



Process Study on the Enzyme-Catalyzed Preparation of Key Chiral Intermediates for Saxagliptin

Shan-Shan Li¹ Zong-Qing Huang² Hao-Ju Hua² Jian-Guang Lu² Wen-Jie Zhao¹ Jun Feng^{1,2,*}

¹ State Key Laboratory of New Drug and Pharmaceutical Process, Shanghai Institute of Pharmaceutical Industry Co., Ltd., China State Institute of Pharmaceutical Industry, Shanghai, People's Republic of China

² Shanghai Duomirui Bio-Technology Co., Ltd., Shanghai, People's Republic of China

Address for correspondence Jun Feng, PhD, State Key Laboratory of New Drug and Pharmaceutical Process, Shanghai Institute of Pharmaceutical Industry, 285 Gebaini Road, Shanghai 201203, People's Republic of China (e-mail: Fengjdmr@163.com).

Pharmaceut Fronts 2022;4:e267–e274.

Abstract

Saxagliptin is a therapeutic drug for diabetes. The key synthesis process of the drug involves catalyzing 2-(3-hydroxy-1-adamantyl)-2-oxoacetic acid (A) into (S)-3-hydroxyadamantane glycine (B), during which enzymes phenylalanine dehydrogenase mutant from *Thermoactinomyces intermedius* (TiPDHm) and formate dehydrogenase (FDH) were most often used for biocatalysis. However, the process was limited due to difficulty in enzyme preparation and a low conversion rate. This study focuses on co-expression of TiPDHm and FDH in recombinant *Escherichia coli*, cell homogenate clarification, enzyme concentration as well as the optimized conditions of enzyme-catalyzed reaction. Our data showed that the wet weight density of bacteria reached 300 g/L, and the yields of TiPDHm and FDH were 7674.24 and 2042.52 U/L, respectively. The combination of ammonium formate and polyethyleneimine favors the clarification of the bacteria homogenate. The clarified enzyme solution obtained can be concentrated by ultrafiltration and directly used in a reductive amination reaction in a high concentration of keto acid A. The reaction time was only 12 hours and the conversion rate reached 95%. Therefore, this process could provide a reference for enzyme-catalyzed preparation of saxagliptin on an industrial scale.

Keywords

- ▶ saxagliptin
- ▶ phenylalanine dehydrogenase
- ▶ formate dehydrogenase
- ▶ clarification
- ▶ biocatalysis
- ▶ reductive amination

Introduction

As a potent dipeptidyl peptidase IV inhibitor, saxagliptin is developed by Bristol Myers Squibb and AstraZeneca, and has shown a great success in treating type II diabetes in adults.^{1,2} Currently, there are many key chiral intermediates in the synthesis of saxagliptin, and approaches involved chemical resolution, asymmetric catalytic synthesis, and biocatalytic semi-synthesis.^{3–6} The latter is environmentally friendly, efficient, and represents the most advanced method. In 2007, Hanson R et al reported co-expression of PDH mutant from *Thermoactinomyces intermedius* (TiPDHm) and the FDH

gene sequence from *Pichia pastoris* (PpFDH) in *Escherichia coli*, which was used to prepare an amino acid intermediate for saxagliptin, namely (S)-3-hydroxyadamantylglycine (C).⁵ As illustrated in ▶Fig. 1, the approach mainly solves the synthesis of the key chiral intermediate of saxagliptin (C), which is prepared by the reductive amination of 2-(3-hydroxy-1-adamantyl)-2-oxoacetic acid (A) with PDH mutant from TiPDHm.⁷ TiPDHm is a hexameric protein and belongs to the class of dehydrogenases. TiPDHm participates in the reductive amination reaction, in which the reduced coenzyme I (nicotinamide adenine dinucleotide, NADH) is required.⁸ Formate dehydrogenase (FDH) is a mainly

received

May 22, 2022

accepted

November 15, 2022

DOI <https://doi.org/>

10.1055/s-0042-1759851.

ISSN 2628-5088.

© 2022. The Author(s).

This is an open access article published by Thieme under the terms of the Creative Commons Attribution License, permitting unrestricted use, distribution, and reproduction so long as the original work is properly cited. (<https://creativecommons.org/licenses/by/4.0/>)

Georg Thieme Verlag KG, Rüdigerstraße 14, 70469 Stuttgart, Germany

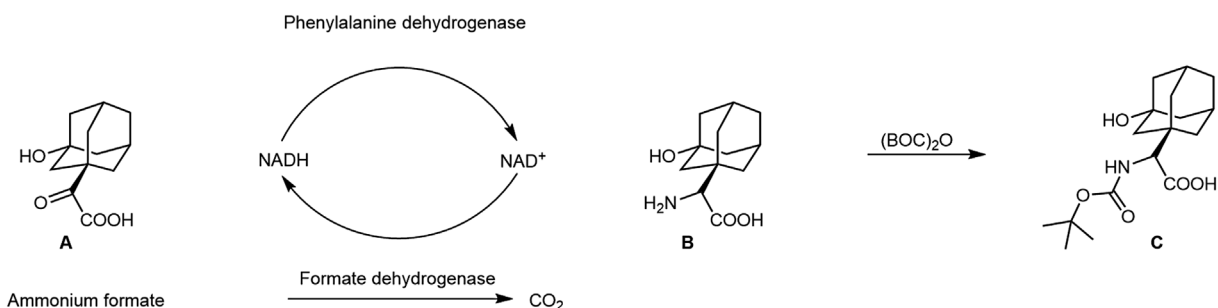


Fig. 1 *Ti*PDHm and *Pp*FDH catalyzed the preparation of (S)-3-hydroxy-1-adamantyl-D-glycine. The image was cited from a reported study.⁵

