

A Four-Step Enzymatic Cascade for Efficient Production of L-Phenylglycine from Biobased L-Phenylalanine

Yuling Zhu^[a], Jifeng Yuan^{[a]*}

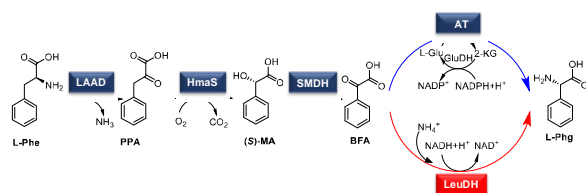
Abstract: Enantiopure amino acids are of particular interest in the agrochemical and pharmaceutical industries. Here, we reported a multi-enzyme cascade for efficient production of L-phenylglycine (L-Phg) from biobased L-phenylalanine (L-Phe). We first attempted to engineer *Escherichia coli* for expressing L-amino acid deaminase (LAAD) from *Proteus mirabilis*, hydroxymandelate synthase (HmaS) from *Amycolatopsis orientalis*, (S)-mandelate dehydrogenase (SMDH) from *Pseudomonas putida*, the endogenous aminotransferase (AT) encoded by *ilvE* and L-glutamate dehydrogenase (GluDH) from *E. coli*. However, 10 mM L-Phe only afforded the synthesis of 7.21 ± 0.15 mM L-Phg. The accumulation of benzoylformic acid suggested that the transamination step might be rate-limiting. We next used leucine dehydrogenase (LeuDh) from *Bacillus cereus* to bypass the use of L-glutamate as amine donor, and 40 mM L-Phe gave 39.97 ± 3.84 mM (6.04 ± 0.58 g/L) L-Phg, reaching 99.9% conversion. In summary, this work demonstrated a concise four-step enzymatic cascade for the L-Phg synthesis from biobased L-Phe, with a potential for future industrial applications.

Enantiopure amino acids are of particular interest in the agrochemical and pharmaceutical industries^[1]. For example, L-phenylglycine (L-Phg) can be used for the synthesis of β -lactam antibiotics such as penicillin^[2], streptogramin B^[3], pristinamycin I^[4] and virginiamycin S^[5]. A number of chemical synthesis routes have been developed for the production of enantiopure amino acid^[6]. For instance, the Strecker reaction is a common method for the industrial production of α -amino acids^[7]. However, chemical approaches typically use environmentally harmful toxic reagents and organic solvents, and the enantioselectivity of the product is relatively low, which are undesirable for sustainable production of enantiopure amino acids^[8].

In comparison to chemical approaches, biocatalytic processes are usually carried out under less harsh conditions such as ambient temperature and atmospheric pressure^[9]. In addition, biocatalytic processes are considered as a suitable alternative for chiral chemical productions because of the excellent enantioselectivity^[10]. Since amino acids such as L-phenylalanine (L-Phe) can be obtained by fermentation or from protein waste hydrolysates in large amounts and at a low cost^[11], they are considered to be cheap and renewable feedstocks for biomanufacturing applications. For instance, it was reported that the production of L-Phg from biobased L-Phe was achieved in the recombinant *Escherichia coli* containing eight reaction steps

with 12 genes^[12]. Under the optimal condition, 40 mM L-Phe was converted to 34 mM (5.1 g/L) L-Phg after 24 h via the whole-cell biotransformation, reaching ~85% conversion. In addition, *de novo* synthesis of L-Phg^[14] and *in vitro* enzyme catalysis^[15] have also been reported for the L-Phg production, the L-Phg yields were relatively low (51.6 mg/g DCW and 91.4 mg/L, respectively).

In this study, we sought to develop a more concise multi-enzyme cascade for synthesizing L-Phg from biobased L-Phe. In particular, our system comprises L-amino acid deaminase (LAAD, Uniprot ID: B2ZHY0) from *Proteus mirabilis*^[13], hydroxymandelate synthase (HmaS, Uniprot ID: O52791) from *Amycolatopsis orientalis*^[14], (S)-mandelate dehydrogenase (SMDH, Uniprot ID: P20932) from *Pseudomonas putida*^[15] and leucine dehydrogenase (LeuDh, Uniprot ID: P0A393) from *Bacillus cereus*^[16]. The four-step enzymatic cascade could efficiently convert 40 mM L-Phe to 39.97 ± 3.84 mM (6.04 ± 0.58 g/L) L-Phg after 12 h, with a conversion rate >99.9%. To the best of our knowledge, our work represents one of the most efficient biocatalytic routes for L-Phg synthesis from L-Phe^[12].



