Supporting Information

Structural diversification of bioactive bibenzyls through modular co-culture leading to the discovery of a novel neuroprotective agent

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Supplementary Material and Methods

1,1-Diphenyl-2-picrylhydrazyl (DPPH) assay

1,1-Diphenyl-2-picrylhydrazyl (DPPH) was weighed and dissolved in anhydrous ethanol with 1×10^{-4} mol/L. 100 µL of different concentrations of test solution and 100 µL DPPH · solution were added to the 96-well plate, and the commonly used antioxidant vitamin C was selected as the positive control (A₁). At the same time, the different concentration of the test solution without DPPH · (100 µL anhydrous ethanol instead of DPPH · solution) was used as the control to eliminate the interference of the color of the test product itself on the test results (A₂). In addition, DPPH · negative control (A₀) was set (100 µL anhydrous ethanol was used instead of the test sample). The 96-well plate was put into a microplate reader, oscillated for 1 min, and stored in this condition (room temperature, away from light) for 30 min. Then the absorbance value was measured at 517 nm.

DPPH clearance rate (%) = $[A_0 - (A_1 - A_2)]/A_0 \times 100\%$ (S1)

Pyrogallol autoxidation assay

180 μ L of 0.05 mol/L Tris-HCl buffer solution (pH 8.2) was added to the 96-well plate, then 40 μ L of sample solution (vitamin C was selected as the positive control) and 16 μ L of 9 mmol/L pyrogallol solution were added. 5 min later, 8 μ L of 3 mol/L HCl solution was added to terminate the reaction, and the absorbance was measured at 299 nm (A₁). Model control group (A₀) replaced the sample solution with 40 μ L water; Reference solution control group (A₁) added 40 μ L of sample solution to 180 μ L of 0.05 mol/L Tris-HCl buffer solution, and then added 16 μ L of water after fully mixing. In blank control group (A₂), pyrogallol and sample solution were replaced with 56 μ L water.

$$O_2^- \cdot \text{clearance rate } (\%) = [A_0 - (A_1 - A_{1'}) + A_2] / A_0] \times 100\%$$
 (S2)

Fenton reaction

30 μ L of 0.75 mmol/L *o*-diphenanthrene solution was added to the 96-well plate. Then 60 μ L PBS solution (pH 7.4) and 30 μ L distilled water were added. After fully mixing, 30 μ L of 0.75 mmol/L ferrous sulfate solution was added. After watering bath at 37 °C for 60 minutes, the absorbance was measured at 536 nm (A₀). The above procedure was repeated with 30 μ L distilled water instead of H₂O₂ to measure absorbance (A₁), then repeated with 30 μ L test solution instead of 30 μ L distilled water to determine absorbance (A₂); Only PBS solution and test solution were added, and the other reagents were supplemented with distilled water. The above procedure was repeated to measure the absorbance (A₃); only PBS solution was added, other reagents with distilled water was replaced to supplement. The above operation was repeated, and the absorbance(A₄) was measured.

OH clearance rate (%) = $[(A_2 - A_3 - A_0 + A_4)/(A_1 - A_0)] \times 100\%$ (S3)

Oxygen radical absorbance capacity (ORAC) assay

20 μ L of sample solution (vitamin C was selected as the positive control) was added to each well of the 96-well plate, then added 20 μ L of 75 mmol/L potassium phosphate buffer and 140 μ L of 18.3 mmol/L AAPH, and finally added 20 μ L of 630 nmol/L sodium fluorescein to start the reaction. The 96-well plate was quickly placed in a fluorescence microplate reader (preset temperature 37 °C) to start the measurement, and a point was measured every 2 min until the fluorescence intensity attenuated to a straight line. The antioxidant capacity of compounds could be reflected by comparing the protected integral area net AUC on the fluorescence decay curve (the integral area under the fluorescence decay curve minus the area under the blank curve without antioxidant).

Determination of 8-hydroxy-2'-deoxyguanosine (8-OHDG)

The level of 8-OHDG was detected following the ELISA kit instruction (Cusabio, Wuhan, China). 100 μ L standard or the supernatant of brain tissue homogenate was added per well, and incubated for 2 h at 37 °C. Then 100 μ L Biotin-antibody was added to each well after removing the liquid, and incubated for 1 h at 37 °C. Each well was aspirated and washed, and the process was repeated two times for a total of three washes. Then the steps were repeated using HRP-avidin before a total of five washes. At last, 90 μ L TMB substrate was added and incubated for 15 min at 37 °C and 50 μ L Stop solution to stop the reaction. The optical density of each well was determined within 5 min by using a microplate reader set to 450 nm.

