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Activation and Stabilization of Engineered Amine Dehydrogenase by Fatty Acids for Bioprocess Intensification of Asymmetric Reductive Amination

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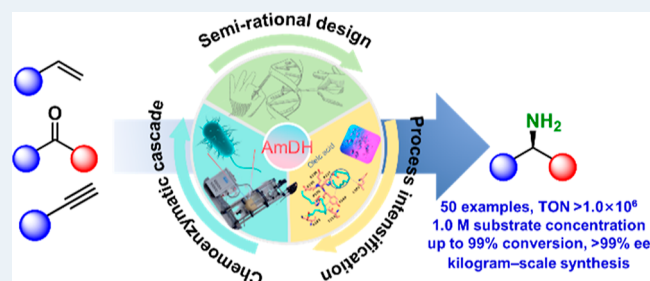
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ABSTRACT: In this study, we present a significant advancement in the field of enzymatic asymmetric reductive amination (ARA) of ketones, a pivotal reaction for chiral amine synthesis. Through a combination of semirational enzyme design and bioprocess development, we achieve the dual activation and stabilization of amine dehydrogenase (AmDH) to meet industrial demands. The engineered AmDH exhibits remarkable catalytic efficiency (turnover number, TON >1,000,000) and exceptional stability (half-life >7 days at 50 °C), with a broadened substrate scope including various aryl alkyl ketones and fatty ketones. Leveraging biobased oleic acid as an activator and stabilizer, we achieved kilogram-scale synthesis of chiral amines. Furthermore, the integration of AmDH with chemical catalysts in chemoenzymatic cascades has enabled the synthesis of a wide array of pharmaceutically relevant amines from diverse substrates, demonstrating the enzyme's versatility and potential to transform synthetic chemistry.

KEYWORDS: amine dehydrogenase, bioprocess intensification, enzyme engineering, reductive amination, chiral amines



INTRODUCTION

Chiral amines are omnipresent structural motifs and building blocks in pharmaceuticals, natural products, and bioactive molecules.^{1,2} Consequently, it is not surprising that a diverse array of chemical synthetic strategies for chiral amines has been developed over the past decades, encompassing asymmetric hydrogenation of enamines and imines,^{3,4} hydroalkylation of enamines,^{5–7} *N*-alkylation of aliphatic amines,⁸ amination of C–H bonds,^{9,10} carbene insertion into N–H bonds of aliphatic amines,¹¹ hydroamination of alkenes,^{12–14} and notably, the asymmetric reductive amination reaction (ARA) of prochiral ketones.^{15–18} These chemical strategies, although effective, commonly require expensive transition metals and synthetically laborious chiral ligands, rendering commercial manufacturing ultimately costly and environmentally unsustainable.

Concurrently, enzymatic alternatives for chiral amine synthesis have rapidly evolved alongside these chemocatalytic methodologies.¹⁹ A pioneering technology involves the hydrolase-catalyzed kinetic resolution (KR) of racemic amines (Scheme 1a), a reaction that is now well-established on an industrial scale.²⁰ Subsequently, the groundbreaking efforts by the group led by Turner introduced the deracemization of racemic amines as a viable route (Scheme 1b),²¹ which, in comparison to the KR approach, is more atom-efficient.

Besides, other elegant methods include Pictet–Spenglerase-catalyzed Pictet–Spengler cyclization (Scheme 1c),^{22,23} cytochrome P450-catalyzed direct C–H amination (Scheme 1d),^{24,25} and ammonia lyase-catalyzed hydroamination of α,β -unsaturated acids (Scheme 1e).^{26,27} In addition, transaminase-catalyzed ARA-type transformations have also garnered attention over the past decade,²⁸ which, however, face significant challenges with pronounced substrate/product-inhibition and equilibrium displacement.²⁹ More recently, imine reductases (IREDs),^{30–34} reductive aminases (RedAms),^{35–39} and amine dehydrogenases (AmDHs)^{40–49} have become the avant-garde in enzymatic ARA (Scheme 1f).

Despite over a decade of intensive research on enzymatic ARA reactions, merely a few of these reactions have transitioned to industrial application,^{31,50–52} and/or met specific performance benchmarks concerning product concentrations and catalyst utilization (Table S1).^{53–55} Presently, the performance of the enzymes catalyzing ARA confine them to

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Scheme 1. Biocatalytic Strategies for Chiral Amine Synthesis