Scheme 1. Schematic diagram of multi-enzyme cascade toward L-Phg synthesis from biobased L-Phe. LAAD, L-amino acid deaminase from *P. mirabilis* (Uniprot ID: B2ZHY0); HmaS, hydroxymandelate synthase from *A. orientalis* (Uniprot ID: O52791); SMDH, (S)-mandelate dehydrogenase from *P. putida* (Uniprot ID: P20932); AT, aminotransferase encoded by *ilvE* from *E. coli* (Uniprot ID: P0AB80); GluDH, L-glutamate dehydrogenase from *E. coli* (Uniprot ID: P00370); LeuDh, leucine dehydrogenase from *B. cereus* (Uniprot ID: P0A393). L-Phe, L-phenylalanine; PPA, phenylpyruvate; (S)-MA, (S)-mandelic acid; BFA, benzoylformic acid; L-Phg, L-phenylglycine; 2-KG, 2-ketoglutarate; L-Glu, L-glutamate.

Recently, our group have demonstrated that LAAD from *P. mirabilis* and HmaS from *A. orientalis* together with SMDH from *P. putida* could effectively synthesize benzyl alcohol and benzylamine from L-Phe^[17]. To enable L-Phg production from benzoylformic acid (BFA), we chose aminotransferase (AT, Uniprot ID: P0AB80) encoded by *ilvE* and L-glutamate dehydrogenase (GluDH, Uniprot ID: P00370) from *E. coli*^[12, 18]. In brief, the multi-enzyme cascade comprises LAAD from *P. mirabilis*, HmaS from *A. orientalis*, SMDH from *P. putida* and AT/GluDH from *E. coli* (Scheme 1). As depicted in Figure 1a, the multi-enzyme cascade was recast into three modules: LAAD together with HmaS to convert L-Phe into (S)-mandelic acid; SMDH and AT to convert (S)-mandelic acid into L-Phg; an

[a] Yuling Zhu, Jifeng Yuan

State Key Laboratory of Cellular Stress Biology

School of Life Sciences, Xiamen University, Fujian 361102, PR

China

E-mail: jfyuan@xmu.edu.cn

Supporting information for this article is given via a link at the end of the document.

additional plasmid expressing GluDH from *E. coli* [12, 18] to improve the L-glutamate regeneration. When the recombinant *E. coli* strain Ec-Phg1.0 harboring three plasmids (pET-LAAD-HmaS, pRSF-SMDH-AT and pACYC-GluDH) was analyzed by the SDS-PAGE, we could clearly observe the bands corresponding to HmaS, SMDH, AT and GluDH (Figure 1b). However, LAAD was not observed from the SDS-PAGE result, probably because LAAD is a membrane-associated protein

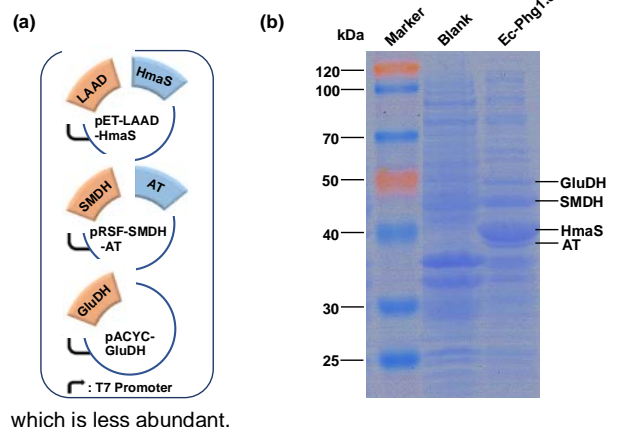
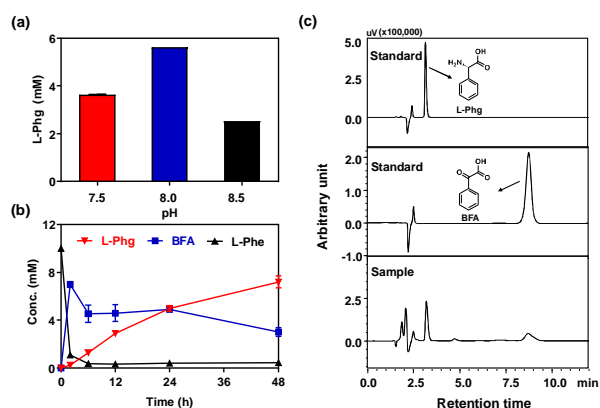