Determination of Protein Carbonyl

Carbonylation of proteins was detected by Protein Carbonyl Colorimetric Assay. The supernatant of brain tissue homogenate was transferred to a clean centrifuge tube, and streptomycin sulfate with 10% volume fraction was dropped, fully mixed, and shaken intermittently at room temperature for 10 min. After centrifugation at 11,000 × g for 5 min, 100 μ L supernatant was added 400 μ L of 10 mmol/ L DNPH (dissolved in 2 mol/ L HCl). A blank control group was set, which was 2 mol/L HCl solution without DNPH. Each reaction system was placed in the dark for 1 h and swirled once every 10 min. After the reaction, 500 μ L of 0.2 kg/L trichloroacetic acid (TCA) solution was added to precipitate the protein hydrazone derivative. Centrifugation was performed at 4 °C at 12,000 × g for 15 min, and the supernatant was discarded. The precipitation was dissolved with 1 mL ethanol and ethyl acetate mixture (V/V = 1:1) for 3 times, and the final precipitation at 12,000 × g for 15 min, the absorbance value of supernatant was measured at 370 nm.

Quantitative RT-PCR

The rat brain tissue was homogenized with Trizol reagent (1 mL for 100 mg of tissue, TransGen Biotech, Cat ET111). 1 mL of homogenate was mixed with 200 µL chloroform in a centrifuge tube and centrifuged at 10,000 × g for 15 min at 4 °C. The supernatant was then mixed with 500 µL of isopropyl alcohol in a new 1.5 mL centrifuge tube and centrifuged at 10,000 × g for 10 min at 4 °C. After discarding the supernatant, the precipitate was rinsed with 1 mL of 75% absolute ethanol (750 µL absolute ethanol and 250 µL of DEPC water). After centrifugation at 10,000 × g for 5 min at 4 °C, the supernatant was discarded and the RNA was resuspended in 50 µL of DEPC water. After uniform quantification, mRNA was reverse transcribed into cDNA using Revert Aid First Strand cDNA Synthesis Kit (Yeasen, Cat 11141ES60). cDNA was generated by reverse transcription at 25 °C for 5 min, 55 °C for 15 min and 85 °C for 5 min. The qRT-PCR conditions were as follows: 95 °C for 30 s, followed by 40 cycles of 95 °C for 10 s, and 60 °C for 30 s. The primer sequences used for qRT-PCR are shown in **Table S4**. The relative expression of objective mRNA was normalized to β-actin mRNA and calculated using the $2^{-\Delta\Delta CT}$ method.

Western Blot

Protein samples from operative hemispheres of rats and SK-N-SH were prepared using RIPA lysis buffer supplemented with complete EDTA-free protease inhibitor mixtures (4693116001, Roche, Indianapolis, IN) and phosphatase inhibitor mixtures (04906845001, Roche, Indianapolis, IN). Protein samples were separated on SDS-polyacrylamide gels and transferred to PVDF membranes. The membrane was blocked with 5% nonfat milk for 2 h and subsequently incubated with the following primary antibodies overnight at 4 °C: anti-β-actin (1:2000, ZSGB-BIO, TA-09), anti-Aifm3 (1:500, proteintech, 14778-1-AP), anti-Nrf-2 (1:2000, proteintech, 16396-1-AP), anti-HO-1 (1:2000, Abcam, ab189491), anti-NQO-1 (1:2000, Abcam, ab80588). Then anti-mouse or anti-rabbit IgG-HRP (1:2000, ZSGB-BIO, ZB-2301; ZB-2305) were used as secondary antibodies for 2 h at room temperature, signals were detected using Image Quant LAS 500 (GE Healthcare). Three samples per group were used for western blot analysis.