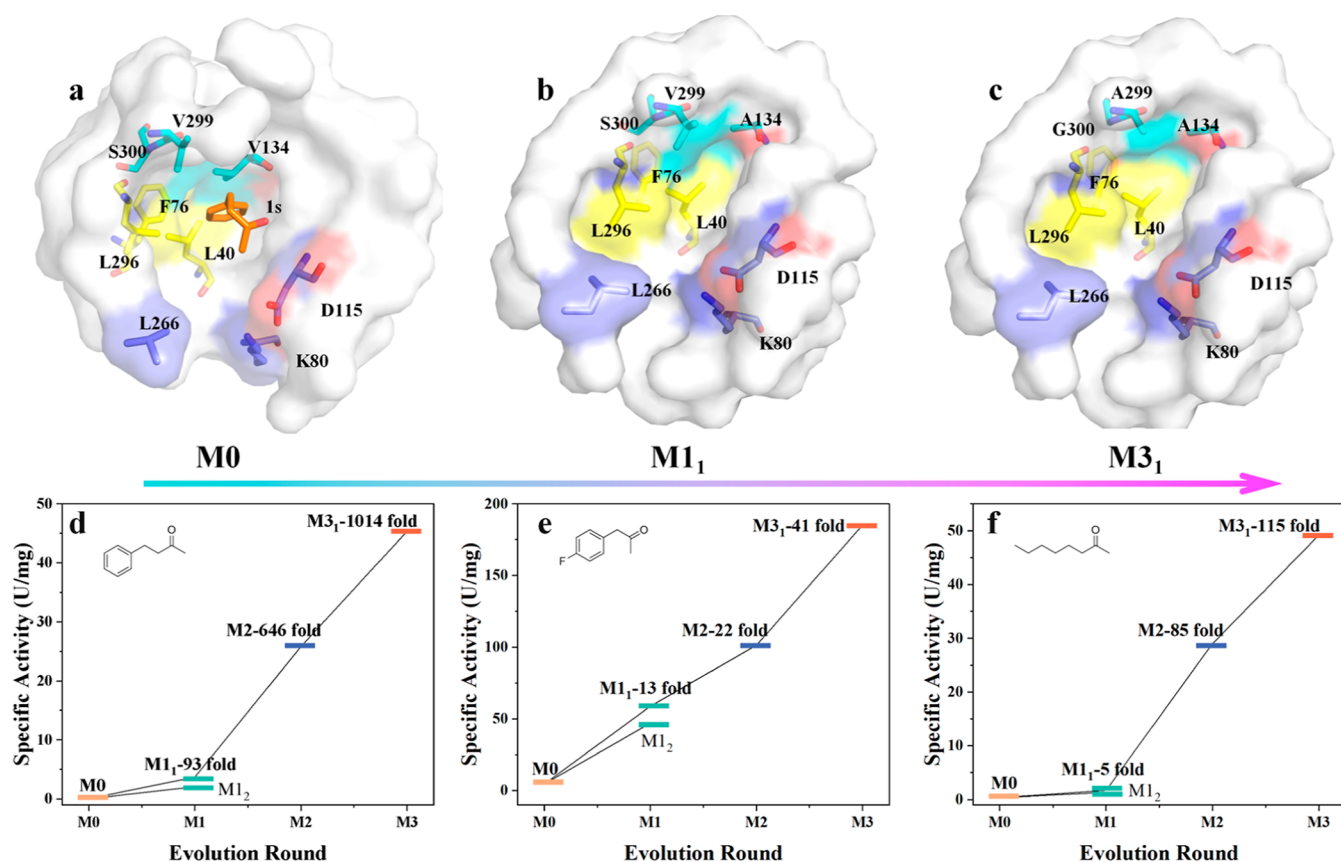
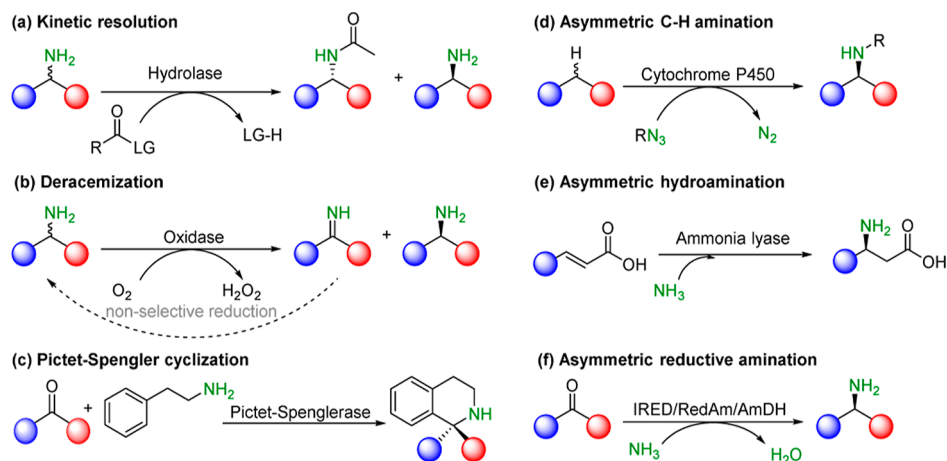


