Supporting information

Engineering *Pseudomonas dacunhae* L-aspartate β-decarboxylase for L-homophenylalanine synthesis

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1. Experimental methods

General methods and materials

L-Aspartate, L-alanine, 3(*R,S*)-methyl-D,L-aspartate, and L-2-amino butyrate were obtained from Aladdin (Shanghai); 3(*R,S*)-hydroxy-D,L-aspartate and L-serine were purchased from TCI (Shanghai); L-homophenylalanine was supplied by Energy Chemical (Shanghai); PrimerSTAR HS, 2× Taq PCR MasterMix, T_4 DNA ligase, and *Dpn* I were obtained from TIANGEN (Beijing). 3(*R,S*)-Benzyl-L-aspartate was prepared according to the methods reported in the literature.[1] ^{1}H NMR, and ^{13}C NMR spectra were recorded on a Bruker AM-400 spectrometer in $CDCl_3$, D_2O. The chemical shift (δ) of 1H NMR and ^{13}C NMR was given in ppm relative to solvent residual peak according to the work of Fulmer *et al.*,[2] Fast column chromatography was carried out using 200–300 mesh silica gel. Thin layer chromatography (TLC) analysis was carried out on glass sheets coated with 0.2 mm thickness silica gel, and visualized using alkaline potassium manganate (VII) solution, and/or UV light at 254 nm. All other reagents and compounds were analytical grade and used without further purification.

Analytic methods

Derivatization of amino acids: To 25 μL reaction solution was added 225 μL acetonitrile-water solution (v/v, 1:1) containing triethylamine (40 mg/mL) and 250 μL 2,3,4,6-tetra-O-acetyl-*β*-D-glucopyranosyl isothiocyanate (GITC, 4 mM) dissolved in acetonitrile, and the resultant mixture was incubated at 30 °C for 30 min.

Shimadzu LC-2010A_{HT} was used for reverse phase HPLC analysis with Hypersil ODS2 column (5μm, 4.6 mm×250 mm). Amino acid derivatives were analyzed using the mobile phase consists of methanol and water (0.005% phosphoric acid) under the following conditions: (1) L-aspartate derivative: 55% (v/v) methanol, 254 nm UV detection, 0.8 mL/min flow rate, and the column temperature was kept at 30°C. (2) 3(*R,S*)-methyl-D,L-aspartate derivative: 45% (v/v) methanol, and the other conditions were the same as (1). (3) 3(*R,S*)-hydroxy-D,L-aspartate derivative: 35% (v/v) methanol, and the other conditions were the same as (1). (4) 3(*R*)-benzyl-L-aspartic acid: 35% (v/v) methanol, 210 nm UV detection, and the other conditions were the same as (1).

Construction of AspBDC variants

The gene sequence of L-aspartate *β*-decarboxylase (AspBDC) from *Pseudomonas dacunhae*[3] was codon optimized and synthesized by Genscript (Nanjing). The vector pET-28a(+) and

host strain *E. coli* BL21 (DE3) were used for protein expression.

AspBDC variants were created by PCR using the AspBDC gene (pET 28a(+)) as the template. Oligonucleotide primers used for the generation of mutants were listed in Table S1. The PCR mixture (total volume 20 μL) contained: template plasmid (1.5 μL, 20 ng/μL), forward and reverse primers (1 μL, 10 μM each), DMSO (1 μL), 2× PrimeSTAR HS (10 μL), and ddH_2O (5.5 μL). The PCR mixture was first subjected to 98 °C for 3 min, followed by 16 cycles of denaturing at 98 °C for 10 s, annealing at 55 °C for 15 s, and elongation at 72 °C for 7 min 16 s. A final extension step at 72 °C for 5 min was conducted at the end the PCR reaction. To the PCR mixture was added 1 μL *Dpn* I and incubated at 37 °C for 5 h to eliminate the template plasmid. The digested PCR product was then used to transform the competent *E. coli* BL21 (DE3) cells.

Enzyme expression and purification

10 μL Bacteria store solution was used to inoculate 4 mL LB medium (containing 50 μg/mL kanamycin) and incubated at 37 °C and 180 rpm overnight. The overnight sub-cultures were transferred to 100 mL LB (1%, v/v) containing 50 μg/mL kanamycin and incubated at 37 °C and 180 rpm until OD_{600} reached 0.6~0.8. Then IPTG (final concentration 0.2 mM) was added to induce AspBDC expression and the culture was then incubated at 16 °C for another 24 h with shaking at 180 rpm. Cells were harvested by centrifugation at 7,000×*g* and 4 °C for 10 min and the supernatant was discarded. The cells were resuspended in the buffer (20 mM phosphate buffer, 0.5 M NaCl, 10 mM β-mercaptoethanol, 10 mM imidazole; pH 7.4) and the target proteins inside the cells were released by ultrasonication. The cell debris was removed by centrifugation at 16,000×*g* for 30 min at 4 °C.

The cell-free extract containing the His-tagged AspBDC was loaded onto a His trap Ni-NTA FF column and eluted with elution buffer (20 mM phosphate buffer, 0.5 M NaCl, 10 mM β-mercaptoethanol, 300 mM imidazole, pH 7.4) to obtain the purified enzyme.

Screening of non-natural substrates

The pH of the reaction mixture (0.5 mL) containing 100 mM KPB buffer (pH 6.0), 150 mM NaCl, substrate (20 mM), PLP (0.5 mM) was adjusted to 6.0 prior to the addition of purified enzyme (4 mg/mL) to initiate the reaction. The reaction was performed at 30 °C and 1000 rpm for 24 h, and the product formed was detected by HPLC and identified by UPLC-MS.

Molecular docking

The monomer crystal structure (PDB: 3FDD) of *Pseudomonas* dacunhae AspBDC has been reported.[2] The reported hexamer (PDB: 2zy4) crystal structure of *Pseudomonas* sp. ATCC 19121 AspBDC showing 93% sequence identity with *Pseudomonas dacunhae* AspBDC was used for docking using Autodock vina.[4]

Determination of total turnover number (TON)

The reaction mixture (0.5 mL) consists of 100 mM KPB (pH 6.0) containing 150 mM NaCl, 0.5 mM PLP, 10 mM substrate, and purified enzyme was incubated at 30 °C and 1000 rpm for 24 hours, and the TON was determined according to the following equation: TON = product (μmol)/enzyme (μmol).

Enzyme assay and kinetic parameters determination

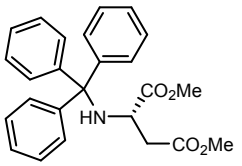
Enzyme assay was performed in a reaction mixture containing 100 mM KPB (pH 6.0), 150 mM NaCl, 10 mM substrate, 0.5 mM PLP, and purified enzyme with different concentrations. The reaction mixture was incubated at 30°C and 1000 rpm for a required period, and the reaction was terminated by metal bath at 95 °C for 10 min to denature the enzyme. The amount of product produced was analyzed by HPLC analysis. One unit of enzyme activity was defined as the amount of enzyme that catalyzes the formation of 1 μmol of product per minute under the assay conditions.

Kinetic constants determination: The reaction mixture (250 μL) consists of 195 μL purified enzyme in100 mM KPB (pH 6.0), 5 μL PLP (final concentration 0.5 mM) and 50 μL substrate with different concentrations was incubated at 30°C and 1000 rpm for a required period, and the product formed was measured by HPLC analysis.

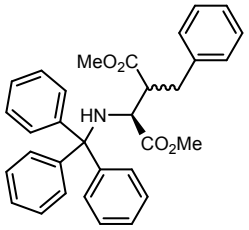
Preparation of L-homophenylalanine

The reaction mixture (15 mL) containing KPB buffer (100 mM, pH 6.0), 3(*R*)-benzyl-L-aspartate (10 mM), 150 mM NaCl and PLP (0.5 mM) was adjusted to a pH value of 6.0, and purified AspBDC R37A/T382G (final concentration 0.07 mg/mL) was added to start the reaction, equal amount of enzyme was supplemented at 5 h. The reaction was stopped by metal bath (95°C for 10 min) for inactivating the enzyme and the denatured protein was removed by centrifugation. L-Homophenylalanine was precipitated by adjusting the pH of the supernatant to 7.0. ^{1}H NMR (400 MHz) and ^{13}C NMR (100 MHz) spectra were all obtained in D_2O for L-homophenylalanine.[5]

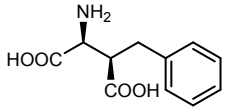
Chemical synthesis of 3(R,S)-benzyl-L-aspartate



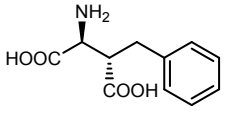
***N*-Trityl aspartate dimethyl ester**: **^{1}H NMR** (400 MHz, $CDCl_3$) *δ/ppm*: 7.50 – 7.48 (m, 6H), 7.28 – 7.24 (m, 6H), 7.19 (d, *J* = 7.3 Hz, 3H), 3.68 (s, 3H), 3.26 (s, 3H), 2.68 – 2.48 (m, 2H), 1.67 (br, 1H). **^{13}C NMR** (100 MHz, $CDCl_3$) *δ/ppm*: 173.9, 171.0, 145.7, 128.8, 127.9, 126.5, 71.2, 53.7, 52.0, 51.8, 40.2.