Supplementary Tables

Gene	Full name	Source organism	Source
DoBBS1	Bibenzyl synthase	Dendrobium officinale	This study
DoBBS2	Bibenzyl synthase	D. officinale	This study
DoBBS3	Bibenzyl synthase	D. officinale	This study
DoBBS4	Bibenzyl synthase	D. officinale	This study
DoBBS5	Bibenzyl synthase	D. officinale	This study
DoBBS6	Bibenzyl synthase	D. officinale	This study
DoBBS7	Bibenzyl synthase	D. officinale	This study
DoBBS8	Bibenzyl synthase	D. officinale	This study
DoBBS9	Bibenzyl synthase	D. officinale	This study
DoOMT1	O-methyltransferase	D. officinale	This study
DoOMT2	O-methyltransferase	D. officinale	This study
DoOMT3	O-methyltransferase	D. officinale	This study
DoOMT4	O-methyltransferase	D. officinale	This study
DoOMT5	O-methyltransferase	D. officinale	This study
DoOMT6	O-methyltransferase	D. officinale	This study
DoOMT7	O-methyltransferase	D. officinale	This study
DoOMT8	O-methyltransferase	D. officinale	This study
DoOMT9	O-methyltransferase	D. officinale	This study
DoOMT10	O-methyltransferase	D. officinale	This study
DoOMT11	O-methyltransferase	D. officinale	This study
metK	S-adenosylmethionine synthetase	Escherichia. coli	Markham et al ¹
PsPT1	Prenyltransferase	Periconia sp. F-31	This study
UGT71E5	Glycosyltransferase	Carthamus tinctorius	Xie et al^2 .
At4CL1	4-coumarate coenzyme A ligase	Aradopsis thaliana	Ehlting et al ³ .
AAE13	Malonyl-CoA synthase	A. thaliana	Chen et al^4 .
MatC	malonate carrier protein	Rhizobium trifolii	An et al^5 .
MK	Mevalonate kinase	Staphylococcus aureus	Wang et al ⁶ .
PMK	Phosphomevalonate kinase	S. aureus	Wang et al ⁶ .
PMD	Mevalonate pyrophosphate decarboxylase	S. aureus	Wang et al ⁶ .
IDI	IPP isomerase	Bacillus subtilis	Wang et al ⁶ .
AACT	Acetoacetyl-CoA thiolase	E. coli	Wang et al 6 .
HMGS	HMG-CoA synthase	Enterococcus. faecalis	Wang et al^6 .
HMGR	Truncated HMG-CoA reductase	E. faecalis	Wang et al ⁶ .

Table S1. Genes used in this study.

Plasmids	Detailed information	Source
pET-28a	T7 promoters, pBR322 ori, Kan ^R	Novagen
pET-21c	T7 promoters, pBR322 ori, Amp ^R	Novagen
pACYCDuet-1	Double T7 promoters, p15A ori, Cm ^R	Novagen
pETDuet-1	Double T7 promoters, ColE1 ori, Amp ^R	Novagen
pCDFDuet-1	Double T7 promoters, CDF ori, Sm ^R	Novagen
p01	pET-28a-DoBBS1	This study
p02	pET-28a-DoBBS2	This study
p03	pET-28a-DoBBS3	This study
p04	pET-28a-DoBBS4	This study
p05	pET-28a-DoBBS5	This study
p06	pET-28a-DoBBS6	This study
p07	pET-28a-DoBBS7	This study
p08	pET-28a-DoBBS8	This study
p09	pET-28a-DoBBS9	This study
p10	pET-28a-DoOMT1	This study
p11	pET-28a-DoOMT2	This study
p12	pET-28a-DoOMT3	This study
p13	pET-28a-DoOMT4	This study
p14	pET-28a-DoOMT5	This study
p15	pET-28a-DoOMT6	This study
p16	pET-28a-DoOMT7	This study
p17	pET-28a-DoOMT8	This study
p18	pET-28a-DoOMT9	This study
p19	pET-28a-DoOMT10	This study
p20	pET-28a-DoOMT11	This study
p21	pCDFDuet-1-metK	This study
p22	pETDuet-1-AAE13-MatC	This study
p23	pCDFDuet-1-DoBBS8	This study
p24	pACYCDuet-1-At4CL1	This study
p25	pCDFDuet-1-PsPT1	This study
p26	pET-28a- <i>UGT71E5</i>	This study
pXL13	pET-28a-MK-PMK-PMD-IDI	This study
pXL17	pET-21c-AACT-HMGS-HMGR	This study

Table S2. Plasmids used in this study.