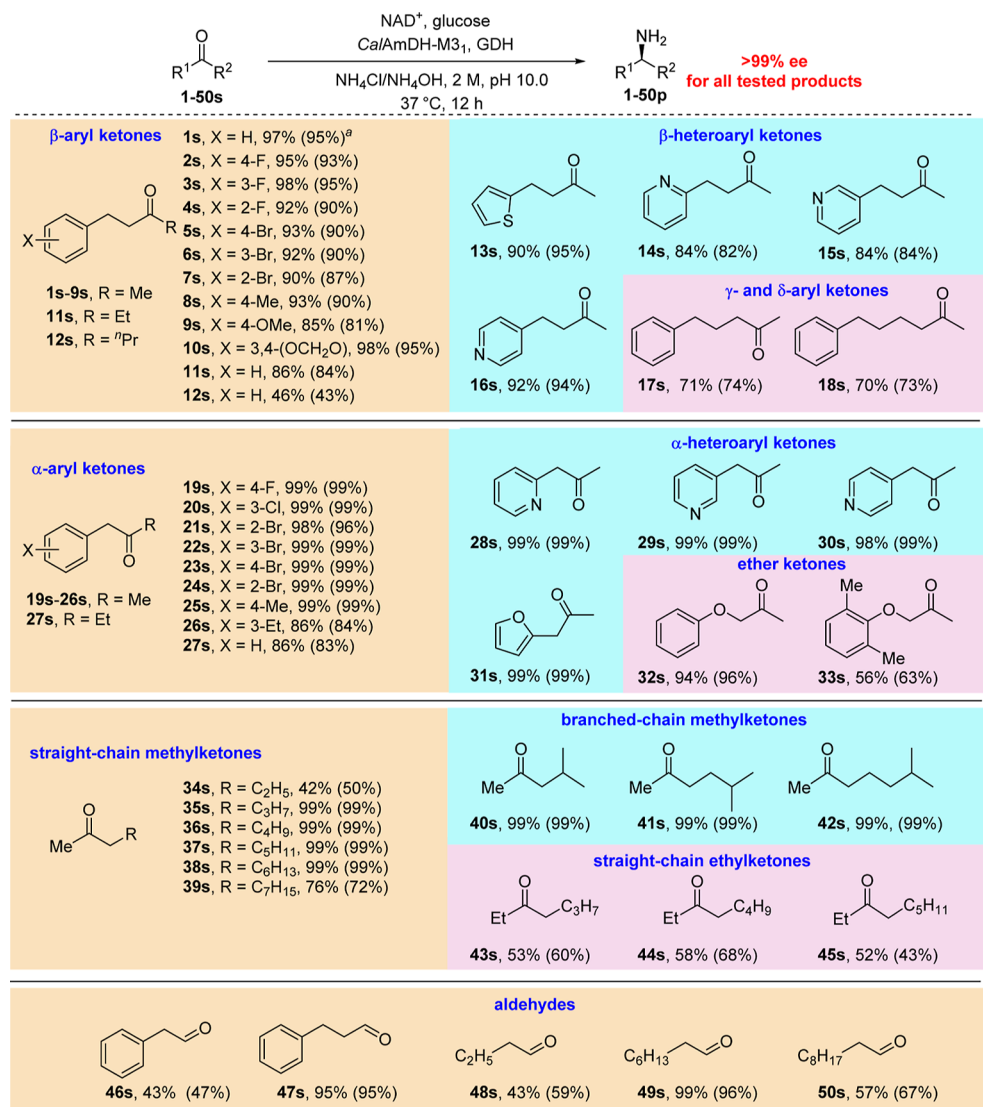
Figure 1. *CalAmDH* variants obtained. (a) Structural model of M0. Mutation sites distribution on the structural model of M1₁ (b) and M3₁. (c) Evolution route of the starting enzyme M0, and the *CalAmDH* mutants toward substrates 1s (d), 19s (e) and 37s (f).

the high-value pharmaceutical domain (Table S2). To broaden the applicability of biocatalytic ARA to encompass larger volume chemicals and thereby significantly enhance its impact on the environmental footprint of the chemical industry, substantial enhancements in the performance of biocatalytic ARA are imperative.

Directed evolution, where mutant libraries are tested against increasing reagent concentrations, has predominantly been the strategy of choice to achieve industrial relevance. Although great progress has been made in engineering of AmDHs, the ARA of bulky (especially aryl-substituted) ketones remains highly challenging, particularly at elevated concen-

trations. An alternative strategy is bioprocess development involving reaction media and reactor design. Interestingly, while this approach has been demonstrated for various enzyme classes, successful examples for ARA-catalyzing biocatalysts are scarce.

In this context, we engineered an AmDH with high activity and substrate scope toward bulky ketones, and achieved the scale-up of this bioprocess in a fatty acid-containing aqueous buffer system. Recently, Pushpanath et al. introduced two mutations (K67S/N266L) into a phenylalanine dehydrogenase (*CalPheDH*) from the thermophilic alkaliphilic bacterium *Caldalkalibacillus therrmarum*, transforming it to an amine

Scheme 2. Substrate Scope of the M3₁-Catalysed Reductive Amination^a

^aStandard reaction conditions for 100 mM scale: substrate (0.5 mmol), glucose (1.2 equiv), NAD⁺ (0.05% equiv), purified M3₁ (75 μg) and GDH (75 μg) in 5.0 mL buffer (NH₄Cl/NH₄OH, 2 M, pH 10.0) at 37 °C; for 1.0 M scale, substrate (5 mmol), M3₁ (lyophilized cell, 20 mg) and GDH (lyophilized cell, 20 mg) in buffer-oleic acid (4:1, v/v) system with other conditions unchanged. The ee values are based on chiral gas chromatography (GC) analysis after the derivatization of the products. GC conversions (results for 1.0 M scale reaction in parentheses).

dehydrogenase (*CalAmDH*), which exhibited high thermostability but suffered from low activity and narrow substrate scope.⁵⁶ To overcome the shortcomings of the variant *CalAmDH* (K67S/N266L), we chose it as the starting point (for the sake of clarity, referred to, in this work, as *CalAmDH-M0*) for semirational enzyme design in this study, yielding *CalAmDH* variants with significantly enhanced substrate range and catalytic efficiency. During process development, we discovered an unexpected activating and stabilizing influence of fatty acids on *CalAmDH*, which stabilize a flexible loop region on the enzyme's surface. This finding led us to engineer *CalAmDH* variants with improved activity. We also validated the potential for chemoenzymatic processes, extending the substrate range from carbonyl groups to simple aryl halides, alkenes, and alkynes. Ultimately, we report kilogram-scale syntheses predicated on advanced enzyme- and reaction-engineering strategies.