Dimethyl (3*S*)-2-benzyl-3-(tritylamino)succinate (3): **^{1}H NMR** (400 MHz, $CDCl_3$) *δ/ppm*: 7.45 (t, *J* = 7.4 Hz, 6H), 7.28 – 7.26 (m, 5H), 7.24 – 7.14 (m, 10H), 3.58(d, *J* = 16.9 Hz, 3H), 3.19 (d, *J* = 19.8 Hz, 3H), 3.06 – 2.81 (m, 2H), 1.64 (br, 1H). **^{13}C NMR** (100 MHz, $CDCl_3$) ^{13}C NMR (100 MHz, $CDCl_3$) *δ/ppm*: 173.1, 172.8, 145.7, 139.4, 129.1, 129.0, 129.0, 128.9, 128.6, 128.5, 128.1, 128.0, 126.7, 126.6, 71.3, 71.2, 58.3, 58.0, 53.1, 52.0, 51.9, 51.9, 51.8, 34.3, 33.7.



3(*R*)-benzyl-L-aspartate: **^{1}H NMR** (400 MHz, D_2O) *δ/ppm*: 7.40 – 7.30 (m, 5H), 3.71 (d, *J* = 4.3 Hz, 1H), 3.21 – 3.18 (m, 1H), 2.90 (ddd, *J* = 20.8, 13.7, 8.0 Hz, 2H). **^{13}C NMR** (100 MHz, D_2O) *δ/ppm*: 138.3, 128.9, 128.8, 126.8, 55.2, 49.2, 35.8. **HRMS** (ESI-TOF): m/z calcd for $C_{11}H_{14}NO_4^+$ 224.0923, found 224.0922.



3(*S*)-benzyl-L-aspartate: **^{1}H NMR** (400 MHz, D_2O) δ*/ppm*: 7.37 – 7.25 (m, 5H), 3.99 (d, *J* = 3.3 Hz, 1H), 3.13-3.08 (m, 1H), 2.90-2.76 (m, 2H). **^{13}C NMR** (100 MHz, D_2O) δ 138.6, 128.8, 128.7, 126.7, 55.5, 48.9, 33.2. [α]D 25 = +14.0 (c x, HCl_{aq} (1 M)). **HRMS** (ESI-TOF): m/z calcd for $C_{11}H_{14}NO_4^+$ 224.0923, found 224.0922.

2. Additional tables

Table S1. List of primers used for the construction of enzyme variants

	Primers	Sequences
Alanine scanning	K17A-F	AGCCCGTTTGAGCTCGCAGATGAGTTGATCAAG
	K17A-R	CTTGATCAACTCATCTGCGAGCTCAAACGGGCT
	L31A-F	GGCGACGGAAACCGCGCAATGCTCAATGCGGGG
	L31A-R	CCCCGCATTGAGCATTGCGCGGTTTCCGTCGCC
	R37A-F	ATGCTCAATGCGGGGGCAGGCAATCCCAATTTT
	R37A-R	AAAATTGGGATTGCCTGCCCCCGCATTGAGCAT
	N39A-F	AATGCGGGGCGGGGCGCACCCAATTTTCTGGCA
	N39A-R	TGCCAGAAAATTGGGTGCGCCCCGCCCCGCATT
	Y134A-F	ATTCTGGGCTGCAATGCACCCGTTCCCCCTCGG
	Y134A-R	CCGAGGGGGAACGGGTGCATTGCAGCCCAGAAT
	F204A-F	ATCGGCATGCCGGTTGCAACTCCGTACATAGAA
	F204A-R	TTCTATGTACGGAGTTGCAACCGGCATGCCGAT
	K315A-F	GTCTATTCATTCTCCGCATACTTTGGTGCCACT
	K315A-R	AGTGGCACCAAAGTATGCGGAGAATGAATAGAC
	T320A-F	AAATACTTTGGTGCCGCAGGCTGGCGTCTGGGT
	T320A-R	ACCCAGACGCCAGCCTGCGGCACCAAAGTATTT
	T382A-F	GTTGCCTTGAACCACGCAGCCGGTCTGTCCACG
	T382A-R	CGTGGACAGACCGGCTGCGTGGTTCAAGGCAAC
R37X	R37G-F	ATGCTCAATGCGGGGGGTGGCAATCCCAATTTT
	R37G-R	AAAATTGGGATTGCCACCCCCCGCATTGAGCAT
	R37V-F	ATGCTCAATGCGGGGGTTGGCAATCCCAATTTT
	R37V-R	AAAATTGGGATTGCCAACCCCCGCATTGAGCAT
	R37L-F	ATGCTCAATGCGGGGCTGGGCAATCCCAATTTT
	R37L-R	AAAATTGGGATTGCCCAGCCCCGCATTGAGCAT
	R37I-F	ATGCTCAATGCGGGGATTGGCAATCCCAATTTT
	R37I-R	AAAATTGGGATTGCCAATCCCCGCATTGAGCAT
	R37S-F	ATGCTCAATGCGGGGAGCGGCAATCCCAATTTT
	R37S-R	AAAATTGGGATTGCCGCTCCCCGCATTGAGCAT
	R37T-F	ATGCTCAATGCGGGGACCGGCAATCCCAATTTT
	R37T-R	AAAATTGGGATTGCCGGTCCCCGCATTGAGCAT
	R37F-F	ATGCTCAATGCGGGGTTTGGCAATCCCAATTTT
	R37F-R	AAAATTGGGATTGCCAAACCCCGCATTGAGCAT
	R37W-F	ATGCTCAATGCGGGGTGGGGCAATCCCAATTTT
	R37W-R	AAAATTGGGATTGCCCCACCCCGCATTGAGCAT
	R37P-F	ATGCTCAATGCGGGGCCGGGCAATCCCAATTTT
	R37P-R	AAAATTGGGATTGCCCGGCCCCGCATTGAGCAT
	R37H-F	ATGCTCAATGCGGGGCATGGCAATCCCAATTTT

	R37H-R	AAAATTGGGATTGCCATGCCCCGCATTGAGCAT
	R37K-F	ATGCTCAATGCGGGGAAAGGCAATCCCAATTTT
	R37K-R	AAAATTGGGATTGCCTTTCCCCGCATTGAGCAT
	R37C-F	ATGCTCAATGCGGGGTGTGGCAATCCCAATTTT
	R37C-R	AAAATTGGGATTGCCACACCCCGCATTGAGCAT
	R37D-F	ATGCTCAATGCGGGGGATGGCAATCCCAATTTT
	R37D-R	AAAATTGGGATTGCCATCCCCCGCATTGAGCAT
	R37E-F	ATGCTCAATGCGGGGGAAGGCAATCCCAATTTT
	R37E-R	AAAATTGGGATTGCCTTCCCCCGCATTGAGCAT
	R37Y-F	ATGCTCAATGCGGGGTATGGCAATCCCAATTTT
	R37Y-R	AAAATTGGGATTGCCATACCCCGCATTGAGCAT
	R37M-F	ATGCTCAATGCGGGGATGGGCAATCCCAATTTT
	R37M-R	AAAATTGGGATTGCCCATCCCCGCATTGAGCAT
	R37N-F	ATGCTCAATGCGGGGAATGGCAATCCCAATTTT
	R37N-R	AAAATTGGGATTGCCATTCCCCGCATTGAGCAT
	R37Q-F	ATGCTCAATGCGGGGCAGGGCAATCCCAATTTT
	R37Q-R	AAAATTGGGATTGCCCTGCCCCGCATTGAGCAT
	T382G-F	GTTGCCTTGAACCACGGTGCCGGTCTGTCCACG
	T382G-R	CGTGGACAGACCGGCACCGTGGTTCAAGGCAAC
	T382V-F	GTTGCCTTGAACCACGTTGCCGGTCTGTCCACG
	T382V-R	CGTGGACAGACCGGCAACGTGGTTCAAGGCAAC
	T382L-F	GTTGCCTTGAACCACCTGGCCGGTCTGTCCACG
	T382L-R	CGTGGACAGACCGGCCAGGTGGTTCAAGGCAAC
	T382I-F	GTTGCCTTGAACCACATTGCCGGTCTGTCCACG
	T382I-R	CGTGGACAGACCGGCAATGTGGTTCAAGGCAAC
	T382S-F	GTTGCCTTGAACCACAGCGCCGGTCTGTCCACG
	T382S-R	CGTGGACAGACCGGCGCTGTGGTTCAAGGCAAC
	T382R-F	GTTGCCTTGAACCACCGTGCCGGTCTGTCCACG
	T382R-R	CGTGGACAGACCGGCACGGTGGTTCAAGGCAAC
T382X	T382F-F	GTTGCCTTGAACCACTTTGCCGGTCTGTCCACG
	T382F-R	CGTGGACAGACCGGCAAAGTGGTTCAAGGCAAC
	T382W-F	GTTGCCTTGAACCACTGGGCCGGTCTGTCCACG
	T382W-R	CGTGGACAGACCGGCCCAGTGGTTCAAGGCAAC
	T382P-F	GTTGCCTTGAACCACCCGGCCGGTCTGTCCACG
	T382P-R	CGTGGACAGACCGGCCGGGTGGTTCAAGGCAAC
	T382H-F	GTTGCCTTGAACCACCATGCCGGTCTGTCCACG
	T382H-R	CGTGGACAGACCGGCATGGTGGTTCAAGGCAAC
	T382K-F	GTTGCCTTGAACCACAAAGCCGGTCTGTCCACG
	T382K-R	CGTGGACAGACCGGCTTTGTGGTTCAAGGCAAC
	T382C-F	GTTGCCTTGAACCACTGTGCCGGTCTGTCCACG
	T382C-R	CGTGGACAGACCGGCACAGTGGTTCAAGGCAAC
	T382D-F	GTTGCCTTGAACCACGATGCCGGTCTGTCCACG