Figure 1. Plasmid design of aminotransferase (AT)-dependent route and SDS-PAGE analysis of protein expression. (a) The recombinant *E. coli* strain Ec-Phg1.0 containing three plasmids (pET-LAAD-HmaS, pRSF-SMDH-AT and pACYC-GluDH). (b) SDS-PAGE analysis of the recombinant *E. coli* strain Ec-Phg1.0. Blank: *E. coli* BL21 (DE3) harboring empty plasmids.

which is less abundant. In the early experiments, we compared the effect of different pH conditions on L-Phg production, and we found that the ideal pH for L-Phg synthesis was around 8.0 (Figure 2a). As shown in Figure 2b and Table S1, when 10 mM L-Phe was fed to the recombinant *E. coli* Ec-Phg1.0 expressing five enzymes, 7.21 ± 0.15 mM L-Phg was obtained after 48 h, which corresponds to ~72.1% conversion. From the HPLC result, we found a



substantial amount of BFA was accumulated during the biocatalytic process (Figure 2c).

Figure 2. Characterization of AT-dependent route for L-Phg synthesis. (a) The efficiency of biotransforming L-Phe (10 mM) to L-Phg under different pH conditions. (b) Time course of biotransforming L-Phe (10 mM) to L-Phg at pH 8.0. (c) Representative HPLC result showing L-Phg produced by the recombinant *E. coli* strain Ec-Phg1.0. All experiments mentioned above were carried out in 200 mM KP buffer with 10 g cdw L⁻¹ recombinant *E. coli* at 30°C.

Data represent the mean value with standard deviations from triplicate of experiments.

According to the literature, LAAD from *P. mirabilis* showed a broad substrate activity on L-amino acids, such as L-His, L-Arg, L-Phe and so on [19]. We hypothesized that LAAD might deaminate L-Phg, which leads to a futile catalytic cycle and results in the accumulation of BFA. To corroborate this hypothesis, we further carried out the L-Phg stability test. When 10 mM L-Phg was treated with the recombinant *E. coli* expressing LAAD, no appreciable degradation of L-Phg was observed even after 48 h (Supplementary Figure S1). Therefore, we suspected that the transamination step catalyzed by AT/GluDH might be the bottleneck limiting the L-Phg production. As it was reported that the production of 34 mM L-Phg from 40 mM L-Phe was achieved in *E. coli* containing eight reaction steps with AT/GluDH and there was no accumulation of BFA in the experimental process [12], the AT activity is unlikely to be rate-limiting. However, LAAD from *P. mirabilis* also effectively deaminates L-glutamate to α -ketoglutarate [20]. Thus, we inferred that the amine donor of L-glutamate was degraded by LAAD, thereby leading to the accumulation of BFA and poor yield of L-Phg.

To overcome the low catalytic efficiency of AT/GluDH-mediated route toward L-Phg production, we next sought to find an alternative strategy to skip the use of amine donor of L-glutamate. From the literature, the preparation of L-Phg in *E. coli* could be realized by expressing an amino acid dehydrogenase from *Bacillus clausii* (BcAADH) with optimal pH around 9.5-10.5 [21], LeuDH from *Exiguobacterium sibiricum* with optimal pH around 10.0, [22] and LeuDH from *B. cereus* with optimal pH around 8.0 [16]. In this study, we decided to replace AT/GluDH with LeuDH from *B. cereus*, which is more compatible with our establishment reaction condition (Scheme 1). As shown in Figure 3a, we further constructed the recombinant *E. coli* strain

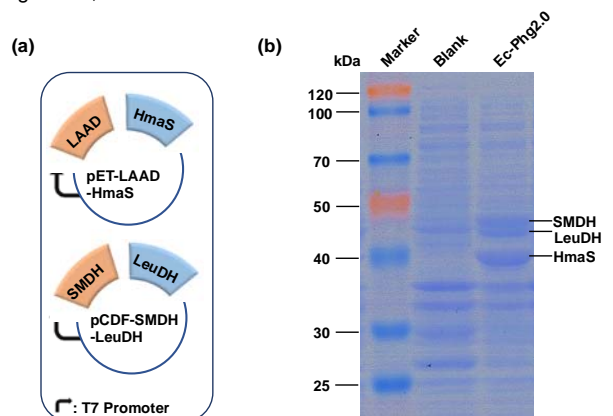


Figure 3. Plasmid design of leucine dehydrogenase (LeuDH)-dependent route and SDS-PAGE analysis of protein expression. (a) The recombinant *E. coli* strain Ec-Phg2.0 containing two plasmids (pET-LAAD-HmaS and pRSF-SMDH-LeuDH). (b) SDS-PAGE analysis of the recombinant *E. coli* strain Ec-Phg2.0. Blank: *E. coli* BL21 (DE3) harboring empty plasmids.