RESULTS AND DISCUSSION

Protein Engineering to Improve Enzymatic Performance. The initial variant, *CalAmDH-M0*, demonstrated minimal activity (in the milliunits per milligram range) toward the targeted ketone substrates (Figure 1d–f). We posited that this could be due to suboptimal binding of the non-native ketone starting materials. To investigate this, we modeled benzylacetone (**1s**) into the active site of M0 (Figure 1a), where **1s** was positioned in a tight hydrophobic pocket, aligning its carbonyl oxygen atom at distances of 8.3 and 5.4 Å from the catalytically significant residues K80–NH₂ and D115–COOH, respectively, and situating the carbonyl carbon atom 6.1 Å away from the NADH-C4 (Figure S2). We hypothesized that the bulky amino acids L40, F76, V134, L296, and V299 might contribute to this nonideal binding (Figure S3), leading us to replace them with smaller residues such as alanine and glycine.

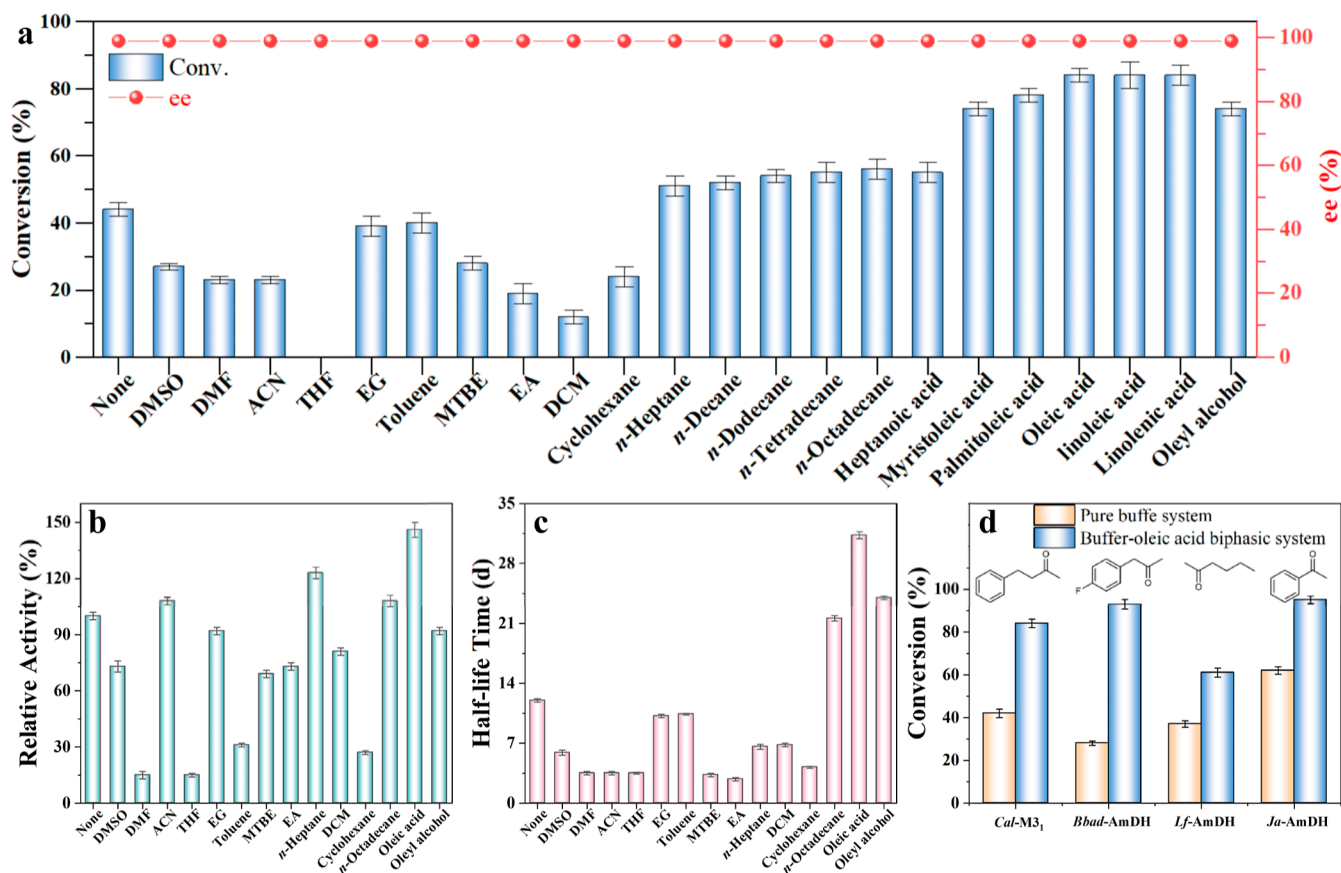


Figure 2. (a) Effect of organic solvents on enzyme performance. (b) Relative activity of M3₁ based on the linear approximation of reaction curves at substrate conversions $\leq 10\%$ (initial rates). (c) Half-life time ($t_{1/2}$) of M3₁ after incubation in 20 vol% organic-aqueous biphasic systems. (d) AMDH-catalyzed ARA in pure buffer and buffer-oleic acid biphasic system.