NAD⁺-dependent enzyme, and could reconvert the oxidized coenzyme to a reduced form.^{9,10} The use of FDH may be associated with the most productive manner to provide NADH in *Ti*PDHm-mediated reductive amination. However, the preparation of enzymes also faces many technical challenges, including higher demands on the yield, activity, and low process costs.

Generation of recombinant enzymes from engineered bacterium *E. coli*, followed by extraction and isolation, is the most common process in industrial production. However, during the extraction process, due to the influence of cell debris, liposomes, nucleic acids, and host cell proteins, the homogenate solution tends to contain considerable turbidity and viscosity, which has significant impact on subsequent purification methods such as ion exchange and ultrafiltration concentration. In addition, the purification methods for biological enzymes are more restricted than other proteins, as they are required to maintain enzymatic activity.

The aim of this study was to improve recombinant expression and pretreatment, and to enhance conversion efficiency, *Ti*PDHm and *Pp*FDH were co-expressed in *E. coli* according to a reported study.⁵ Then high-density fermentation process, clarification method, reaction conditions, and other aspects are optimized to improve the catalytic efficiency. The preparation process provides a reference for producing biological enzymes and saxagliptin intermediates on an industrial scale.

Materials and Methods

Construction and Verification

*Ti*PDHm and *Pp*FDH were translated into DNA sequences according to codon bias of *E. coli* BL21 (DE3). The GGAG-GAAAAAAA sequence was inserted between *Pp*FDH and *Ti*PDHm, thus constituting the target gene sequence *Pp*FDH-*Ti*PDHm and expressed under the control of the same promoter. Restriction sites *Nco*I (CCATGG) and *Eco*RI (GAATTC) were added to the 5' and 3' ends of the sequence. The sequence was then cloned into *Nco*I-*Eco*RI sites of the expression vector pET28a, and the plasmid pET28a-*Pp*FDH-*Ti*PDHm was generated finally. The plasmid was transferred into *E. coli* BL21(DE3), and the recombinant strain *E. coli* BL21(DE3)/pET28a-*Pp*FDH-*Ti*PDHm, namely DMR532, was obtained.

After expansion in Luria-Bertani (LB) media, 1% inoculum was added to 30 mL of LB shake flask medium, and incubated

at 37°C and 220 rpm for 6 hours. The culture temperature was lowered to 25°C. Cells were induced by adding 15 μ L of isopropyl-D-1-thiogalactopyranoside (IPTG, Sangon Biotech, Shanghai) at a final concentration of 0.1 mmol/L, and then cultured for 18 hours. The fermentation broth (4 mL) was centrifuged at 12,000 \times g for 5 minutes to obtain wet cells, which were resuspended in 1 mL of Tris-HCl (25 mmol/L, pH = 8.0), then fragmented by ultrasonication, and centrifuged at 12,000 \times g for 10 minutes. The supernatant was verified by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). Materials for electrophoresis were obtained from commercial kits (Shanghai Epizyme Biotech Co., Ltd.). The samples were denatured and added to the gels for separation. After that, the gels were stained with Coomassie brilliant blue R250 and decolorized with acetic acid solution until the protein bands were visualized.

Enzyme Activities Assay

Since NADH has a maximum absorption at 340 nm,¹¹ the absorbance values of different molar concentrations of NADH at 340 nm were measured at 30°C using the enzyme-labeled Assay instrument (SpectraMax I3X Microplate reader, Molecular Devices Company, Austria), and a concentration-OD₃₄₀ standard curve was plotted. The activity of *Ti*PDHm was measured in a medium containing NADH (4 mmol/L), sodium phenylpyruvate (5 mmol/L), and ammonium chloride buffer (0.75 mmol/L), with pH = 9.0 adjusted with ammonium hydroxide. The decrease in absorption values was monitored. The activity assay of *Pp*FDH was measured in a medium containing oxidized coenzyme I (NAD⁺, 4 mmol/L), ammonium formate (20 mmol/L), and glycine buffer (50 mmol/L), with pH = 10.4 adjusted with potassium hydroxide.¹¹ The increase in absorption values was monitored. "Enzyme activity unit (U)" was defined as the amount of enzyme required to consume or generate 1 μ mol/L NADH per minute in the buffer system at a temperature of 30°C.