Ec-Phg2.0 containing two plasmids (pET-LAAD-HmaS and pRSF-SMDH-LeuDH). From the SDS-PAGE analysis, we could observe the bands corresponding to HmaS, SMDH and LeuDH in the recombinant *E. coli* strain Ec-Phg2.0 upon the IPTG induction (Figure 3b).

As can be seen from Figure 4a and Table S2, when 10 mM L-Phe was used as the substrate, 9.92 ± 0.39 mM L-Phg was

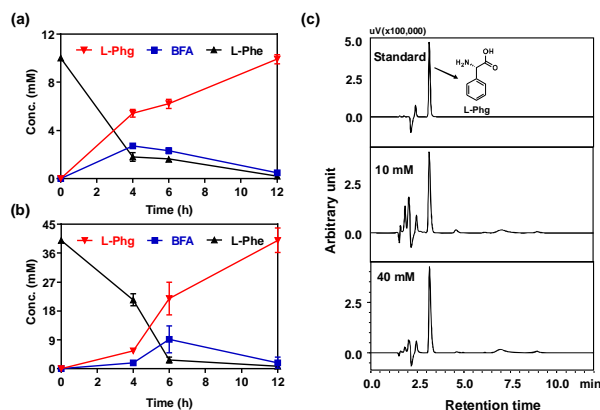
produced after 12 h. Interestingly, the problem of BFA accumulation was addressed by replacing AT/GluDH module with LeuDh from *B. cereus* (Figure 4c). To compare the catalytic efficiency of our system with that of the recombinant *E. coli*

appreciable accumulation of intermediates for *E. coli* strain Ec-Phg2.0, our biocatalytic method would greatly simplify the product separation process, with a great potential for future industrial applications.

Acknowledgements

This work was supported by Xiamen University under grant no. 0660-X2123310 and ZhenSheng Biotech, China.

Keywords: L-phenylglycine; L-amino acid deaminase; multi-enzyme cascade; leucine dehydrogenase; whole-cell biocatalyst.



expressing 12 genes [12], we also examined high substrate concentration of 40 mM L-Phe. When 40 mM L-Phe was fed to the recombinant *E. coli*, approximately 39.97 ± 3.84 mM (6.04 ± 0.58 g/L) L-Phg was obtained after 12 h (Figure 4b, Table S3), which corresponds to >99.9% conversion.

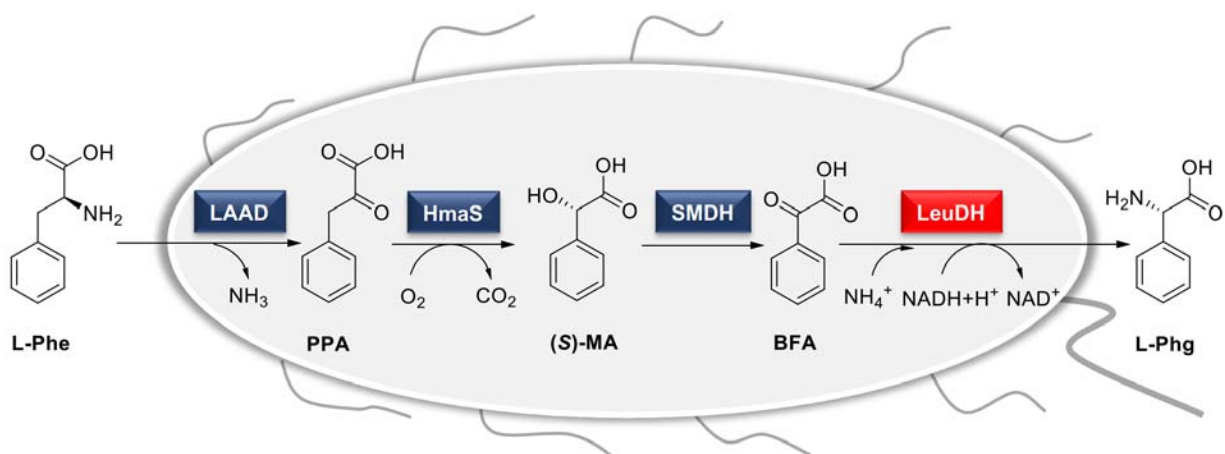
Figure 4. Characterization of LeuDh-dependent route for L-Phg synthesis.