Contrary to our expectations, modifications at positions 40, 76, and 296 led to a further decline in activity. However, variants V134A (M1₁) and V299A (M1₂) exhibited significant enhancements in activity toward **1s**, with 93-fold and 42-fold increases, respectively, compared to M0 (Figure 1d and Table S3). Similarly, these modifications notably amplified the activity toward model compounds **19s** and **37s** (Figure 1e,f). This improvement might be attributed to the expanded surface area and volume of the active sites in M1₁ and M1₂ (Table S4), potentially facilitating the formation of a productive transition state. Supporting this notion, both molecular docking (with calculated binding energies, Figure S4 and Table S5) and kinetic analyses (showing up to 95-fold increases in k_{cat}) corroborate our hypothesis. Combining the mutations from M1₁ and M1₂ to create mutant M2 led to a synergistic enhancement in catalytic activity for substrates **1s** (Figures 1d and S5 and Table S6) and **37s** (Figures 1f and S6 and Table S7). For substrate **19s**, the mutant M2 only led to a moderate enhancement in catalytic activity, which is due to that the k_{cat} values of M1₁ and M1₂ for **19s** were already higher than that of substrates **1s** and **37s**, achieving 54.0 and 44.8 s⁻¹, respectively (Figures 1e and S7 and Table S8). This enhancement can primarily be attributed to an increased k_{cat} , while the affinity of M2 for **1s** remained largely unchanged (Table S6). The introduction of an additional mutation, replacing hydrophilic S300 with glycine (V134A/V299A/S300G, M3₁), further augmented the enzyme's activity (Figure 1d–f). M3₁ also exhibited slight improvements in thermal and pH stability compared to M0. For example, at 50 °C and pH 10, M3₁

demonstrated half-lives ($t_{1/2}$) of 168 and 228 h, respectively, compared to 132 and 192 h for M0 (Figures S8–S11).

Subsequent experiments explored the substrate (100 mM) scope of M3₁ (Scheme 2), in which glucose dehydrogenase (GDH) was used for cofactor regeneration. While M0 showed no detectable conversion for substrates **1s–18s**, M3₁ achieved over 80% conversion for all tested β -(hetero)aryl ketones (**1s–16s**) except the propyl-bearing ketone **12s** (46%) under the same conditions. Conversions for the bulkier ketones **17s** (71%) and **18s** (70%) were lower. The aromatic ring substitution pattern had minimal impact on the conversion rates. The optical purity of the (*R*)-amine products was consistently greater than 99% enantiomeric excess (ee), with **1s** and **10s** being precursors for the antihypertensive drugs dilevalol and medroxalol.

For ketones **19s–33s**, M3₁ showed a specific activity significantly higher than M0, converting all α -(hetero)aryl ketones (**19s–31s**) to their corresponding 1-arylpropan-2-amines with greater than 98% conversion and greater than 99% ee, except the bulkier **26s** (86%). M3₁ was also effective with ether ketones **32s** and **33s**, and despite **33s'** steric hindrance, its amination product (**33p**, i.e., mexiletine, an antiarrhythmic drug) was obtained in 56% conversion and greater than 99% ee.

While M0 exhibited minimal activity with aliphatic methylketones (**37s–42s**), M3₁ displayed significantly higher activity, with the conversion rates varying based on the alkyl chain length. Moreover, M3₁ efficiently converted more challenging ethyl ketones (**43s–45s**) with high enantioselectivity.