	T382D-R	CGTGGACAGACCGGCATCGTGGTTCAAGGCAAC
	T382E-F	GTTGCCTTGAACCACGAAGCCGGTCTGTCCACG
	T382E-R	CGTGGACAGACCGGCTTCGTGGTTCAAGGCAAC
	T382Y-F	GTTGCCTTGAACCACTATGCCGGTCTGTCCACG
	T382Y-R	CGTGGACAGACCGGCATAGTGGTTCAAGGCAAC
	T382M-F	GTTGCCTTGAACCACATGGCCGGTCTGTCCACG
	T382M-R	CGTGGACAGACCGGCCATGTGGTTCAAGGCAAC
	T382N-F	GTTGCCTTGAACCACAATGCCGGTCTGTCCACG
	T382N-R	CGTGGACAGACCGGCATTGTGGTTCAAGGCAAC
	T382Q-F	GTTGCCTTGAACCACCAGGCCGGTCTGTCCACG
	T382Q-R	CGTGGACAGACCGGCCTGGTGGTTCAAGGCAAC

Table S2. The decarboxylation of 3(*R*)-benzyl-L-aspartate by AspBDC and its variants[a]

Entry	Mutants	TON (μmol product/μmol enzyme)
1	WT	9.1 ± 0.1
2	K17A	91 ± 0.1
3	L31A	12 ± 2
4	R37A	53 ± 5
5	N39A	9.0 ± 0.1
6	Y134A	21 ± 0.3
7	F204A	20 ± 1
8	K315A	4.0 ± 0.5
9	T320A	7.0 ± 0.3
10	T382A	184 ± 3

[a] The reaction mixture (0.5 mL) consists of 100 mM KPB (pH 6.0) containing 150 mM NaCl, 0.5 mM PLP, 10 mM substrate, and purified enzyme (6 mg/mL) was incubated at 30°C and 1000 rpm for 24 hours, and the TON was determined according to the following equation: TON = product (μmol)/enzyme (μmol).

Table S3. Specific activity of AspBDC and its variants R37A/T382G towards 3(*R*)-benzyl-L-aspartate[a]

Entry	Enzymes	Specific activity (mU/$mg_{protein}$)	Fold
1	WT	0.014 ± 0.002	1
2	T382G	60.6 ± 0.9	4320
3	T382G/R37A	216 ± 0.3	15400
4	T382G/R37F	37.1 ± 0.5	2650
5	T382G/K17A	145 ± 1.7	10357
6	T382G/Y134A	59.8 ± 0.5	4270
7	T382G/R37A/K17A	198 ± 1.5	14100
8	T382G/R37A/Y134A	14.1± 0.5	1000

[a] The reaction mixture containing 100 mM KPB (pH 6.0), 150 mM NaCl, 10 mM substrate, 0.5 mM PLP, and purified enzyme with different concentrations was incubated at 30°C and 1000 rpm for a required period, and the amount of product produced was analyzed by HPLC analysis.

3. Additional figures

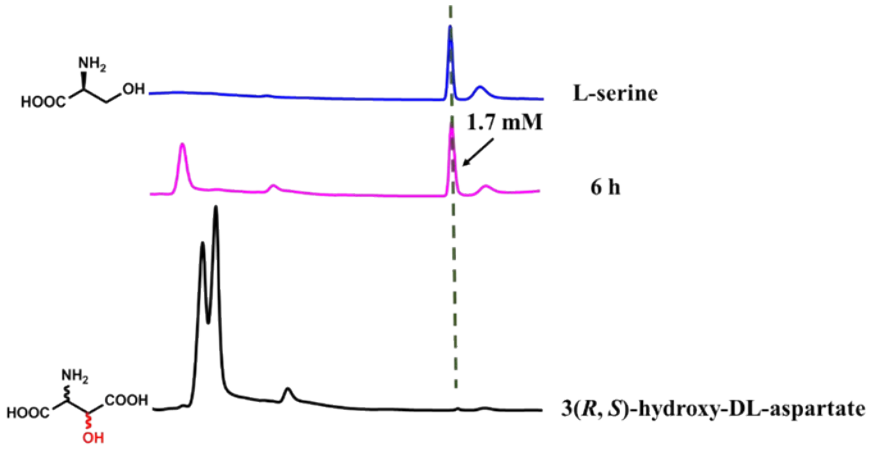


Figure S1. HPLC chromatograph of wild-type AspBDC catalyzed decarboxylation of 3(*R*, *S*)-hydroxy-DL-aspartate.

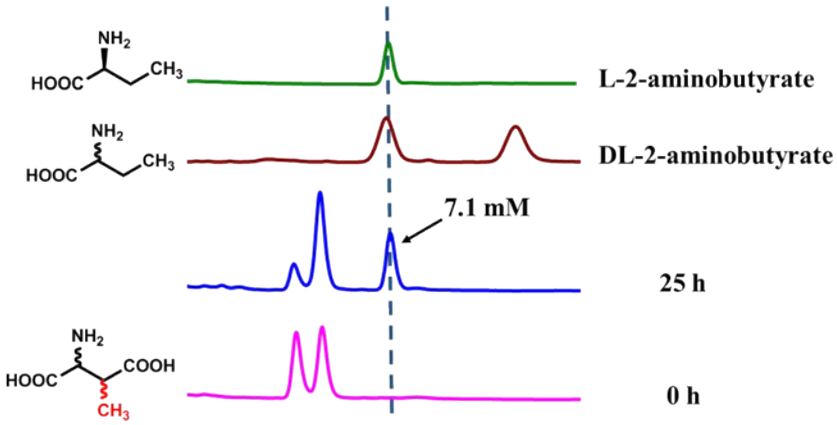


Figure S2. HPLC chromatograph of wild-type AspBDC catalyzed decarboxylation of 3(*R*, *S*)-methyl-DL-aspartate.

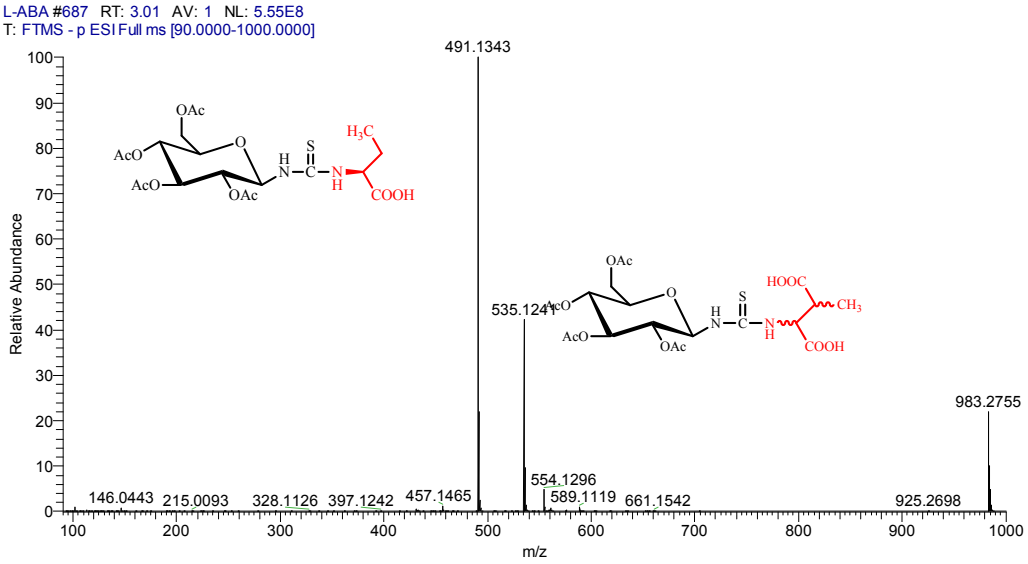


Figure S3. UPLC-MS analysis of the product produced by wild-type AspBDC catalyzed decarboxylation of 3(*R*,*S*)-methyl-DL-aspartate.