Strains	Detailed information	Source
E01	Transetta (DE3): p01	This study
E02	Transetta (DE3): p02	This study
E03	Transetta (DE3): p03	This study
E04	Transetta (DE3): p04	This study
E05	Transetta (DE3): p05	This study
E06	Transetta (DE3): p06	This study
<i>E07</i>	Transetta (DE3): p07	This study
E08	Transetta (DE3): p08	This study
E09	Transetta (DE3): p09	This study
E10	Transetta (DE3): p10	This study
E11	Transetta (DE3): p11	This study
E12	Transetta (DE3): p12	This study
E13	Transetta (DE3): p13	This study
E14	Transetta (DE3): p14	This study
E15	Transetta (DE3): p15	This study
E16	Transetta (DE3): p16	This study
E17	Transetta (DE3): p17	This study
E18	Transetta (DE3): p18	This study
E19	Transetta (DE3): p19	This study
E20	Transetta (DE3): p20	This study
E-DoBBS8	BL21(DE3): p22, p23, p24	This study
E-DoOMT1	BL21(DE3): p10, p21	This study
E-DoOMT6	BL21(DE3): p15, p21	This study
E-PsPT1	BL21(DE3): p25, pXL13, pXL17	This study
E-UGT71E5	Transetta (DE3): p26	Xie et al^2 .

Table S3. Strains used in this study.

Table S4. Primers used in this study.

Primer	Sequence (5'→3')
DoBBS1-F	CAGCAAATGGGTCGCGGATCCATGCCGAGCCTTGAATCCATCAG
DoBBS1-R	GTGGTGGTGGTGGTGCTCGAGTCAGAGATGGACACTGCGTAGAAC
DoBBS2-F	CAGCAAATGGGTCGCGGATCCATGCCGAGCCTTGAATCCATCAG
DoBBS2-R	GTGGTGGTGGTGGTGCTCGAGTCAGAGATGGACACTGCGTAGAAC
DoBBS3-F	CAGCAAATGGGTCGCGGATCCATGCCGAGCCTTGAATCCATCAG
DoBBS3-R	GTGGTGGTGGTGGTGCTCGAGTCAGAGATGGACACTGCGTAGAAC
DoBBS4-F	CAGCAAATGGGTCGCGGATCCATGCCGAGCCTTGAATCCATCAG
DoBBS4-R	GTGGTGGTGGTGGTGCTCGAGTCAGAGATGGACACTGCGTAGAAC
DoBBS5-F	CAGCAAATGGGTCGCGGATCCATGCCGAGCCTTGAATCCATCAG
DoBBS5-R	GTGGTGGTGGTGGTGCTCGAGTCAGAGAGGGACACTGCGTAGAAC
DoBBS6-F	CAGCAAATGGGTCGCGGATCCATGCCGAGCCTTGAATCCATCAG
DoBBS6-R	GTGGTGGTGGTGGTGCTCGAGTCAGAGAGGGACACTGCGTAGAAC
DoBBS7-F	CAGCAAATGGGTCGCGGATCCATGAAAGCTGTTAGAAAAGTAAC
DoBBS7-R	GTGGTGGTGGTGGTGCTCGAGTCAAACAAGAGGAGCGCTACGAAG
DoBBS8-F	CAGCAAATGGGTCGCGGATCCATGCCGAGCCTTGAATCCATCAA
DoBBS8-R	GTGGTGGTGGTGGTGCTCGAGTCAAATTGGAACACTGCGGAGGAT
DoBBS9-F	CAGCAAATGGGTCGCGGATCCATGCCGAGCCTTGAATCCATCAA
DoBBS9-R	GTGGTGGTGGTGGTGCTCGAGTCAAATTGGAACACTGCGGAGGAT
DoOMT1-F	CAGCAAATGGGTCGCGGATCCATGGATTCAGAATCTCATCAG
DoOMT1-R	GTGGTGGTGGTGGTGCTCGAGTTTGCTCAACTCCATTATCCAAGC
DoOMT2-F	CAGCAAATGGGTCGCGGATCCATGGGCAGTTACAACGCCACCG
DoOMT2-R	GTGGTGGTGGTGGTGCTCGAGCTTGATGAATTCCATAACCCAAC
DoOMT3-F	CAGCAAATGGGTCGCGGATCCATGGGTTCAGAATCTCATAAAC
DoOMT3-R	GTGGTGGTGGTGGTGCTCGAGTTTGCTCAACTCCATTATCCAAGC
DoOMT4-F	CAGCAAATGGGTCGCGGATCCATGGCGGCCTCCGGCGGAGAAAT
DoOMT4-R	GTGGTGGTGGTGGTGCTCGAGCTTCTGGAACTCTAGAACAGTA
DoOMT5-F	CAGCAAATGGGTCGCGGATCCATGCCAGAATTAAGCAATAAAAC
DoOMT5-R	GTGGTGGTGGTGGTGCTCGAGAATCCAAGCTTCTATGACATGC
DoOMT6-F	CAGCAAATGGGTCGCGGATCCATGGACGGTGATGATCTCTCC
DoOMT6-R	<u>GTGGTGGTGGTGGTGCTCGAG</u> GACGACGCGGCGGCAAATCGTG
DoOMT7-F	CAGCAAATGGGTCGCGGATCCATGGACGTTGATGATCTCTCCAC
DoOMT7-R	GTGGTGGTGGTGGTGCTCGAGGACGACGCGGCGGCAAATCGTG
DoOMT8-F	CAGCAAATGGGTCGCGGATCCATGGCTAATCCTGGTAGAATTTTC
DoOMT8-R	GTGGTGGTGGTGGTGCTCGAGAGCAACCCGCCTACAAATGG
DoOMT9-F	CAGCAAATGGGTCGCGGATCCATGGCGATATCACCTCCGTCCC
DoOMT9-R	GTGGTGGTGGTGGTGCTCGAGCTCCCTTTTGCGGCAGATTGTC
DoOMT10-F	CAGCAAATGGGTCGCGGATCCATGGCGACCGCCACCGCGGAGG