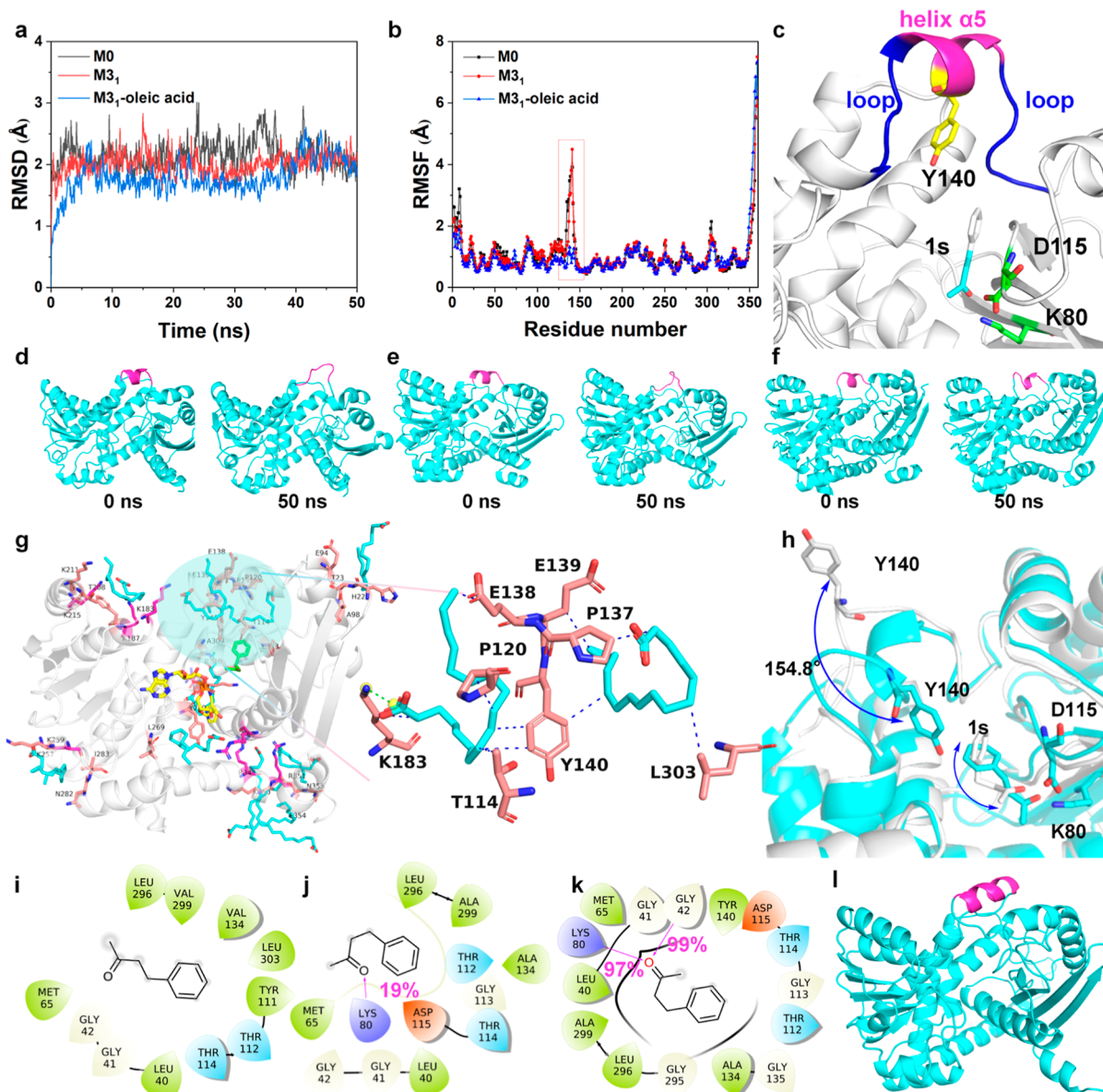


Figure 3. Variation of RMSD (a) and RMSF (b). (c) Cartoon models of the loop- α 5-loop region. Snapshots of M0 (d) and M3₁ (e) in buffer solution, and of M3₁ in oleic acid-buffer solution (f). (g) Spatial distribution of oleic acid (shown in blue) on M3₁ within 4 Å in the MD simulations (left), and the interaction between oleic acid and α -helix 5 (right). (h) The direction of Y140 in oleic acid-buffer (blue) and pure buffer (gray) systems. Arrows indicate the flipping angle of Y140 and the shifting of substrates, respectively. The binding modes of 1s to M0 (i) and of 1s to M3₁ in the absence (j) and presence (k) of oleic acid (hydrophobic amino acids are represented by green water droplets, glycine by light-yellow water droplets, alkaline lysine by blue water droplets, and acidic amino acids by red water droplets). (l) Snapshots of M4 in buffer solution.

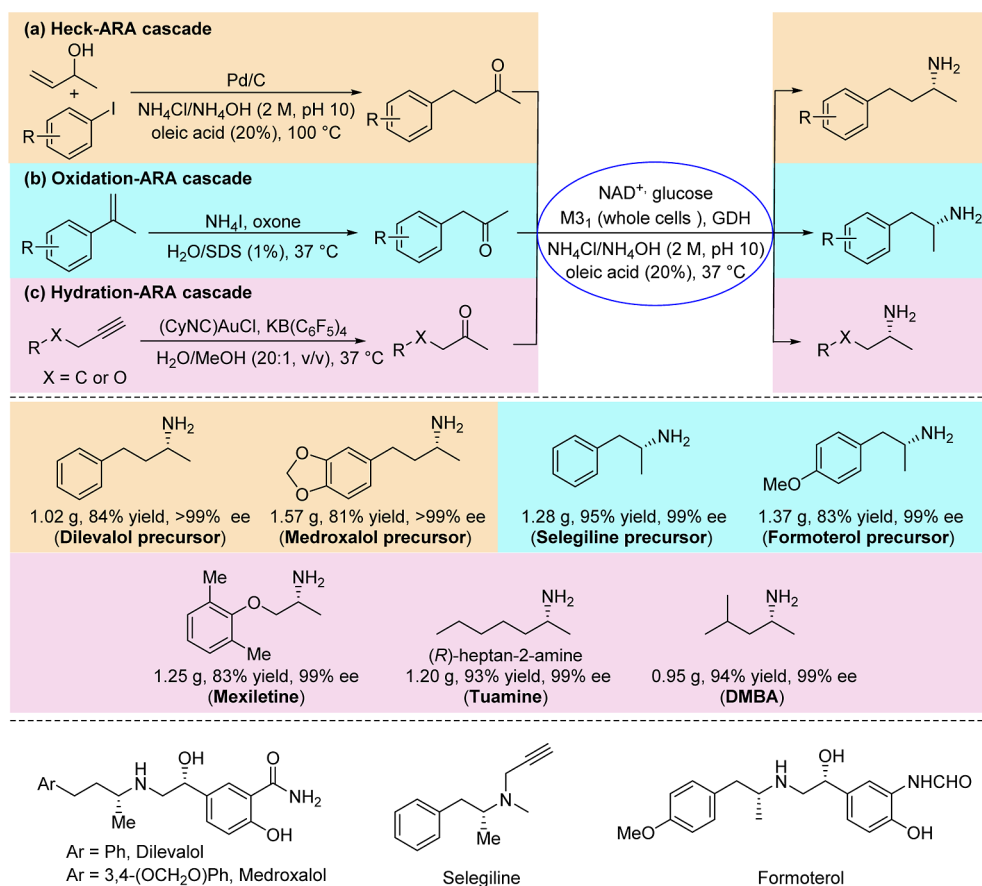
tivity. These products include sympathomimetic stimulants.¹⁶ M3₁ also catalyzed the amination of aldehydes (46s–50s), with the conversion efficiency influenced by the steric demands of the substrates.