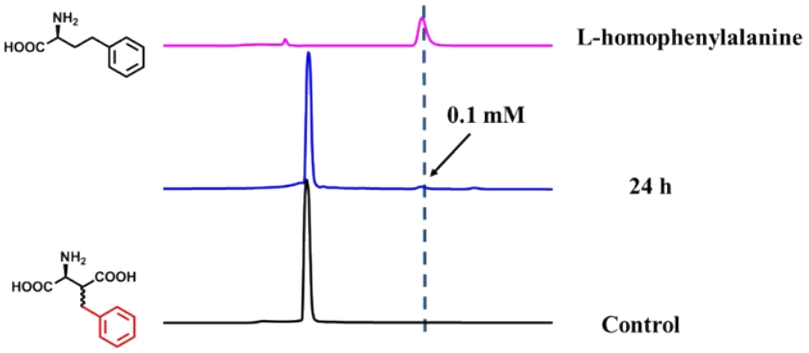


Figure S4. HPLC chromatograph of wild-type AspBDC catalyzed decarboxylation of 3(*R*, *S*)-benzyl-L-aspartate.

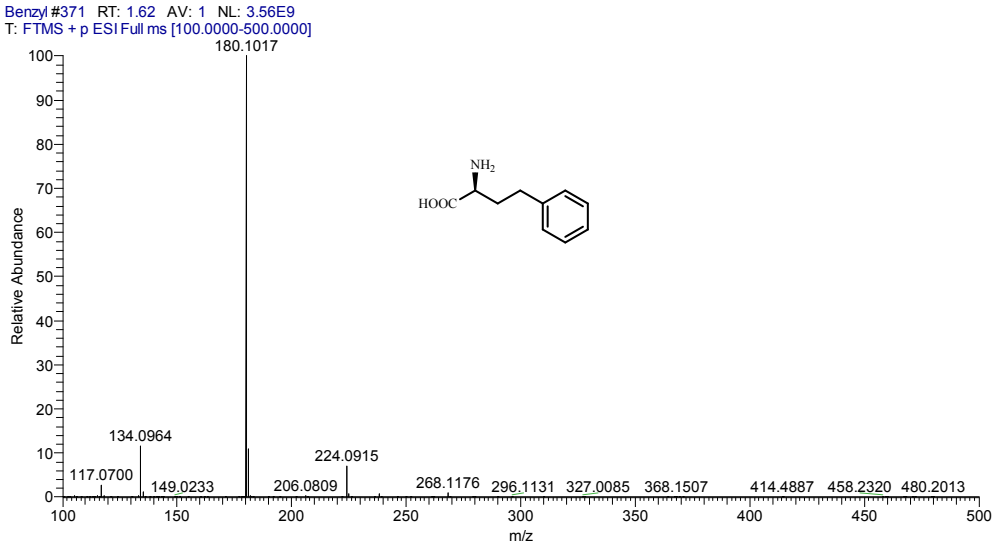


Figure S5. UPLC-MS analysis of the product produced by wild-type AspBDC catalyzed decarboxylation of 3(*R*,*S*)-benzyl-L-aspartate.

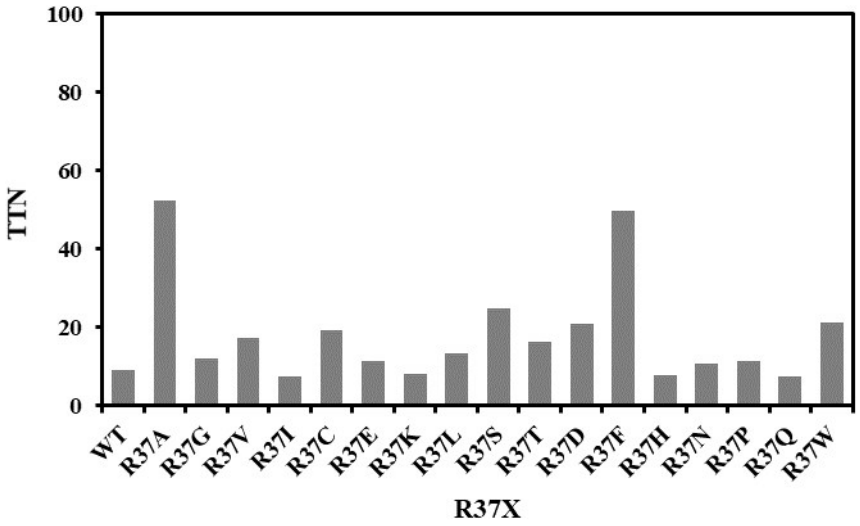


Figure S6. Decarboxylation of 3(*R*)-benzyl-L-aspartate by R37X variants of AspBDC.

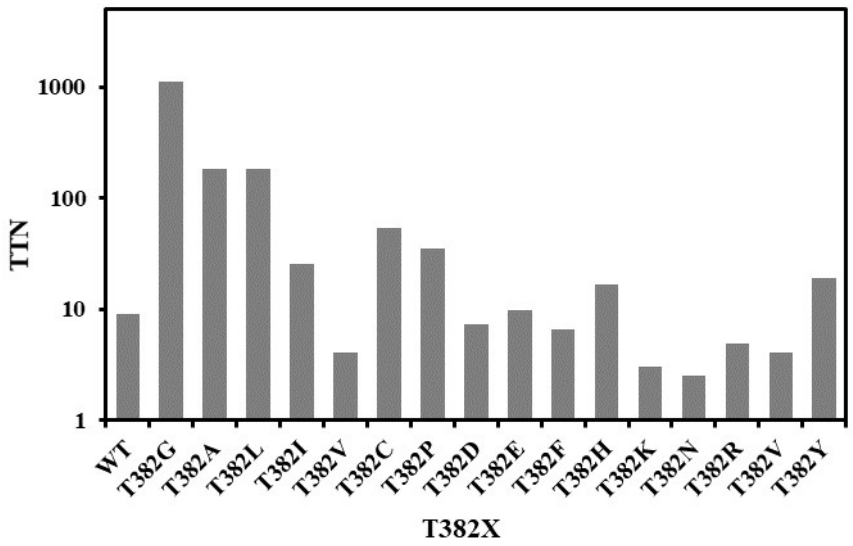


Figure S7. Decarboxylation of 3(*R*)-benzyl-L-aspartate by T382X variants of AspBDC.

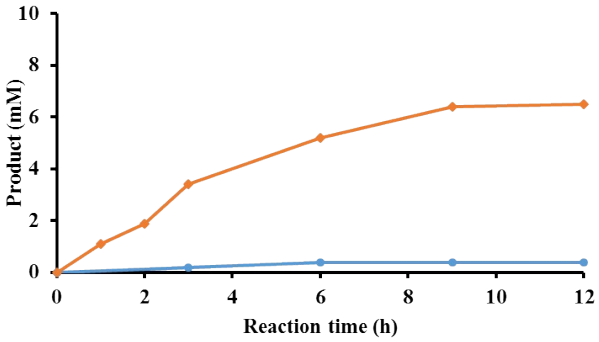


Figure S8. Reaction progress curves of 3(*R*)-benzyl-L-aspartate (orange) and 3(*S*)-benzyl-L-aspartate (blue) catalyzed by AspBDC R37A/T382G.

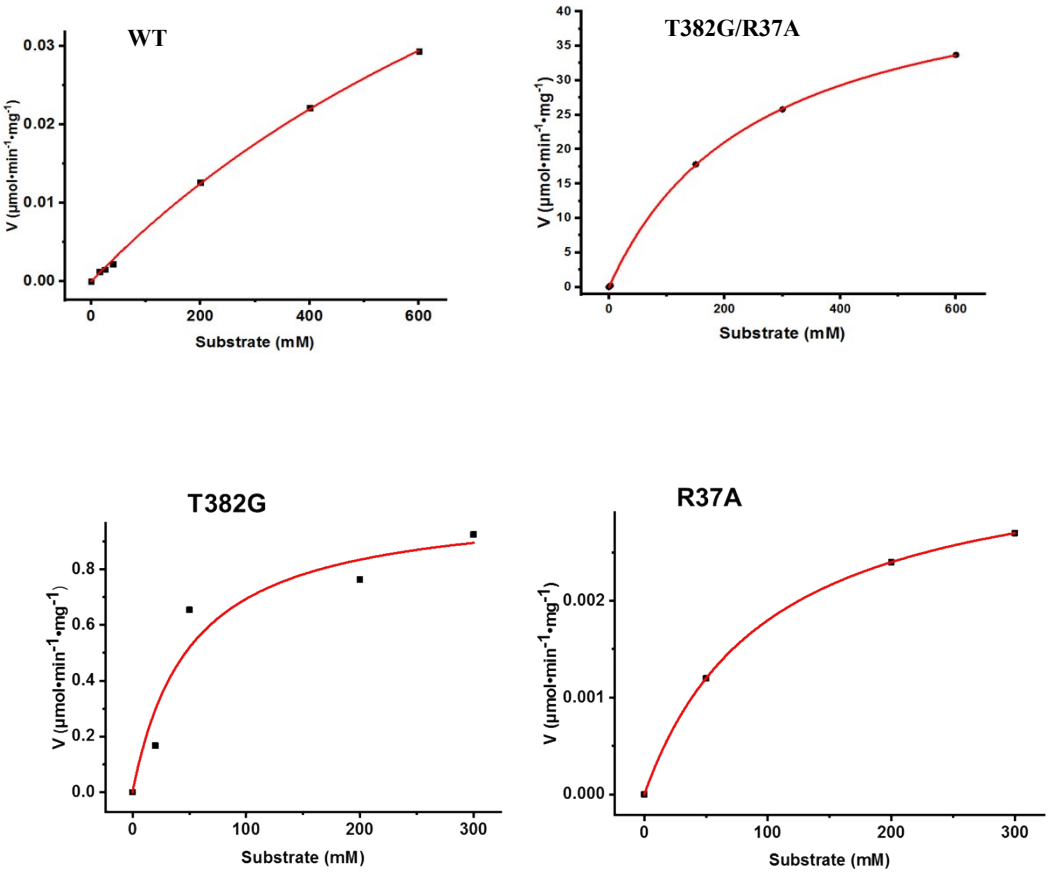


Figure S9. Kinetic study of wild-type AspBDC and mutants R37A, T382G, and T382G/R37A towards 3(*R*)-benzyl-L-aspartate.