DoOMT10-R	GTGGTGGTGGTGGTGCTCGAGGCTAACACGGCGGCAGAGAGTA
DoOMT11-F	CAGCAAATGGGTCGCGGATCCATGCAGTGCCTATTGCAGAGTC
DoOMT11-R	GTGGTGGTGGTGGTGCTCGAGTTTGATTCGCCTGCAAATGGTG
pACYC-At4CL1-F	GCAGATCTCAATTGGATGGCGCCACAAGAACAAGC
pACYC-At4CL1-R	ATCGCGTGGCCGGCCTCACAATCCATTTGCTAG
pCDF-DoBBS8-F	GCAGATCTCAATTGGATGCCGAGCCTTGAATCC
pCDF-DoBBS8-R	ATCGCGTGGCCGGCCTTAAATTGGAACACT
pETD-MatC-F	<u>GCAGATCTCAATTGG</u> ATGGGTATTGAACTGC
pETD-MatC-R	ATCGCGTGGCCGGCCTTAAACCAGACCCGG
pETD-AAE13-F	<u>GCAGGTCGACAAGCTT</u> ATGGAAGTGTTTAAAGC
pETD-AAE13-R	CCGCTCGACTTAAGCATTATTCTTGATTTTCCAGAG
pCDF- <i>metK</i> -F	ATGGCAGATCTCAATTGGATGGCAAAACACCTTTTTACG
pCDF-metK-R	<u>GCGATCGCGTGGCCGGCCG</u> ATATTTACTTCAGACCGGCAG
pCDF-PsPT1-F	ATGGCAGATCTCAATTGGATGTCTCACACCGTCGT
pCDF-PsPT1-R	<u>GCGATCGCGTGGCCGGCCG</u> ATATCTAGTTGGGGAGATAG
β -actin-F	TGAAAAGATGACCCAGGACTCTC
β -actin-R	TGATCTCATCTGGGAAAGAGCA
Aifm 3-F	CAGGACTGTGTGGAGGCTAC
Aifm 3-R	GGGACAGCACCTTTCACC
Bax-F	AGAGGATGATTGCTGATGTGG
Bax-R	CCCAGTTGAAGTTGCCGT
Bcl-2-F	GATAACGGAGGCTGGGATGC
Bcl-2-R	ATGCACCCAGAGTGATGCAG
Caspase-3-F	GAGCTTGGAACGCGAAGAAA
Caspase-3-R	AGTCCATCGACTTGCTTCCA
Cytochrome c-F	CCAGCCCGGACCGAATTTA
Cytochrome c-R	CTGTCTTCCGCCCAAACAGA

Group	Drug concentration	Relative survival rate (%)			Improved survival rate (%)	P value
Control		100	100	100	-	-
Model	29 mM	62.53	63.02	65.01	-	0.000
Resveratrol	10 µM	72.80	78.16	75.45	18.83	0.017
12	10 µM	71.21	72.30	76.29	15.32	0.006
13	10 µM	65.95	72.23	76.19	12.43	0.076
9	10 µM	65.45	70.90	72.09	9.36	0.061
4	10 µM	64.05	68.10	73.73	7.97	0.133
15	10 µM	65.34	67.50	67.75	5.27	0.028
1	10 µM	64.08	67.35	66.91	4.08	0.098
10	10 µM	63.89	67.50	66.64	3.93	0.131
20	10 µM	64.19	66.35	67.41	3.88	0.036
21	10 µM	62.94	65.22	66.38	2.08	0.126
14	10 µM	63.55	64.37	63.87	0.67	0.654
7	10 µM	60.63	62.85	65.73	-0.74	0.613
22 and 23	10 µM	58.92	62.52	66.06	-1.65	0.534
16	10 µM	60.68	62.15	63.99	-1.98	0.054
19	10 µM	59.06	59.69	63.89	-4.19	0.074
11	10 µM	59.39	54.87	57.91	-9.63	0.057

Table S5. Evaluation the neuroprotective effect of the bibenzyl derivatives on the damaged cells induced by glutamate.