Analysis and Identification of Compounds A, B, and C

High-performance liquid chromatography (HPLC) was used to monitor peak areas of keto acid **A** (Tianjin Minxiang Biomedical Co., Tianjin) and amino acid **B** using an evaporative light scattering detector (ELSD; Agilent 1260 HPLC-ELSD system, Agilent Technologies, United States). There were some difficulties in making a standard curve for **A** and **B** by the ELSD-HPLC method. Therefore, the method of peak

area normalization was used to define the efficiency of the reaction. The conversion of the product (**B**) was calculated by Equation (1).

$$\text{Conversion efficiency (\%)} = \frac{\text{Peak area of B}}{\text{Total peak areas of A and B}} \times 100 \quad (1)$$

HPLC was performed on a Kromasil 100–3.5–C18 (4.6 × 150 mm) column at 40°C. UV absorption at 214 nm was recorded. Mobile phases A and B were 0.1% formic acid solution in water and 90% methanol solution, respectively. ELSD parameters were set as follows: the temperature for both evaporator and nebulizer were 35°C; the gas flow rate was 1.6 standard liter per minute. Other parameters were kept at their default values. Peak time for compound **B** is 12 minutes and for compound **A** is 16 to 17 minutes.

The chiral column CHIRALPAK MA(+) (0.46 cm I.D. × 5 cm L × 3 μm) was used to identify **B** and **C** with a mobile phase of 2 mmol/L CuSO₄. The peak time of **B** was 14.1 minutes. With trifluoro acetic acid treatment, the BOC protecting group of the standard intermediate **C** (Tianjin Minxiang Biomedical Co., Tianjin) was removed to obtain standard **B**.

High-Density Fermentation at a 300 L Scale

The fermentation process of DMR532 strain was first explored and optimized using a 5 L fermenter. A scale-up production was performed at a 300 L fermenter. Seed culture of the DMR532 strain, which had been activated by the LB medium, was mixed well and inoculated at 1% (v/v) into a sterilized fermentation medium (2 g glucose, 15 g yeast extract, 17.2 g Na₂HPO₄ 12H₂O, 3 g KH₂PO₄, 0.5 g NaCl, 3 g (NH₄)₂SO₄, 1 g KCl, 0.5 g MgSO₄, 0.011 g CaCl₂, glycerol 20 g dissolved in 1 L of deionized water) in a volume of 200 L. The incubation temperature was 37°C. During incubation, dissolved oxygen was controlled at 30 to 50% and pH was maintained at 6.9 to 7.0. The feeding medium was 75% glycerol, 2.25% yeast extract, and 1.5% anhydrous magnesium sulfate (m/v). When the glycerol was exhausted, the fermentation medium was added at a flow rate of 50 mL/h. When the OD₆₀₀ reached 80 to 90, the culture temperature was gradually reduced to 25°C, then, IPTG at a final concentration of 0.1 mmol/L was also added for induction. After 12 hours, the fermentation broth was processed by disc centrifuge and the solid content was controlled at 50 to 70%. Wet cells from high-density fermentations were resuspended using Tris-HCl buffer (25 mmol/L, pH 8.0), wet cells: buffer (m:v, 1:10), homogenized at high pressure (750 bar, three times), and then centrifuged at 12,000 × g for 20 minutes to remove cell debris and other insoluble material to obtain a homogenate of DMR532.

Exploration and Optimization of Clarification Processes

To each 100 mL of DMR532 homogenate was added 0.05 to 0.2% chitosan solution, 0.5 to 1.5 mol/L of (NH₄)₂SO₄, as well as 13% diatomite plus 0.08% polyethyleneimine (PEI) solution, separately. The mixture was stirred for 60 minutes at room temperature and the supernatant was obtained by

centrifugation at 12,000 × g for 20 minutes. In the final group of homogenate, 0.6 mol/L of ammonium formate was added. The mixture was heated at 40°C for 60 minutes and centrifuged. To the supernatant was added PEI (Sigma-Aldrich, Shanghai, China) at a final concentration of 0.06%, stirred at room temperature for 30 minutes, and centrifuged at 12,000 × g for 10 minutes. Then, a clarified enzyme solution was obtained. The activity of *Ti*PDHm in the solution was detected and the supernatant was graded for turbidity according to the first method of clarity check in Pharmacopoeia of the People's Republic of China (ChP), which was a visual method and divided into five grades (0.5, 1, 2, 3, and 4). Samples with a judged grade ≤ 2 were considered as clarified solutions, where insoluble particles are invisible and will not affect the microfiltration or ultrafiltration.

Effects of different salt solutions ((NH₄)₂SO₄, NH₄H₂PO₄, (NH₄)₂CO₃, and ammonium acetate), different experimental temperatures (5–60°C), and different concentrations of ammonium formate (0.1–1.2 mol/L) on clarification of the homogenate were further explored according to the steps described above. After an optimized clarification process, the homogenate was concentrated to one-fifth of the volume using an ultrafiltration membrane with a molecular weight cutoff of 100 kDa.

Reaction Condition Optimization

Reaction mixture **1** contained keto acid **A** (0.1 mol/L), ammonium formate (0.6 mol/L), NAD (1 mmol/L), and DTT (0.1 mmol/L). pH was adjusted with 10 mol/L NaOH. The reaction volume was 2 mL per group (1 mL reaction mixture and 1 mL clarified solution). The reaction was performed for 12 hours. HPLC was used for analysis. Furthermore, reaction conditions including pH (6–8), temperature (20–60°C), as well as **A** concentration were also explored, using a concentrated clarified solution. Reaction mixture **2** contained: keto acid **A** (0.1–0.5 mol/L), ammonium formate (0.9 mol/L), NAD (1 mmol/L), and DTT (0.1 mmol/L). pH was adjusted with 10 mol/L NaOH. The reaction volume was 2 mL per group (1 mL reaction mixture and 1 mL concentrated clarified solution), and samples were taken for analysis at 8 and 12 hours, respectively.