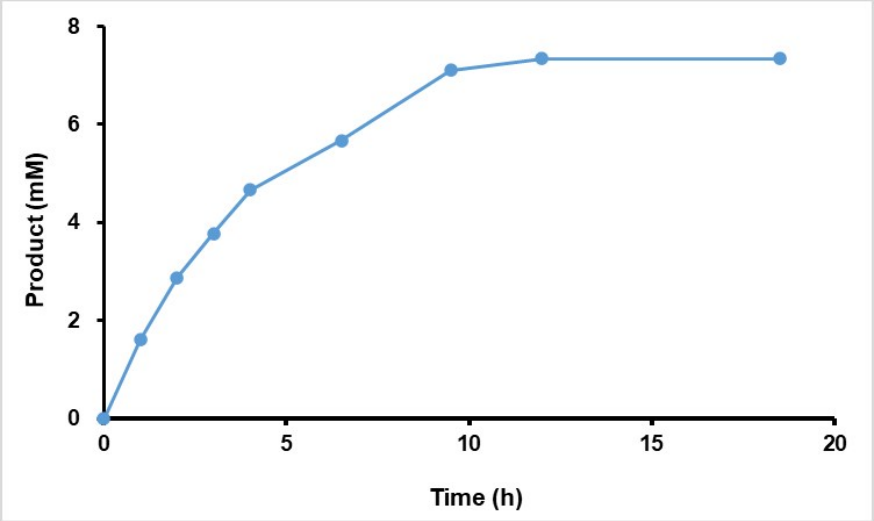
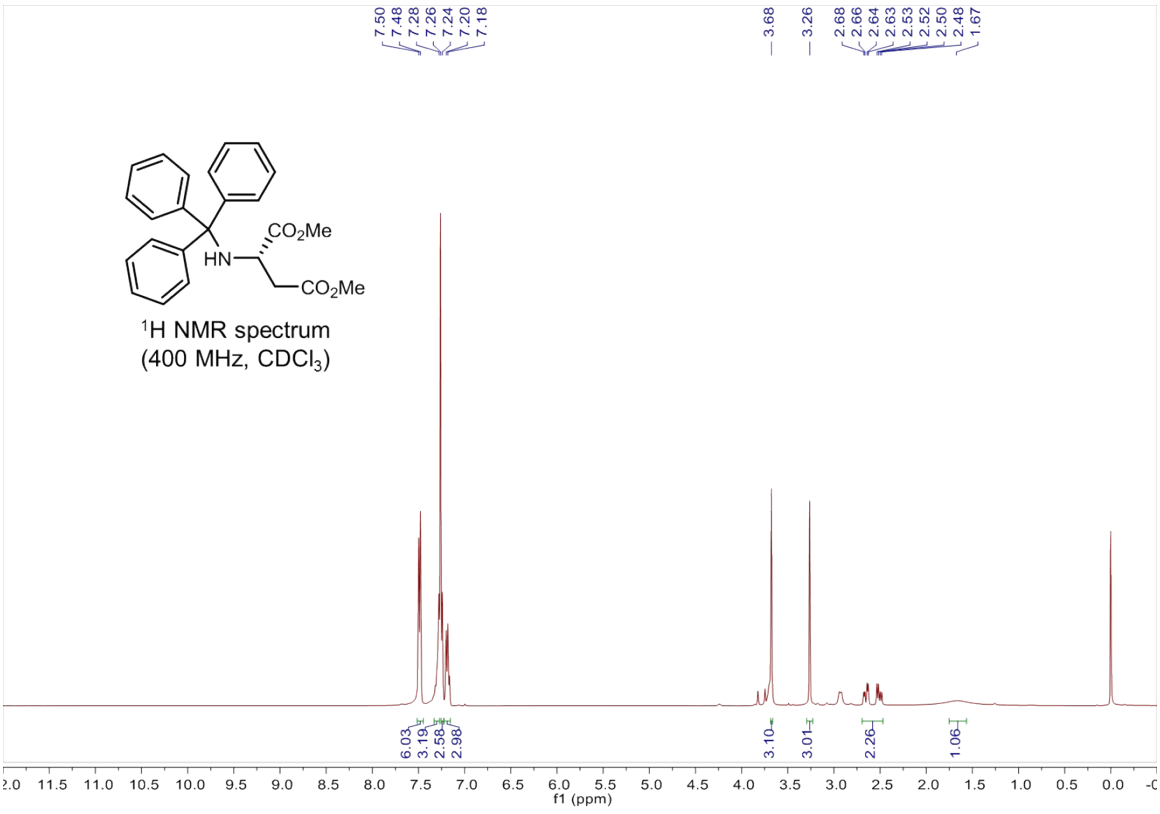


Figure S10. Reaction progress curve of AspBDC R37A/T382G catalyzed decarboxylation of 3(*R*)-benzyl-L-aspartate for the synthesis of L-homophenylalanine.


7.50
7.48
7.28
7.26
7.24
7.20
7.18
3.68
3.26
2.68
2.66
2.64
2.63
2.53
2.52
2.50
2.48
1.67
CO2Me
HN
CO2Me
1H NMR spectrum
(400 MHz, CDCl3)
6.03
3.19
2.58
2.98
3.10
3.01
2.26
1.06
f1 (ppm)

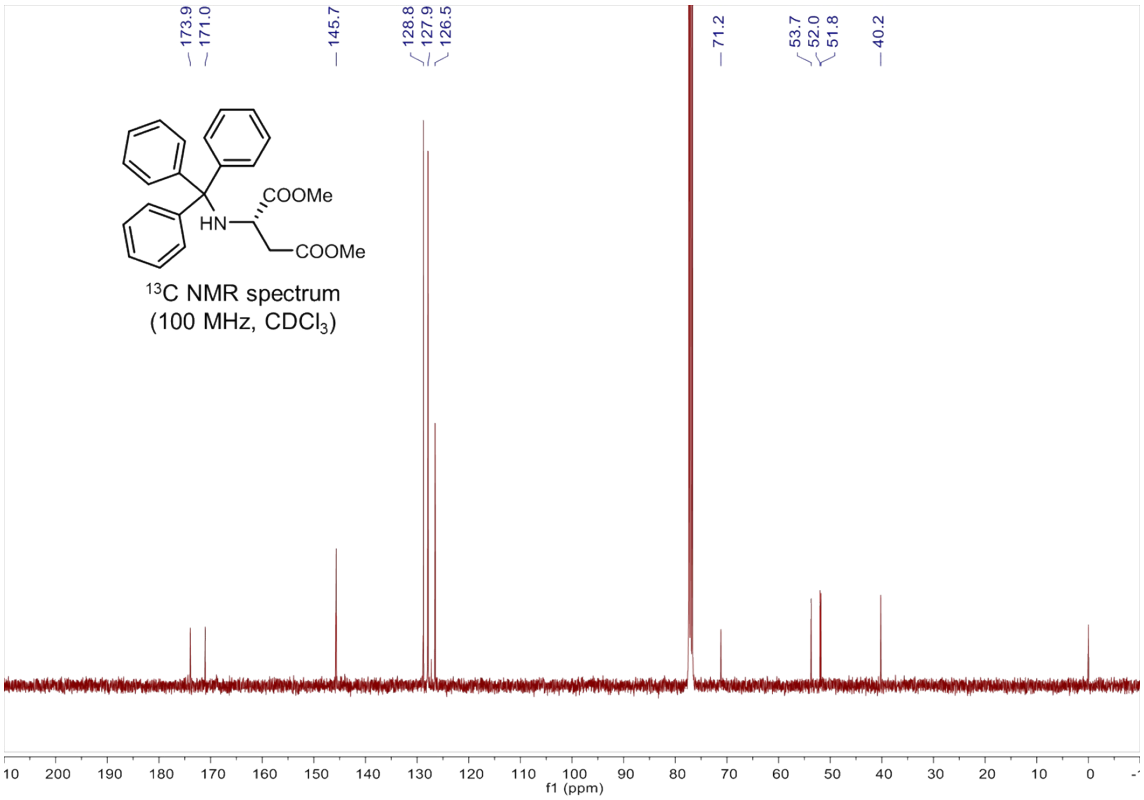


Figure S11. ^{1}H NMR and ^{13}C NMR spectra of *N*-trityl aspartate dimethyl ester.