Method	Solvent A	Solvent B	Gradient	
1	0.1% formic acid aqueous solution	Acetonitrile	15–45% B, 25 min; 45–100% B, 10 min; 100% B, 5 min	Analysis for bibenzyl derivatives
2	0.1% trifluoroacetic acid aqueous solution	Acetonitrile	0% B, 5 min; 0–40% B, 20 min; 40–100% B, 3 min; 100% B, 3 min	Analysis for the CoA derivatives
3	ddH ₂ O	Acetonitrile	20–40% B, 20 min; 40–100% B, 5 min; 100% B, 5 min	Preparation for the methylated bibenzy derivatives
4	0.1% formic acid aqueous solution	Acetonitrile	15–40% B, 20 min; 40–100% B, 5 min; 100% B, 5 min	Preparation for the prenylated bibenzyl derivatives
5	ddH ₂ O	Acetonitrile	15–30% B, 15 min; 30–100% B, 5 min; 100% B, 5min	Preparation for the glycosylated bibenzyl derivative
6	ddH ₂ O	Acetonitrile	15–45% B, 25 min; 45–100% B, 2 min; 100% B, 5min	Preparation for the methylated/ prenylated and glycosylated bibenzyl derivative:

 Table S6. HPLC methods used in this study.

Supplementary Figures

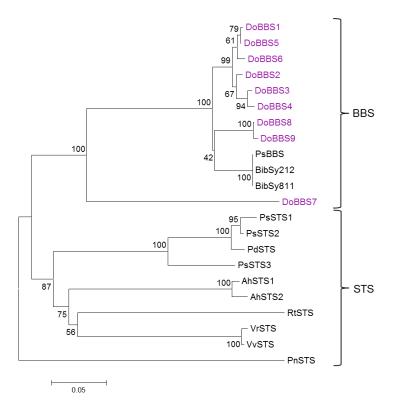


Figure S1. Phylogenetic analysis of DoBBSs with plant bibenzyl synthases (BBSs) and stilbene synthases (STSs). The results were calculated using the MEGA version 6 software. Method: Neighbor-joining, Bootstrap: 1000. The branch lengths represent relative genetic distances. The protein sequences and corresponding accession numbers that were used for this comparasion are as follows: PsBBS (P53416); BibSy212 (CAA56276); BibSy811 (CAA56277); PsSTS1 (AAB24341); PsSTS2 (CAA43165); PdSTS (BAA94953); PsSTS3 (P48407); AhSTS1 (BAA78617); AhSTS2 (P20178); VrSTS1 (AAF00586); VvSTS (CAA54221); RtSTS (AAP13782); PnSTS (BAA87925).