However, arylketones (such as the 4 examples shown in Figure S12) were somewhat sluggish substrates, which may be due to the existence of resonance and field effects derived from the phenyl ring, yielding a maximally 47% conversion under the reaction conditions chosen. The low reactivity of arylketones was also found by Mutti and co-workers.⁵⁸

Unexpected Influence of Fatty Acids on CalAmDH. Despite the improved performance of M3₁, only 45% conversion was achieved under 500 mM substrate (1s) concentration (Figure S13). In anticipation of the preparative application of M3₁, we explored various cosolvents to facilitate

relevant reactant concentrations (Figure 2a).⁵⁷ Water-soluble cosolvents hindered the M3₁-catalyzed ARA of 1s, whereas most hydrophobic cosolvents slightly enhanced the reaction compared to its absence. A similar phenomenon was also found by Au and co-workers.⁵⁹ Notably, the conversion of 1s nearly doubled in the presence of fatty acids. In particular, oleic acid not only augmented M3₁'s activity (Figure 2b) but also substantially bolstered its robustness (Figure 2c). Notably, the oleic acid-induced conversion improvement for other AmDHs toward their respective substrates was also found (Figure 2d), including the enzymes from *Bacillus badius* (*Bbad*-AmDH⁴¹), *Lysinibacillus fusiformis* (*Lf*-AmDH⁴⁴) and *Jeotgaliococcus aerolatus* (*Ja*-AmDH⁴⁶), demonstrating the versatility of this approach.

Scheme 3. Chemoenzymatic Synthesis of Chiral Pharmaceutically Relevant Amines



To elucidate the unexpected activating and stabilizing impact of fatty acids on M3₁, we conducted molecular dynamics (MD) simulations. The root-mean-square deviations (RMSD, Figure 3a) for M0, M3₁, and M3₁ in the presence of oleic acid stabilized after approximately 10 ns, indicating no significant impact on the structural integrity of the enzyme. Similarly, the enzyme's secondary structure and amino acid residue interactions remained largely unchanged (Figures S14 and S15). However, the root-mean-square fluctuation (RMSF, Figure 3b) revealed a significant effect of oleic acid. In its absence, helix α 5 (P137–N143) exhibited considerable flexibility (Figure 3c), eventually transitioning into a loop (Figures 3d,e and S16), a shift not observed with oleic acid present (Figure 3f). As shown in Figures 3g and S17, the presence of the carboxyl group gives oleic acid a completely different distribution position on the protein surface compared to *n*-octadecane. In particular, two oleic acid molecules are distributed in the α 5 region and interact strongly with the α 5 residues through hydrophobic interactions and salt bridges, blocking the helix-to-loop transition and thus stabilizing the enzyme conformation (Figure S18). In contrast, no enzyme stabilization effect was found in the case of *n*-octadecane molecules due to their absence in this region. In addition, the amphiphilic oleic acid can form micelles, thereby solubilizing the substrate and facilitating mass transfer, which is not possible with *n*-octadecane. Therefore, the carboxyl group of oleic acid plays an important role in improving enzymatic performance.

The significance of the helix-to-loop transition is underscored by examining Y140 (Figure 3h). In the helix state, Y140

forms close contacts (within hydrogen-bonding distance to K80 and G42) and is near the nicotinamide cofactor (Figure S19), facilitating substrate interaction. Conversely, in the loop state, Y140 points outward, disrupting these interactions. M0 did not exhibit this hydrogen bonding (Figure 3i), and it was only partially present in M3₁ (18% hydrogen bonding occupancy, Figure 3j). Oleic acid significantly enhanced these interactions (97% and 99% occupancy with K80 and G42, respectively, Figure 3k), explaining the observed rate acceleration. Additionally, oleic acid decreased the solvent-accessible surface area (SASA, Figure S20), enhancing interior packing interactions and potentially contributing to M3₁'s increased stability.

To experimentally confirm the important role of the α 5 region, a helix engineering was performed by elongating the α 5 fragment. As shown in Figure 3l, a α 5-elongated new mutant (M4) was obtained by introducing 7 additional amino acids (PEEYGGN), which, as expected, exhibited further improvement in activity, stability, and kinetic parameters compared to M3₁ (Figures S10–S11 and Tables S6–S8). These findings not only underscored the significant impact of mutations distant from the active site on enzymatic performance, but also provided evidence that oleic acid, beyond serving as reaction media, can modulate enzyme's catalytic conformation, as directed evolution did. Notably, despite the further improved activity of AmDH-M4, it suffered from low soluble protein expression due to the partial formation of inclusion bodies, making its scale-up application problematic.

Equipped with M3₁ and optimized reaction conditions, we executed a semipreparative synthesis of (*R*)-4-phenylbutan-2-

amine (**1p**) from **1s** (0.5 M). Employing a mere $20 \text{ mg} \times \text{L}^{-1}$ of purified M3₁ and 0.25 mM of NAD⁺ in a biphasic system comprising buffer and oleic acid (4:1, v/v) at 37 °C for 12 h, we achieved a 95% yield and >99% ee (Figure S21). This equates to a total turnover number for M3₁ of 1,020,000 ($\text{mol}_{\text{1p}} \times \text{mol}_{\text{M3}_1}^{-1}$, translating to a product to biocatalyst ratio of $3540 \text{ g} \times \text{g}^{-1}$) and an average turnover frequency of 23.6 s^{-1} over the 12 h period. The yield escalated to >99% when using lyophilized whole cells at a concentration of $4 \text{ g} \times \text{L}^{-1}$ (Figure S22), and the amount of oleic acid can be reduced to 8% (v/v) with 90% conversion (Figure S23). Consequently, the substrate concentration for all previously tested substrates could be increased to 1.0 M without any noticeable impact on conversions or enantioselectivities.