(a) Time course of biotransforming L-Phe (10 mM) to L-Phg. (b) Time course of bioconverting L-Phe (40 mM) to L-Phg. (c) Representative HPLC result showing L-Phg produced by the recombinant *E. coli* strain Ec-Phg2.0. All experiments mentioned above were carried out in 200 mM KP buffer with 10 g cdw L⁻¹ recombinant *E. coli* at 30°C. Data represent the mean value with standard deviations from triplicate of experiments.

In summary, we have developed two artificial enzymatic cascades to synthesize enantiopure amino acid of L-Phg from biobased L-Phe. The first enzymatic cascade comprises co-expressing five enzymes in the recombinant *E. coli* strain Ec-Phg1.0 harboring three corresponding plasmids (pET-LAAD-HmaS, pRSF-SMDH-AT and pACYC-GluDH). However, under the optimal pH condition, only 7.21 ± 0.15 mM L-Phg was obtained from 10 mM L-Phe after 48 h and the accumulation of intermediate product BFA was observed. Further experiments revealed that LAAD from *P. mirabilis* could not deaminate L-Phg (Supplementary Figure S1), indicating that the transamination step is rate-limiting. Next, we attempted to use LeuDh from *B. cereus* to replace AT/GluDH and the recombinant *E. coli* strain Ec-Phg2.0 harboring two corresponding plasmids (pET-LAAD-HmaS and pRSF-SMDH-LeuDh) was constructed. The four-step enzymatic cascade could efficiently convert 40 mM of L-Phe to 39.97 ± 3.84 mM (6.04 ± 0.58 g/L) L-Phg, reaching >99.9% conversion after 12 h. Although we did not further optimize and scale-up the biocatalytic process, it would be possible to achieve even higher L-Phg titer as more active enzyme alternatives are available for L-Phg synthesis from mandelate [21-22, 25]. Based on these findings, the four-step enzymatic cascade outperformed all the previously established biocatalytic systems for L-Phg synthesis from biobased L-Phe [12, 24]. Since there was no