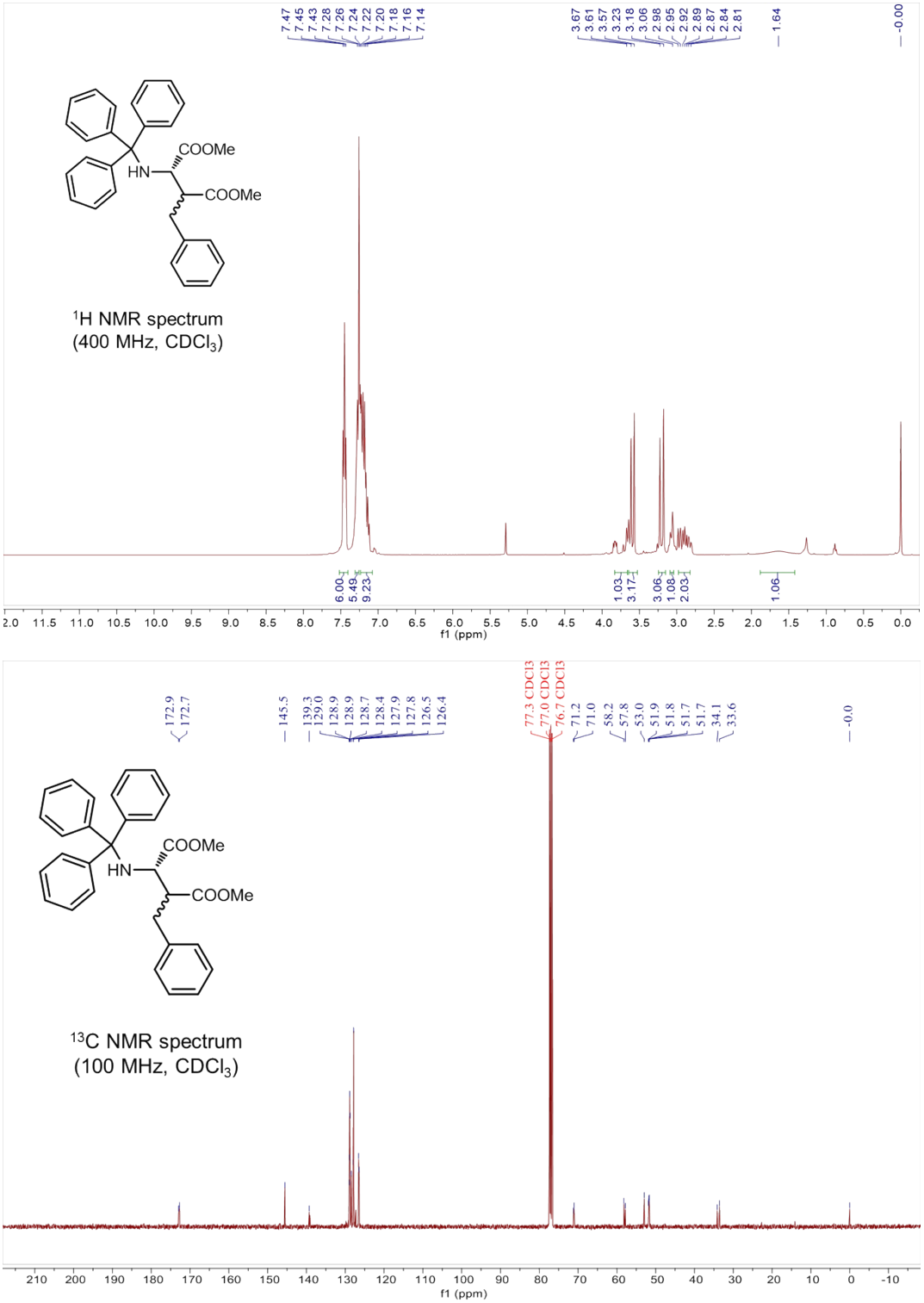
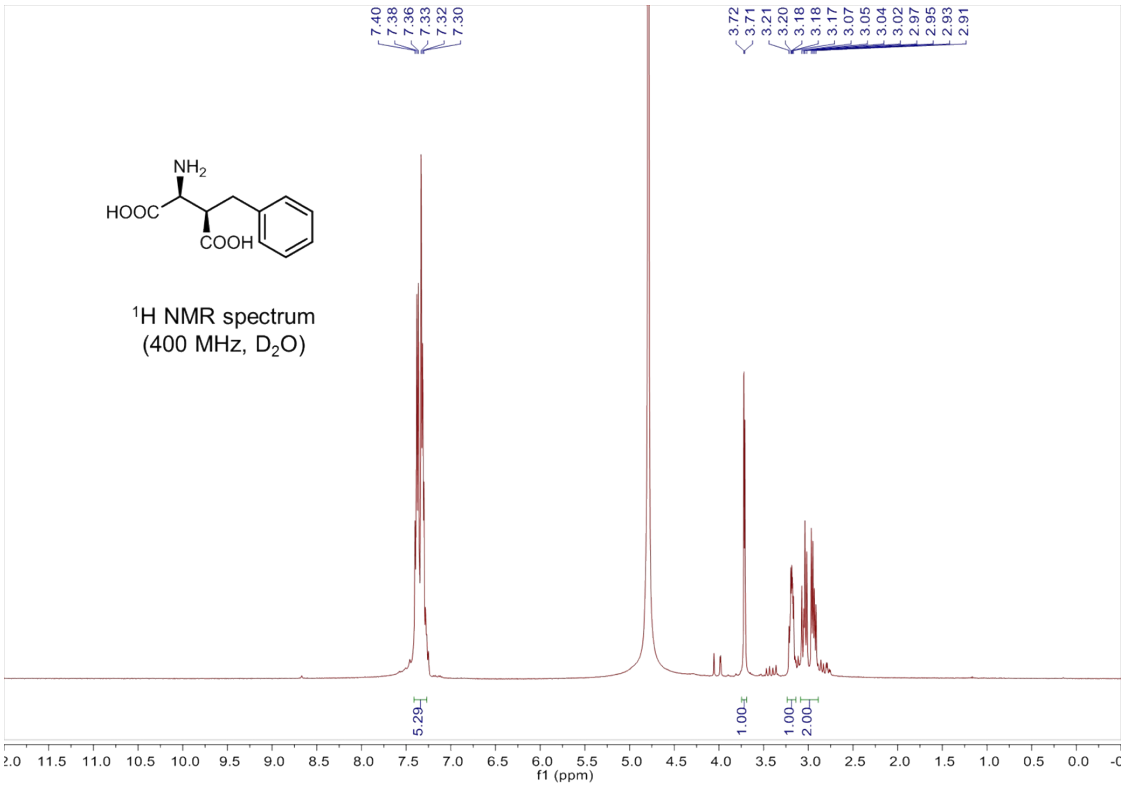


Figure S12. ^{1}H NMR and ^{13}C NMR spectra of *N*-tritylamino dimethyl ester *β*-benzylaspartate.



