] a) C. You, R. Huang, X. L. Wei, Z. G. Zhu, Y. H. P. Zhang, Synth. Syst. Biotechnol. 2017, 2, 208–218; b) P. M. Thompson, N. J. Turner, ChemCatChem 2017, 9, 3833–3836; c) J. K. B. Cahn, C. A. Werlang, A. Baumschlager, S. Brinkmann-Chen, S. L. Mayo, F. H. Arnold, ACS Synth. Biol. 2017, 6, 326–333; d) A. M. Chánique, L. P. Parra, Front. Microbiol. 2018, 9, 194.
- [14] F. Tonin, N. Alvarenga, J. Z. Ye, I. W. C. E. Arends, U. Hanefeld, Adv. Synth. Catal. 2019, 361, 2448–2455.

- [15] Z. N. You, Q. Chen, S. C. Shi, M. M. Zheng, J. Pan, X. L. Qian, C. X. Li, J. H. Xu, ACS Catal. 2019, 9, 466–473.
- [16] a) N. S. Scrutton, A. Berry, R. N. Perham, *Nature* 1990, *343*, 38–43; b) A. Lerchner, A. Jarasch, W. Meining, A. Schiefner, A. Skerra, *Biotechnol. Bioeng.* 2013, *110*, 2803–2814.
- [17] a) S. Kochhar, N. Chuard, H. Hottinger, J. Biol. Chem. 1992, 267, 20298–20301. b) F. Sha, Y. Zheng, J. Chen, K. Chen, F. Cao, M. Yan, P. Ouyang, Green Chem. 2018, 20, 2382–2391. c) B. Beer, A. Pick, V. Sieber, Metab. Eng. 2017, 40, 5–13.
- [18] a) Q. Li, B. Huang, Q. He, J. Lu, X. Li, Z. Li, H. Wu, Q. Ye, *Bioresour. Bioprocess.* **2018**, *5*, 41. b) M. S.

Rahman, C. C. Xu, W. Qin, *Bioresour. Bioprocess.* **2018**, *5*, 3. c) K. Y. San, G. N. Bennett, S. J. Berríos-Rivera, Vadali, R. V.; Y. T. Yang, E. Horton, F. B. Rudolph, B. Sariyar, K. Blackwood, *Metab. Eng.* **2002**, *4*, 182–192.

- [19] G. Carrea, R. Bovara, R. Longhi, S. Riva, *Enzyme Microb. Technol.* **1985**, 7, 597–600.
- [20] E. Fossati, F. Polentini, G. Carrea, S. Riva, *Biotechnol. Bioeng.* 2006, 93, 1216–1220.
- [21] P. P. Giovannini, A. Grandini, D. Perrone, P. Pedrini, G. Fantin, M. Fogagnolo, *steroids* 2008, 73, 1385–1390.

Accepted Manuscrip

COMMUNICATION

Efficient Synthesis of 12-Oxochenodeoxycholic Acid Using a 12α-Hydroxysteroid Dehydrogenase from *Rhodococcus ruber*

Adv. Synth. Catal. Year, Volume, Page – Page

Shou-Cheng Shi,^{+a} Zhi-Neng You,^{+a} Ke Zhou,^a Qi Chen,^{a, b} Jiang Pan,^{a, b} Xiao-Long Qian,^c Jian-He Xu,^{a, b,*} and Chun-Xiu Li^{a, b,*}