Synthesis of Saxagliptin Intermediate

Considering the reaction efficiency and cost control, 0.4 mol/L of substrate was chosen for the following study. To 20 to 40 mL of double-distilled water was added **A** (17.92 g) and ammonium formate (11.35 g), adjusting pH = 9.2 with 10 mol/L NaOH. Then, NAD 0.133 g, DTT 0.03 g, and 100 mL of the concentrated clarified solution (containing 11435.34 U/L of *Ti*PDH) were added. The reaction volume was fixed to 200 mL with double-distilled water. The pH was adjusted to 9.0 at room temperature and then controlled it at 49 to 51°C. During the reaction process, the pH was regularly monitored and maintained between 8.9 and 9.1. At the end of the reaction, the mixture was heated to 70 to 90°C for 30 minutes,⁷ cooled to room temperature, and centrifuged at 12,000 × g for 15 minutes to obtain the supernatant containing product **B**, which had a purity over 90%.

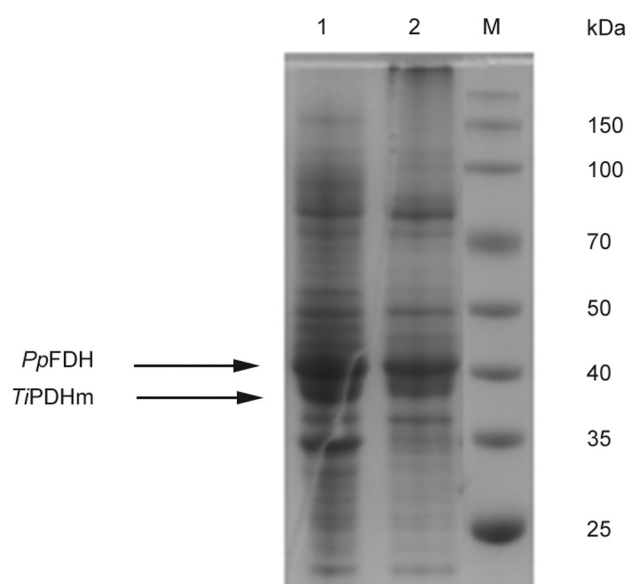


Fig. 2 SDS-PAGE analysis of fermentation expression of DMR532. Lane 1: cell homogenate of DMR532. Lane 2: clarified solution of DMR532. SDS-PAGE, sodium dodecyl sulphate-polyacrylamide gel electrophoresis.

Results

Identification of Co-expressed Enzymes and High-Density Fermentation

SDS-PAGE analysis showed that the relative molecular weight of the mixed homogenate of *TiPDHm* and *PpFDH* was 40 kDa, which was consistent with the theoretical value (►Fig. 2). The protein band of *PpFDH* was located above the *TiPDHm*. Furthermore, activity of *PpFDH* and *TiPDHm* was 63.65 and 214.16 U/L respectively in the fermentation broth from shake flasks (►Table 1).

Zhao et al reported that the maximal cell density (OD_{600}) reached 103.87 with the dry cell weight (DCW) of 52.32 g/L. However, in this study, the OD_{600} reached 186.77, which may be associated with a much higher DCW than the reported result.¹² High-density fermentations at the 5 L and 300 L scales yielded 301.93 and 296.60 g/L of wet cells, respectively (►Table 1), both close to 30% of total weight, indicating that this medium is suitable for DMR532 growth. Moreover, 300 L scale fermentations reached a final enzyme activity of 2,042.52 U/L (*PpFDH*) and 7,674.24 U/L (*TiPDHm*), respectively, which are approximately 32- and 35-fold increase compared with the shake flasks (LB). The fermentation time

was only 24 hours, much shorter than the reported study (36.5–40 hours).^{5,13} Given above, the fermentation process is stable and reproducible and meets the requirements for scale-up production.

Exploration of the Clarification Process for Homogenate

Clarification Methods for Screening

Our preliminary research showed that FDH easily catalyzes the coenzyme NADH cycle, and *TiPDH* is a key enzyme that restricts the conversion rate of reductive amination. Thus, a higher concentration of the enzyme may be associated with higher conversion efficiency. Considering the low concentration of the enzyme in the homogenate, the enzyme needs to be concentrated. Ultrafiltration technology is widely used for the separation and concentration of biomacromolecules due to its mildness and efficient characteristics. But the premise is that the feed liquid should have a certain degree of clarity to avoid the rapid decline of the processing speed caused by the clogging of the membrane pores. In our process, the crude enzyme was used to catalyze the reaction directly, which avoids the fine purification of the crude enzyme solution and makes a simple preparation of the enzymes. Therefore, it is necessary to explore clarification methods of the turbid homogenate to facilitate the ultrafiltration, while removing impurities as much as possible and retaining the catalytic activity of the *TiPDH* to the greatest extent.