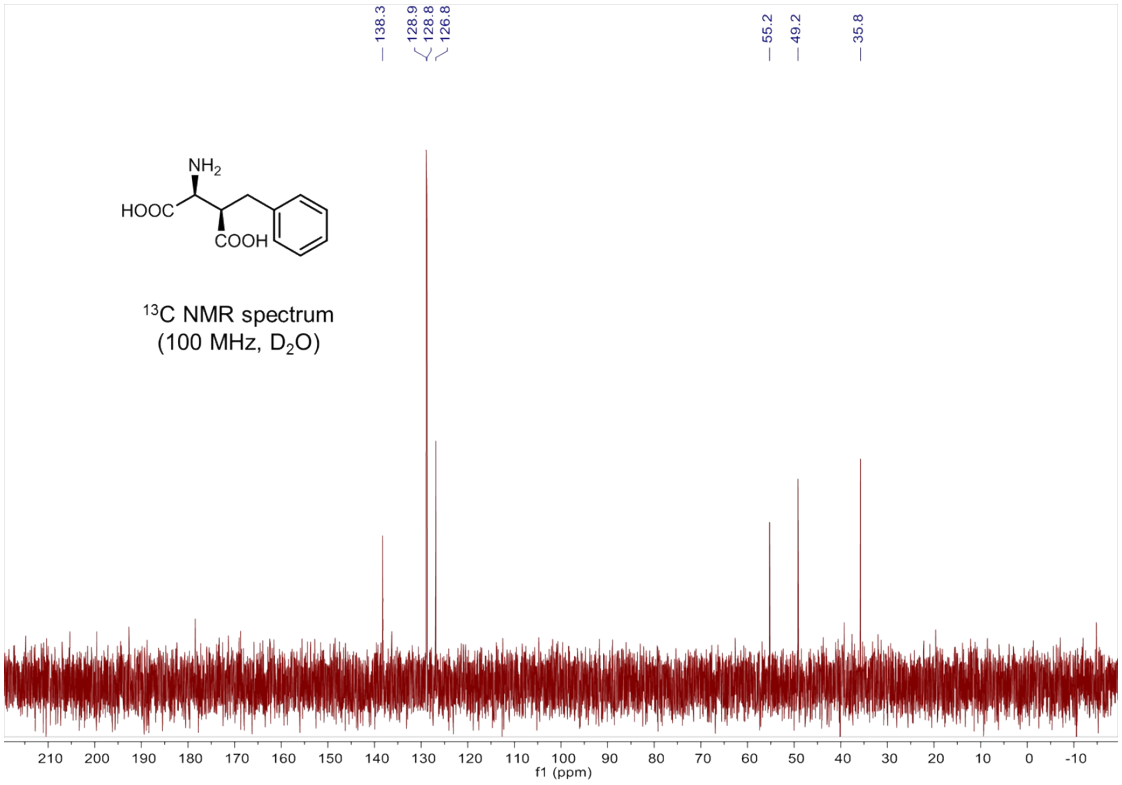
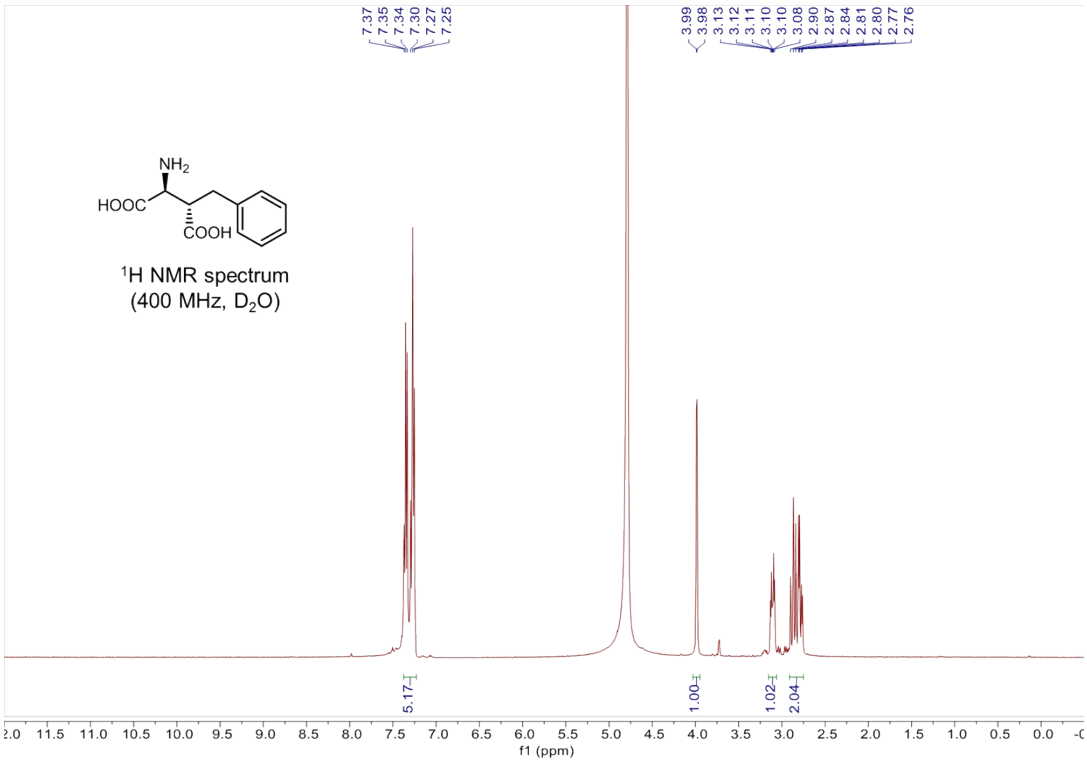


Figure S13. ^{1}H NMR and ^{13}C NMR spectra of 3(*R*)-benzyl-L-aspartate.


7.37
7.35
7.34
7.30
7.27
7.25
3.99
3.98
3.13
3.12
3.11
3.10
3.10
3.08
2.90
2.87
2.84
2.81
2.80
2.77
2.76
NH2
HOOC
COOH
1H NMR spectrum
(400 MHz, D2O)
5.17
1.00
1.02
2.04
f1 (ppm)

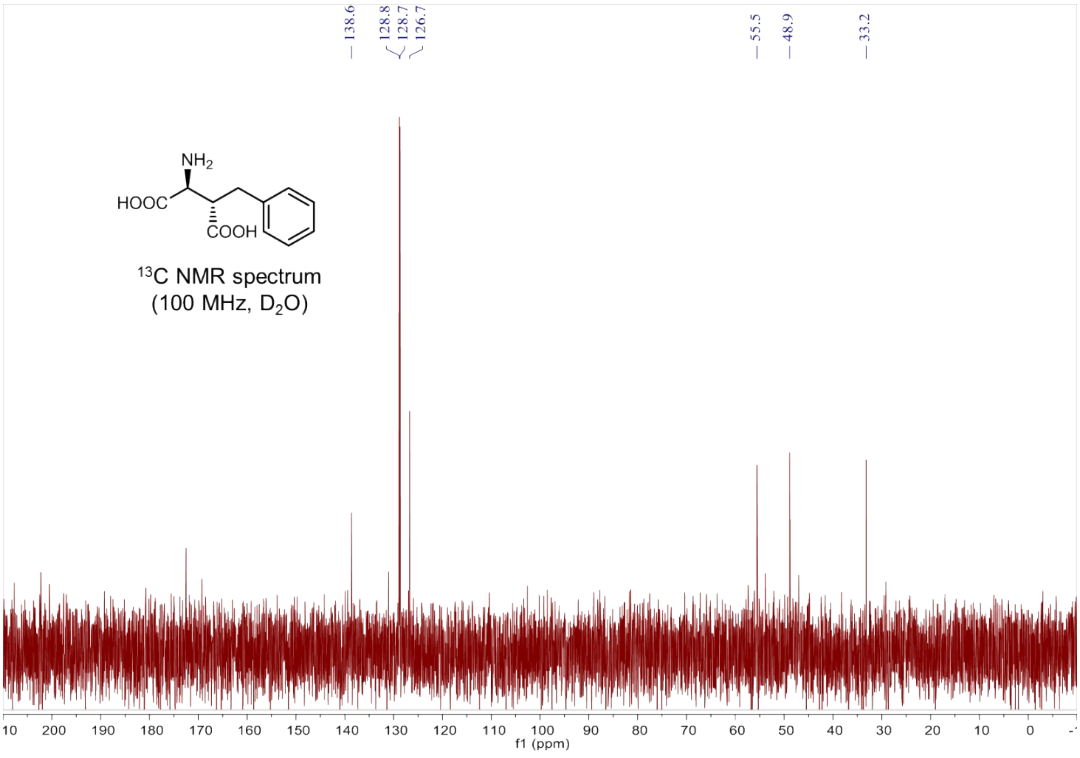
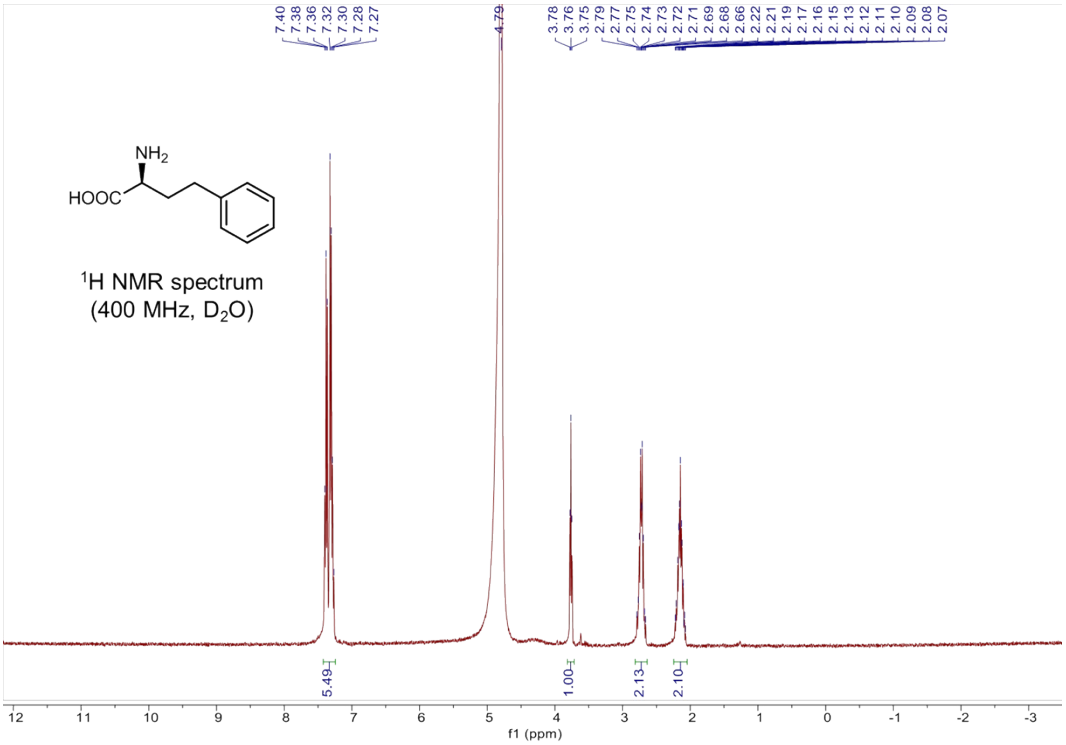


Figure S14. ^{1}H NMR and ^{13}C NMR spectra of 3(*S*)-benzyl-L-aspartate.