A kilogram-scale demonstration was conducted in a 10 L reactor using **1s** as a model substrate (refer to Supporting Information Methods, Figure S24). Traces of unreacted substrate were eliminated via extraction with ethyl acetate in acidic conditions, followed by a second extraction under basic conditions. Without any additional purification steps, 1.01 kg of the amine product (*R*)-**1p** was isolated (85% yield) with >99.9% ee. The total impurities remained below the gas chromatography detection threshold (<0.15%), satisfying the criteria for Good Manufacturing Practice (GMP) in active pharmaceutical ingredient (API) synthesis.

Constructing Chemoenzymatic Cascades to Expand the Feedstock Scope. Given the instability, costliness, or difficulty in obtaining certain ketone substrates, the utilization of cost-effective and readily accessible ketone precursors like olefins, alkynes, or alcohols is deemed advantageous. Toward this aim, three chemoenzymatic cascades were developed by amalgamating M3₁ with Pd-catalyzed Heck reaction of allylic alcohols,⁶⁰ hypiodite-catalyzed anti-Markovnikov oxidation of alkenes,⁶¹ and Au-catalyzed hydration of alkynes.⁶²

In the Heck-ARA cascade, both processes were executed in the previously delineated buffer-oleic acid biphasic system. Owing to the Heck reaction's requirement for elevated temperatures (100 °C), it was carried out sans the biocatalyst. Post completion, the heterogeneous catalyst was recuperated, and the biocatalyst was incorporated for the ARA reaction at 37 °C. This one-pot sequential cascade facilitated the generation of chiral precursors for dilevalol and medroxalol from allyl alcohol and aryl halides (Scheme 3a).

For the subsequent cascades, the chemical catalysts displayed incompatibility with oleic acid, necessitating its addition after the chemical transformation and catalyst recycling, alongside the biocatalyst. The oxidation-ARA cascade enabled the asymmetric synthesis of amphetamine, precursors for formoterol, from olefins (Scheme 3b). Meanwhile, the hydration-ARA cascade produced mexiletine, heptan-2-amine (tuamine), and 1,3-dimethylbutylamine (DMBA) from alkynes (Scheme 3c). Conducted on a gram scale, these chemoenzymatic cascades showcased over 80% overall yield and greater than 99.9% ee, highlighting their practical application in synthesizing pharmaceutically relevant amines.

CONCLUSION

In conclusion, the application of molecular docking and dynamic simulations for the enhancement of a thermostable AmDH's activity has proven to be a successful strategy in engineering catalysts that are both highly active and stable. Our

findings underscore the significance of the often-overlooked loop regions in enzymes, highlighting their importance in catalysis. The product yields and catalyst efficiencies achieved with the engineered AmDH mutants suggest their potential applicability in the synthesis of commodity and even bulk chemicals. Thus, we demonstrate a pathway to liberate biocatalytic asymmetric reductive amination (ARA) from the confines of pharmaceutical niches. To date, however, biocatalytic reactions have been predominantly confined to this sector due to the insufficient efficiency of enzymes for the production of larger-scale (and more cost-effective) products.

The modest production volumes within the pharmaceutical sector constrain the potential of biocatalysis to significantly enhance environmental sustainability. We are convinced that this contribution adds a series of thought-provoking insights aimed at transcending this limitation, positioning biocatalysis as a transformative technology for the chemical industry.

Methods. Enzyme Activity Assay. The activities of AmDHs were measured by monitoring the change in the absorbance of NADH at 340 nm using a SpectraMax190 spectrophotometer (Molecular Devices, USA). The activity assay was conducted in a 1 mL reaction mixture comprising NH₄Cl/NH₄OH buffer (2.0 M, pH 10.0), 1 mM NADH, 50 mM substrate, and 15 μg/mL of purified enzyme, at 37 °C for a duration of 1.0 min. One unit of activity was defined as the amount of enzyme that catalyzes the conversion of 1 μmol of substrate per minute.

Enzymatic ARA. Substrate (5.0 mmol), glucose (1.2 equiv), NAD⁺ (0.05% equiv), lyophilized whole cells of M3₁ (20.0 mg) and lyophilized whole cells of GDH (20.0 mg) in 5.0 mL buffer (NH₄Cl/NH₄OH, 2.0 M, pH 10.0)-oleic acid (4:1, v/v) were added to a 25 mL round-bottom flask. The mixture was stirred at 37 °C for 12 h. After the reaction was completed, the reaction solution was extracted with Et₂O (5 mL × 3). The organic phase was dried using anhydrous Na₂SO₄, and concentrated in vacuo to obtain the crude products. The products were purified by column chromatography using dichloromethane and methanol (10:1, v/v) as eluent.

ASSOCIATED CONTENT

Supporting Information

The Supporting Information is available free of charge at <https://pubs.acs.org/doi/10.1021/acscatal.4c05904>.

Materials and methods, optimization details, general catalytic procedure, figures, tables and analytical data (PDF)

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Author Contributions

The manuscript was written through contributions of all authors. All authors have given approval to the final version of the manuscript.

Notes

The authors declare no competing financial interest.

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