- [1] a) G. Helmchen, A. Pfaltz, *Acc Chem. Res.* **2000**, *33*, 336-345; b) M. Breuer, K. Dittrich, T. Habicher, B. Hauer, M. Kessler, R. Sturmer, T. Zelinski, *Angew. Chem. Int. Ed.* **2004**, *43*, 788-824.
- [2] L. M. Van Langen, F. Van Rantwijk, V. K. Švedas, R. A. Sheldon, *Tetrahedron Asymmetry.* **2000**, *11*, 1077-1083.
- [3] a) R. S. Al Toma, C. Briek, M. J. Cryle, R. D. Süßmuth, *Nat. Prod. Rep.* **2015**, *32*, 1207-1235; b) L. J. Marcos-Zambrano, P. Escribano, E. Bouza, J. Guinea, *Int. J. Med. Microbiol.* **2014**, *304*, 1192-1198.
- [4] Y. J. Mast, W. Wohlleben, E. Schinko, *J. Biotechnol.* **2011**, *155*, 63-67.
- [5] C. Cocito, *Microbiol. Rev.* **1979**, *43*, 145-192.
- [6] J. Wang, X. Liu, X. Feng, *Chem Rev* **2011**, *111*, 6947-6983.
- [7] a) S. Aiba, N. Takamatsu, T. Sasai, Y. Tokunaga, T. Kawasaki, *Chem. Commun. (Camb)* **2016**, *52*, 10834-10837; b) S. Miyagawa, K. Yoshimura, Y. Yamazaki, N. Takamatsu, T. Kuraishi, S. Aiba, Y. Tokunaga, T. Kawasaki, *Angew. Chem. Int. Ed.* **2017**, *56*, 1055-1058; c) I. Baglai, M. Leeman, K. Wurst, B. Kaptein, R. M. Kellogg, W. L. Noorduin, *Chem. Commun.* **2018**, *54*, 10832-10834.
- [8] a) S. Saravanan, A. Sadhukhan, N. U. Khan, R. I. Kureshy, S. H. Abdi, H. C. Bajaj, *J. Org. Chem.* **2012**, *77*, 4375-4384; b) W. H. Boesten, J. P. Seerden, B. de Lange, H. J. Dielemans, H. L. Elsenberg, B. Kaptein, H. M. Moody, R. M. Kellogg, Q. B. Broxterman, *Org. Lett.* **2001**, *3*, 1121-1124.
- [9] J. Muschiol, C. Peters, N. Oberleitner, M. D. Mihovilovic, U. T. Bornscheuer, F. Rudroff, *Chem. Commun.* **2015**, *51*, 5798-5811.
- [10] a) J.-B. Wang, M. T. Reetz, *Nat. Chem.* **2015**, *7*, 948-949; b) S. Servi, D. Tessaro, G. Pedrocchi-Fantoni, *Coordin. Chem. Rev.* **2008**, *252*, 715-726.
- [11] a) W. Leuchtenberger, K. Huthmacher, K. Drauz, *Appl. Microbiol. Biotechnol.* **2005**, *69*, 1-8; b) A. Rodriguez, J. A. Martinez, N. Flores, A. Escalante, G. Gosset, F. Bolivar, *Microb. Cell Fact.* **2014**, *13*, 126-141.
- [12] Y. Zhou, S. Wu, Z. Li, *Angew. Chem. Int. Ed.* **2016**, *128*, 11819-11822.
- [13] a) G. Massad, H. Zhao, H. L. Mobley, *J. Bacteriol.* **1995**, *177*, 5878-5883; b) Y. Hou, G. S. Hossain, J. Li, H. D. Shin, L. Liu, G. Du, *Appl. Microbiol. Biotechnol.* **2015**, *99*, 8391-8402.
- [14] U. Müller, F. van Assema, M. Gunsior, S. Orf, S. Kremer, D. Schipper, A. Wagemans, C. A. Townsend, T. Sonke, R. Bovenberg, M. Wubboldts, *Metab. Eng.* **2006**, *8*, 196-208.
- [15] B. Mitra, J. A. Gerlt, P. C. Babbitt, C. W. Koo, G. L. Kenyon, D. Joseph, G. A. Petsko, *Biochemistry.* **1993**, *32*, 12959-12967.
- [16] Q. Liu, J. Zhou, T. Yang, X. Zhang, M. Xu, Z. Rao, *Appl. Microbiol. Biotechnol.* **2018**, *102*, 2129-2141.
- [17] a) L. Liu, Y. Zhu, Y. Chen, H. Chen, C. Fan, Q. Mo, J. Yuan, *Chem. Asian J.* **2020**, *15*, 1018-1021; b) Y. Zhu, T. Yang, Y. Chen, C. Fan, J. Yuan, *ChemistrySelect.* **2020**, *5*, 14292-14295.

- [18] S. Wu, Y. Zhou, T. Wang, H.-P. Too, D. I. C. Wang, Z. Li, *Nat. Commun.* **2016**, *7*, 11917.
- [19] G. Molla, R. Melis, L. Pollegioni, *Biotechnol. Adv.* **2017**, *35*, 657-668.
- [20] J. O. Baek, J. W. Seo, O. Kwon, S. I. Seong, I. H. Kim, C. H. Kim, *J. Basic Microbiol.* **2011**, *51*, 129-135.
- [21] J. Cheng, G. Xu, R. Han, J. Dong, Y. Ni, *RSC Adv.* **2016**, *6*, 80557-80563.
- [22] C.-W. Fan, G.-C. Xu, B.-D. Ma, Y.-P. Bai, J. Zhang, J.-H. Xu, *J. Biotechnol.* **2015**, *195*, 67-71.
- [23] S. P. Liu, R. X. Liu, A. A. El-Rotail, Z. Y. Ding, Z. H. Gu, L. Zhang, G. Y. Shi, *J. Biotechnol.* **2014**, *186*, 91-97.
- [24] S. P. Liu, R. X. Liu, J. Mao, L. Zhang, Z. Y. Ding, Z. H. Gu, G. Y. Shi, *Biotechnol. Bioproc. E.* **2016**, *21*, 153-159.
- [25] V. Resch, W. M. F. Fabian, W. Kroutil, *Adv. Synth. Catal.* **2010**, *352*, 993-997.



Graphical abstract: a concise four-step enzymatic cascade for the L-phenylglycine synthesis from biobased L-phenylalanine was devised. 40 mM L-phenylalanine afforded the synthesis of 39.97 ± 3.84 mM (6.04 ± 0.58 g/L) L-phenylglycine, reaching 99.9% conversion.