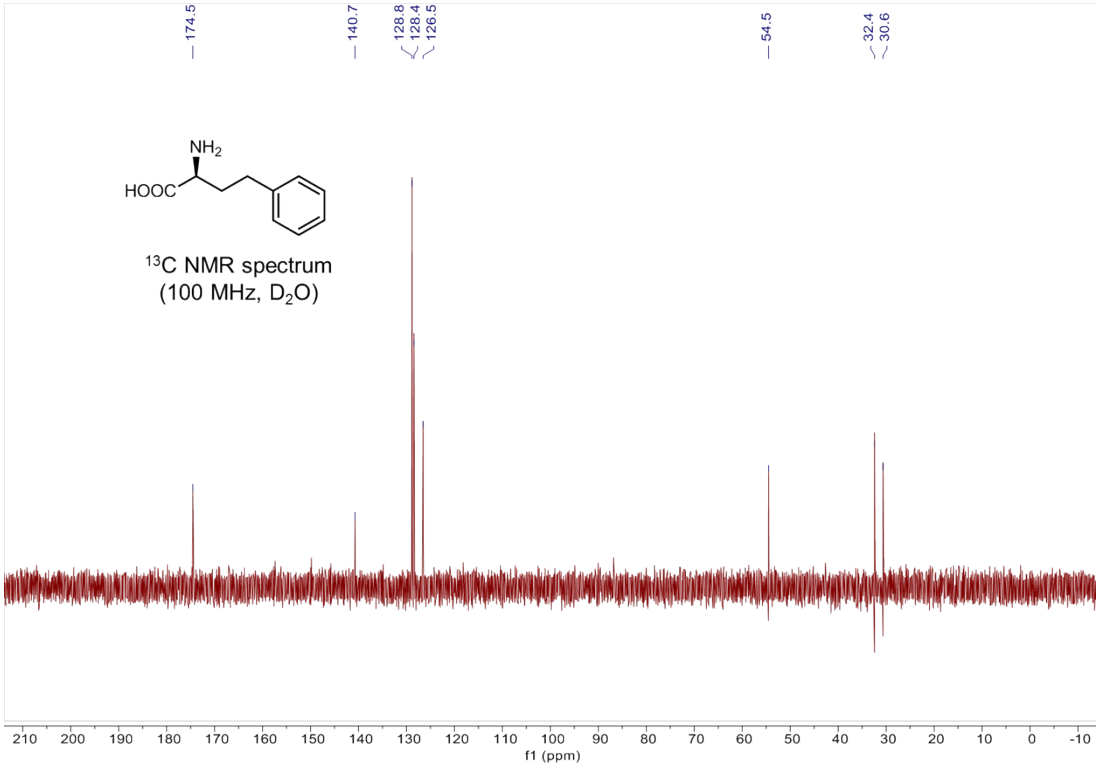


Figure S15. ^{1}H NMR and ^{13}C NMR spectra of L-homophenylalanine.

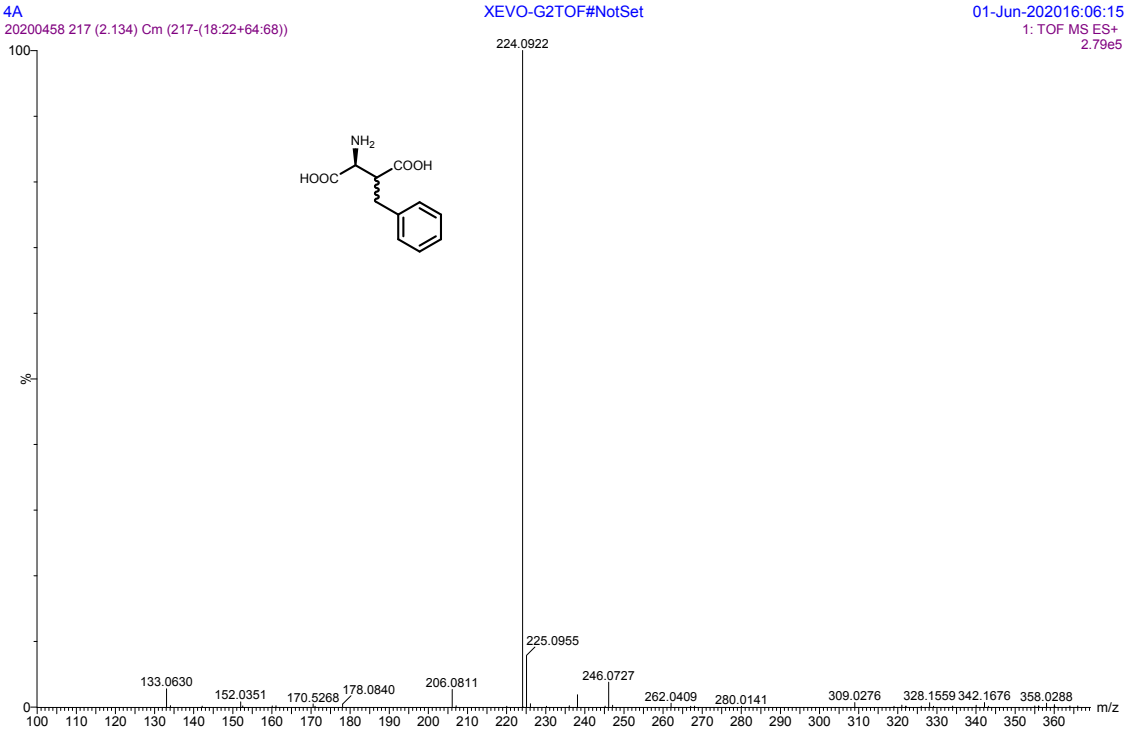


Figure S16. HRMS of chemically synthesized 3(*R*,*S*)-benzyl-L-aspartate.

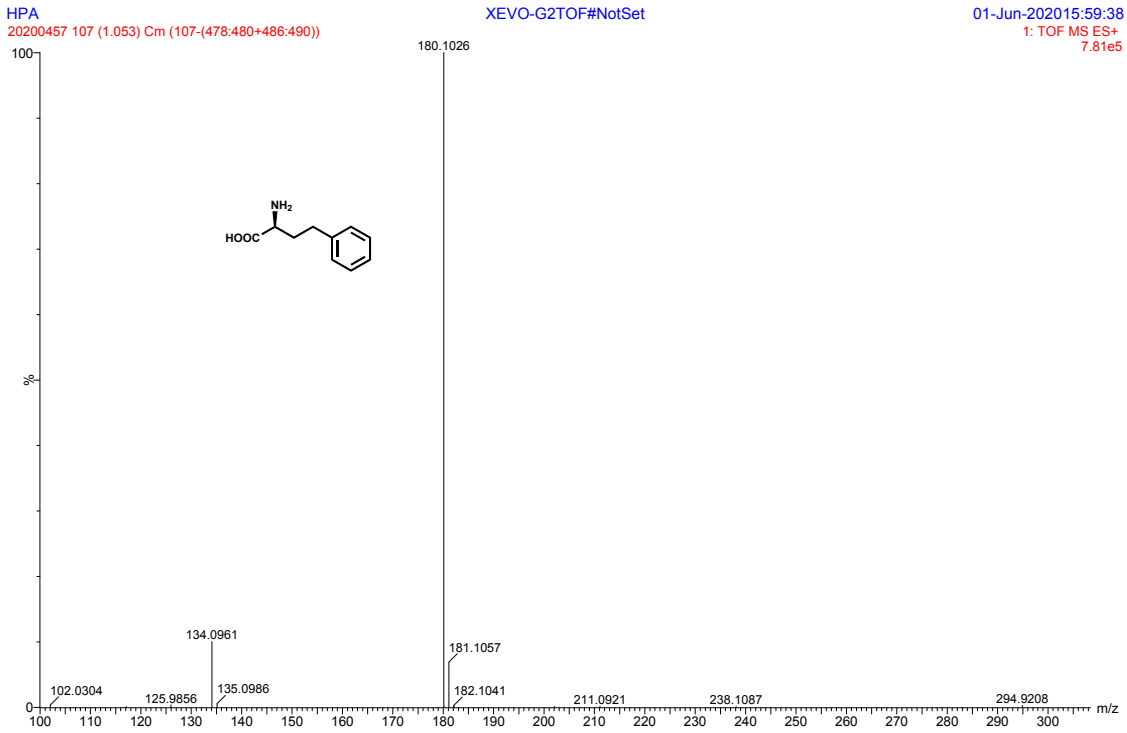


Figure S17. HRMS of L-homophenylalanine produced by AspBDC catalyzed decarboxylation of 3(*R*)-benzyl-L-aspartate.

4. References

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