DoBBS1 DoBBS2 DoBBS3 DoBBS4 DoBBS5 DoBBS6 DoBBS7 DoBBS8 DoBBS9 BibSy212 AhSTS Consensus	MESIESIRAH ANGHASILAIGANE DNFILOSTYFLFFFRITNSEHIVCLKKKE CRICKTAIRKRHFVWNEDFITAN MESIESIRAH ANGHASILAIGANE DNFILOSTYFLFFFRITNSEHIVCLKKE CRICKTAIRKRHFVWNEDFITAN MISIESIRAH ANGHASILAIGANE DNFILOSAYFLFFFRITNSEHIVCLKKE CRICKTAIRKRHFVWNEDFITAN MISIESIRAH ANGHASILAIGANE DNFILOSAYFLFFFRITNSEHIVCLKKE CRICKTAIRKRHFVWNEDFITAN MISIESIRAH ANGHASILAIGANE DNFILOSAYFLFFFRITNSEHIVCLKKE CRICKTAIRKRHFVWNEDFITAN MISIESIRAH ANGHASILAIGANE DNFILOSAYFLFFFRITNSEHIVCLKKE CRICKTAIRKRHFVWNEDFITAN MISIESIRAH ANGHASILAIGANE DNFILOSAYFLFFFRINSEHIVCLKKE CRICKTAIRKRHFVWNEDFITAN MISIESIRAH ANGHASILAIGANE DNFILOSAYFLFFFRINSEHIVCLKKE CRICKTAIRKRHFVWNEDFITAN MISIESIRAH ANGHASILAIGANE DNFILOSAYFLFFFRINSEHIVCLKKE CRICKTAIRKRHFVWNEDFITAN MISIESIRAH ANGHASILAIGANE DNFILOSAYFLFFRINSEHIVCLKKE CRICKTAIRKHFVWNEDFITAN MISIESIRAH ANGHASILAIGANE DNFILOSAYFLFFRINSEHIVCLKKE CRICKTAIRKHFVWNEDFITAN MISIESIRAH ANGHASILAIGANE DNFILOSAYFLFFRINSEH TINSEHIVCLKKE CRICERTAIRKHFVWNEDFITAN	80 80 80 80 80 77 80 80 80 80
DoBBS1 DoBBS2 DoBBS3 DoBBS4 DoBBS5 DoBBS7 DoBBS7 DoBBS7 DoBBS8 DoBBS9 BibSy212 AhSTS Consensus	PCLHTEMEKSIEVRÇEVAIREIEKIÇAFAAAAIÇEWGÇEKSRITHLIFCTTSGMELFCAPYQLIQILGINENVERVMLY PCLHTEMEKSIEVRÇEVAIREIEKIÇAFAAAAIÇEWGÇEKSRITHLIFCTTSGMELFCAPYQLIQILGINENVERVMLY PCLHTEMEKSIEVRÇEVAIREIEKIÇAFAAAAIÇEWGÇEKSCITHLIFCTTSGMELFCAPYQLIQILGINENVERVMLY PCLHTEMEKSIEVRÇEVAIREIEKIÇAFAAAAIÇEWGÇEKSCITHLIFCTTSGMELFCAPYQLIQILGINENVERVMLY PSLHTEMEKSINIRÇEVAIREIEKIÇAFAAAAIÇEWGÇEKSCITHLIFCTTSGMELFCAPYQLIQILGINENVERVMLY PSLHTEMEKSINIRÇEVAIREIEKIÇAFAAAAIÇEWGÇEKSCITHLIFCTTSGMELFCAPYQLIQILGINENVERVMLY PCLHTEMEKSINIRÇEVAIREIEKIÇAFAAAAIÇEWGÇEKSCITHLIFCTTSGMELFCAPYQLIQILGINENVERVMLY PCLHTEMEKSINIRÇEVAIREIEKIÇAFAAAAAIÇEWGÇEKSCITHLIFCTTSGMELFCAPYQLIQILGINENVERVMLY PCLHTEMEKSINIRÇEVAIREIEKIÇAFAAAAAIÇEWGÇEKSCITHLIFCTTSGALFSAPVILIFCIIGINENVERVMLY PCLETEMAAFSINIRÇEVAIREIEKIÇAFAATAIÇEWGÇEKSCITHLIFCTTSGMELFCAPYQLIQILGINENVERVMLY PCCESTEMEKSINIRÇEVAIREIEKIÇAFAATAIÇEWGÇEKSRITHLIFCTTSGMELFCAPYQLIQILGINENVERVMLY PCFSTEMEKSINIRÇEVAIREIEKIÇAFAATAIÇEWGÇEKSRITHLIFCTTSGMELFCAPYQLIQILGINENVERVMLY PCFSTEMEKSINIRÇEVAIREIEKIÇAFAATAIFIEWGÇEKSRITHLIFCTTSGMELFCAPYQLIQILGINENVERVMLY PCFSTEMEKSINIRÇEVAIREIEKIÇAFAATAIFIEWGÇEKSRITHLIFCTTSGMELFCAPYQLIQILGINENVERVMLY PCFSTEMEKSINIRÇEVAIREIEKIÇAFAATAIFIEWGÇEKSRITHLIFCTTSGMELFCAPYQLIQILGINENVERVMLY PCFSTEMEKSINIRÇEVAIREIEKIÇAFAATAFIEFWÇEKSRITHLIFCTTSGMELFCAPYQLIQILGINENVERVMLY PCFSTEMEKSINIRÇEVAIREIEKIÇAFAATAFIEFWÇEKSRITHLIFCTTSGMELFCAPYQLICTIGINENVERVMLY PCFSTEMEKSINIRÇEVAIREIEKIÇAFAATAFIEFWÇEKSRITHLIFCTTSGMELFCAPYQLICTIGIN	160 160 160 160 160 157 160 160 160