As shown in ►Table 2, the combination of ammonium formate and PEI gave the best effect, which not only achieved the clarification effect of the homogenate, but also retained 95.30% activity of *TiPDHm*. The centrifuged precipitate, treated with ammonium formate, was viscous, indicating that the salt had a better removal effect on viscous impurities such as cell debris in a warm bath. Further use of PEI removed negatively charged impurities, and finally yielded a clarified enzyme solution. In the reductive amination experiments, ammonium formate was also a reaction substrate, which avoids additional introduction outside the reaction system that may affect the conversion rate.

Optimization of the Clarification Process

As shown in ►Fig. 3, the better clarifying categories were ammonium formate and ammonium acetate. The optimum concentration of ammonium formate was 0.6 to 0.9 mol/L and the temperature was within 40 to 50°C. With an

Table 1 Results of fermentation expression and activity assays of DMR532

Fermentation methods	OD_{600}	Wet cells ^a (g/L)	Activity of <i>PpFDH</i> ^b (U/L)	Activity of <i>TiPDHm</i> ^c (U/L)
Shake Flask	9.33	10.61	63.65	214.16
5 L Fermenter	197.65	301.93	2,181.30	7,753.56
300 L Fermenter	186.77	296.60	2,042.52	7,674.24

^aThe content of wet cells per liter of fermentation broth.

^b*PpFDH* activity per liter of fermentation broth.

^c*TiPDHm* activity per liter of fermentation broth.

Table 2 Effect of different treatments on clarification of DMR532 crude enzyme solution

Processing	Turbidity ^a	Activity recovery ^b
0.05% chitosan	>4	80.21%
0.1% chitosan	>4	75.22%
0.2% chitosan	>4	20.38%
0.5 mol/L (NH ₄) ₂ SO ₄	>4	96.33%
1 mol/L (NH ₄) ₂ SO ₄	>4	69.59%
1.5 mol/L (NH ₄) ₂ SO ₄	>4	1.47%
13% diatomaceous earth + 0.08% PEI	>4	57.85%
0.6 mol/L ammonium formate + 0.06% PEI	= 2	95.30%

Abbreviation: PEI, polyethyleneimine.

^aBased on the first method of clarity check in ChP.

^bActivity ratio of *Ti*PDHm in treatment solution to homogenate.

economical point in mind, DMR532 homogenate was treated with 0.6 mol/L ammonium formate at 40°C, and concentrated to one-fifth volume by ultrafiltration. Our data showed that both *Ti*PDHm and *Pp*FDH maintained high yields during the processes of clarification and ultrafiltration (► **Table 3**). However, the molecular weight of the dimeric form of *Pp*FDH is similar to that retained by the ultrafiltration membrane, resulting in a small amount of permeation during ultrafiltration, with a loss of activity of *Pp*FDH approximately 10% after ultrafiltration. As shown in ► **Fig. 2**, the clarified solution (lane 2) has a lighter *Ti*PDHm band by comparison to the homogenate (lane 1), and bands with molecular weight >150 kDa appeared. It is presumed that a high concentration of ammonium formate promoted the formation of the *Ti*PDHm molecule in a polymeric form. We directly used the enzyme solution containing high concentrations of *Ti*PDHm and *Pp*FDH, obtained from the above clarification and ultrafiltration treatment, to catalyze the formation of amino acid **B** from keto acid **A**.

*Ti*PDHm- and *Pp*FDH-Mediated Reductive Amination Reaction

Reaction Condition Optimization

In this study, a lower concentration of **A** (0.1 mol/L) was used to avoid substrate inhibition according to a reported study.¹⁴ Results from pH screening (► **Fig. 4A**) showed that when pH = 8 to 10, a high conversion efficiency was achieved with the maximum being seen at pH = 9.0. Results from temperature screening (► **Fig. 4B**) showed that the catalytic activity of the enzymes is significantly at 40 to 50°C with the highest conversion being at 50°C. However, the enzyme was gradually deactivated above 50°C, leading to a low conversion of the reaction. Thus, pH = 9.0 and a reaction temperature of 50°C were chosen for the following study. Results from substrate concentration screening (► **Fig. 4C**) suggested that the conversion efficiency was gradually inhibited with an increase in substrate concentration. When substrate concentration was within 0.3 mol/L, more than 95% of the conversion could be

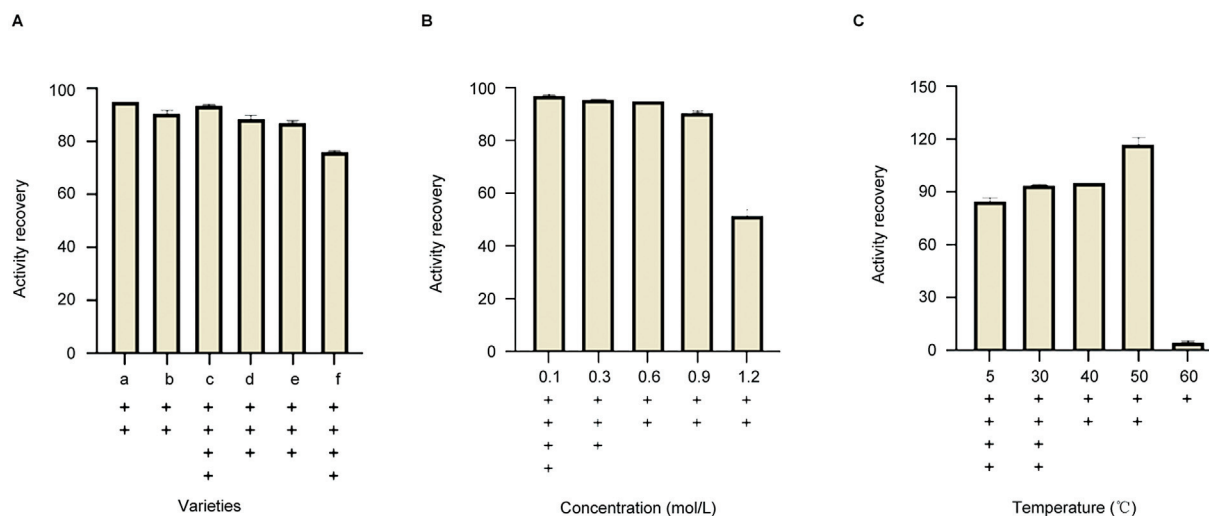


Fig. 3 Optimization of treatment method of DMR532 homogenizing solution using ammonium formate. (A) Different neutral salts: a = ammonium formate; b = ammonium acetate; c = ammonium citrate; d = (NH₄)₂SO₄; e = NH₄H₂PO₄; f = (NH₄)₂CO₃. (B) Different concentrations of ammonium formate. (C) Different experiment temperatures. The “+” symbol means turbidity level with “+” for 1, “++” for 2, “+++” for 3, and “++++” for greater than or equal to 4.

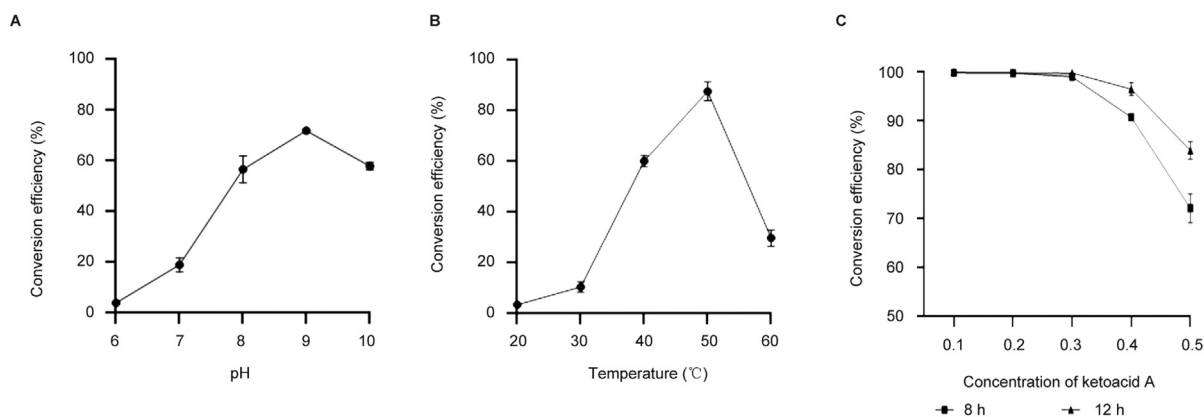


Fig. 4 Optimization of reaction conditions using (A) different pH; (B) different temperatures; and (C) different concentrations of compound A.

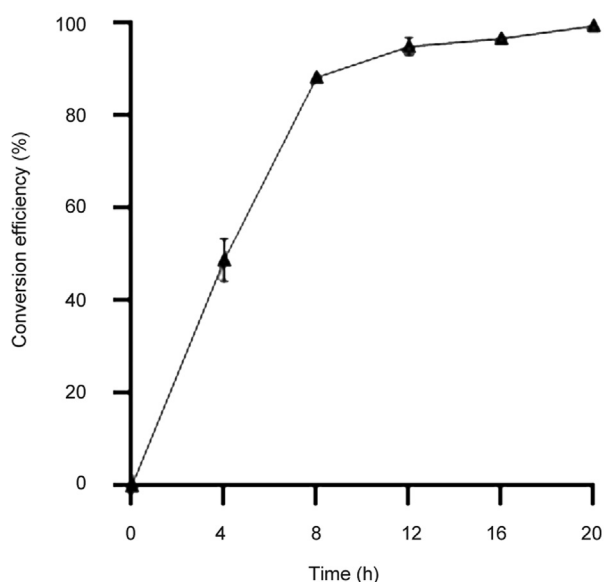


Fig. 5 Conversion efficiency of reductive amination reaction with a 1:1 ratio of concentrated clarified solution to substrate.

completed in 8 hours. When the concentration was increased to 0.4 mol/L, it needs to take 12 hours to complete 95% of the conversion. In Basch et al reports, the reaction time of catalyzing **A** (0.45 mol/L) into **B** was approximately 42 hours⁷; how-

ever, in the present study, under the optimized reaction conditions, the reaction time is greatly reduced.

Efficient Preparation of Saxagliptin Intermediate Materials

As shown in ▶**Fig. 5**, when a concentrated enzyme solution was used to catalyze the generation of **B** from **A** (0.4 mol/L), the conversion rate could reach 95% at 12 hours. At 20 hours, a complete conversion was achieved. In fact, during industrial preparation, the remaining 3 to 5% may be discarded to control reaction time and save production costs. Therefore, it is feasible to achieve efficient conversion of chiral amino acids by concentrating enzymes.

The prepared **B** was subjected to HPLC (▶**Fig. 6**) and chiral analysis with the standard control. Our data showed that peak positions of the sample and the control were consistent. Chiral analysis showed an enantiomeric excess value of the sample >99.9%. Liquid chromatography-tandem mass spectrometry showed that the molecular weight of **B** was in agreement with the theory, indicating that the amino acid **B** prepared by biocatalysis was correct in structure.

Discussion

Biocatalytic synthesis of chiral compounds is identified of mild reaction conditions, high stereoselectivity, and high

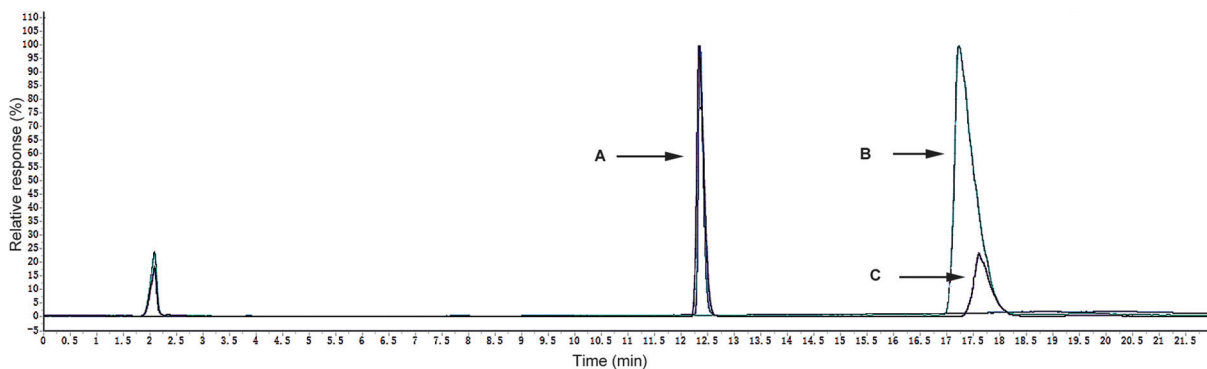


Fig. 6 HPLC analysis of compound **B**. Line A: a standard curve of compound **B**; line B: curve of reductive amination reaction at 0 hour; line C: curve of reductive amination reaction at 8 hours. HPLC, high-performance liquid chromatography.

Table 3 Enzyme activity changes after clarification and concentration

	Turbidity ^a	Activity (F) ^b (U/L)	Activity (P) ^c (U/L)	Activity (F) recovery ^d	Activity (P) recovery ^e
Clarified solution	2	701.22	2,446.74	96.37%	95.30%
Concentrated solution	3	3,146.37	11,435.34	89.60%	93.27%

^aBased on the first method of clarity check in ChP.

^b*Pp*FDH concentration in solution.

^c*Ti*PDHm concentration in solution.

^dActivity ratio of *Pp*FDH in clarified solution or concentrated solution to homogenate.

^eActivity ratio of *Ti*PDHm in clarified solution or concentrated solution to homogenate.

specificity.¹⁵ In this study, a double-gene co-expression strategy was used to introduce the protease genes, *Ti*PDHm and *Pp*FDH, into *E. coli* for expression. Then, high-density fermentation culture was investigated. *Ti*PDHm was used to catalyze the synthesis of key intermediate of saxagliptin (compound **B**). *Pp*FDH was used for regeneration of NAD(P)H. The co-expression of the recombinant organisms solved the complicated preparation problem of multi-enzymes, and to some extent had the effect of cooperative expression, which is verified on the 300 L fermentation scale.

*Ti*PDHm is a hexameric enzyme. Compared with monomers, oligomerization confers structural stability and kinetic changes to the protein, leading to improved catalytic efficiency of the enzyme.^{16,17} Protein–salt interaction regulates protein solubility and stability, and ion concentration influences protein hydrophobicity.¹⁸ In the present study, ammonium formate was found to have the ability to clarify the solution, and this may be due to the fact that ammonium formate, as an organic ammonium salt, could not only stabilize the structure of the oligomeric enzyme, but also remove other impurities. The clarifying enzyme solution can be directly used to catalyze the reaction, or purified by hydrophobic and affinity chromatography, with a wide range of applications.

Increasing the concentration of enzyme per unit volume is important to improve the catalytic efficiency of the enzyme. An aqueous two-phase system (ATPS) technique was used by Zhao et al.¹² to concentrate and purify PDH, which was achieved in the middle layer with the insoluble product and may bring difficulty for subsequent application. Although ATPS technology is mature and economical, the operational process is complicated, leading to instability in industrial production. Ultrafiltration may be an alternative, which requires good clarity of the enzyme solution. The homogenate clarification method developed in this study allows for an unrestricted process of ultrafiltration concentration and the clarified solution retains more than 90% of the enzyme activity. The concentrated enzyme solution catalyzes high concentration **A** (0.4 mol/L) into **B** within only 20 hours, which performs the functional advantages of the enzyme for the synthesis of chiral compounds.

Conclusion

The preparation process of enzyme solution described in this article is different from the previous method. The

enzyme solution can be used for catalytic reactions without purification. The conversion efficiency is higher. The clarification is the key process, which allows a low loss of enzyme activity, simple operation and easy access to raw materials, and is suitable for scale-up production. The study provides a sufficient and feasible basis for industrial production of the key intermediate of saxagliptin with the application of *Ti*PDHm.

Supplementary Information

The results of liquid chromatography–tandem mass spectrometry (LC-MS) analysis and chiral analysis of product **B** are shown in the Supporting Information (► **Supplementary Figs. S1 and S2** [online only]).

Conflict of Interest

None declared.

References

- Thareja S, Aggarwal S, Malla P, Haksar D, Bhardwaj TR, Kumar M. Saxagliptin: a new drug for the treatment of type 2 diabetes. *Mini Rev Med Chem* 2010;10(08):759–765
- Gu W, Liang L, Wang S, et al; SUNSHINE Study Group. Efficacy and safety of saxagliptin monotherapy or added to metformin in Chinese patients with type 2 diabetes mellitus: results from the 24-week, post-marketing SUNSHINE study. *J Diabetes* 2016;8(06):809–815
- Chen Y, Wang A, Tao Z, Deng Y, Hu X. A facile synthesis of saxagliptin intermediate N-Boc-3-hydroxyadamantylglycine. *Res Chem Intermed* 2015;41(07):4113–4121
- Liao Q, Jiang L, Li C, et al. An efficient and practical method for the synthesis of saxagliptin intermediate 2-(3-hydroxy-1-adamantane)-2-oxoacetic acid and its optimization. *J Chem* 2019;2019:5375670
- Hanson RL, Goldberg SL, Brzozowski DB, et al. Preparation of an amino acid intermediate for the dipeptidyl peptidase IV inhibitor, saxagliptin, using a modified phenylalanine dehydrogenase. *Adv Synth Catal* 2007;349(8–9):1369–1378
- Chen GS, Dong JZ, Qin LG, Li Q. A method for the preparation of saxagliptin intermediates. CN Patent 202010276487.1. April, 2020
- Basch J, Franceschini T, Liu SW, Chiang SJ. Genetically stable plasmid expressing and enzymes. U.S. Patent 8158394. April, 2012
- Ohshima T, Takada H, Yoshimura T, Esaki N, Soda K. Distribution, purification, and characterization of thermostable phenylalanine dehydrogenase from thermophilic actinomycetes. *J Bacteriol* 1991;173(13):3943–3948
- Jormakka M, Byrne B, Iwata S. Formate dehydrogenase—a versatile enzyme in changing environments. *Curr Opin Struct Biol* 2003;13(04):418–423

- 10 Schirwitz K, Schmidt A, Lamzin VS. High-resolution structures of formate dehydrogenase from *Candida boidinii*. *Protein Sci* 2007; 16(06):1146–1156
- 11 Wu T, Mu X, Xue Y, Xu Y, Nie Y. Structure-guided steric hindrance engineering of *Bacillus badius* phenylalanine dehydrogenase for efficient L-homophenylalanine synthesis. *Biotechnol Biofuels* 2021;14(01):207
- 12 Zhao C, Wang L, Li D, et al. High-cell-density fermentation of *Escherichia coli* for expression of a recombinant phenylalanine dehydrogenase mutant and its purification. *J Chem Technol Biotechnol* 2021;96(01):199–206
- 13 Steinmann B, Christmann A, Heiseler T, Fritz J, Kolmar H. In vivo enzyme immobilization by inclusion body display. *Appl Environ Microbiol* 2010;76(16):5563–5569
- 14 Zhou F, Mu X, Nie Y, Xu Y. Enhanced catalytic efficiency and coenzyme affinity of leucine dehydrogenase by comprehensive screening strategy for L-tert-leucine synthesis. *Appl Microbiol Biotechnol* 2021;105(09):3625–3634
- 15 Zheng GW, Xu JH. New opportunities for biocatalysis: driving the synthesis of chiral chemicals. *Curr Opin Biotechnol* 2011;22(06):784–792
- 16 Fatmi MQ, Chang CE. The role of oligomerization and cooperative regulation in protein function: the case of tryptophan synthase. *PLOS Comput Biol* 2010;6(11):e1000994
- 17 Mishra SK, Sankar K, Jernigan RL. Altered dynamics upon oligomerization corresponds to key functional sites. *Proteins* 2017;85(08):1422–1434
- 18 Arosio P, Jaquet B, Wu H, Morbidelli M. On the role of salt type and concentration on the stability behavior of a monoclonal antibody solution. *Biophys Chem* 2012;168–169:19–27