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DoBBS1 DoBBS2 DoBBS3 DoBBS4 DoBBS5 DoBBS7 DoBBS8 DoBBS9 BibSy212 AhSTS Consensus	VSTSQVIIEDSACAIGGHVSEGCILATIHREVEKIVSKNVEKCIEE2.ETBEGITUMNTIEWVEB2GGFAILEQVEERV VSTSQVIIEDSACAIGGHVSEGCILATIHREVEHIVSKNVGKCIEE2.ETBEGITUMNSIEWVEB2GGFAILEQVEERV VSTSQVIIEDSACAIGGHVSEGCILATIHREVEHIVSKNVGKCIEE2.ETBEGITUMNSIEWVEB2GGFAILEQVEERV VSTSQVIIEDSACAIGGHVSEGCILATIHREVEHIVSKNVGKCIEE2.ETBEGITUMNSIEWVEB2GGFAILEQVEERV VSTSQVIIEDSACAIGGHVSEGCILATIHREVEKIVSKNVGKCIEE2.ETBEGITUMNSIEWVEB2GGFAILEQVEERV VSTSQVIIEDSACAIGGHVSEGCILATIHREVEKIVSKNVGKCIEE2.ETBEGITUMNSIEWVEB2GGFAILEQVEERV VSTSQVIIEDSACAIGGHVSEGCILATIHREVEKIVSKNVGKCIEE2.ETBEGITUMNTIEWVEB2GGFAILEQVEERV VSTSQVIIEDSACAIGGHVSEGCILATIHREVEKIVSKNVGKCIEE2.ETBEGITUMNTIEWVEB2GGFAILEQVEERV VSTSQVIIEDSACAIGGHVSEGCILATIHREVEKIVSKNVGKCIEE2.ETBEGITUMNTIEWVEB2GGFAILEQVEERV VSTSQVIIEDSACAIGGHVSEGCILATIHREVEKIVSKNVGKCIEE2.ETBEGITUMNTIEWVEB2GGFAILEQVEERV VSTSQVIIEDSACAIGGHVSEGCILATIHREVEKIVSKNVGKCIEE2.ETBEGISTUMSIEWVEB2GGFAILEQVEESV VSTSQVIIEDSACAIGGHVSEGCILATIHREVEQIVSKNVGKCIEE2.ETBEGISTUMSIEWVEB2GGFAILEQVEESV VSTSQVIIEDSACAIGGHVSEGCILATIHREVEQIVSKNVGKCIEE2.ETBEGISTUMSIEWVEB2GGFAILEQVEESV VSTSQVIIEDSACAIGGHVSEGCILATIHREVEQIVSKNVGKCIEE2.ETBEGISTUMSIEWVEB2GGFAILEQVEESV VSTSQVIIEDSACAIGGHVSEGCILATIHREVEQIVSKNVGKCIEE2.ETBEGISTUMSIEWVEB2GGFAILEQVEESV VSTSQVIIEDSACAIGGHVSEGCILATIHREVEQIVSKNVGKCIEE2.ETBEGISTUMSIEWVEB2GGFAILEQVEESV VSTSQVIIEDSACAIGGHVSEGCILATIHREVEQIVSKNVGKCIEE2.ETBEGISTUMSIEWVEB2GGFAILEQVEESV VSTSQVIIEDSACAIGGHVSEGCILATIHREVEQIVSKNVGKCIEE2.ETBEGISTUMSIEWVEB2GGFAILEQVEEV VSTSQVIIEDSACAIGGHVSECGILATIHREVEQIVSKNVGKCIEF2.ETBEGISTUMSIEWVEB2GGFAILEQVEEV S q l p s gai e q p s l a f p d n ifw Dggraildq ee	318 318 318 318 318 318 318 317 318 318 318 318 317
DoBBS1 DoBBS2 DoBBS3 DoBBS4 DoBBS5 DoBBS7 DoBBS7 DoBBS8 DoBBS9 BibSy212 AhSTS Consensus	CIKFEKLIVSREVIAEYCNYSSVCVHEALDENRKFSAIEGKATTGEGLEWGVIFGFGFGITVETVVLRSVHL CIKFEKLIVSREVIAEYCNYSSVCVHEALDENRKFSAFEGKATTGEGLEWGVIFGFGFGITVETVVLRSVHL CIKFEKLIVSREVIAEYCNYSSVCVHEALDENRKFSAFEGKATTGEGLEWGVIFGFGFGITVETVVLRSVHL CIKFEKLIVSREVIAEYCNYSSVCVHEALDENRKFSAFECKATTGEGLEWGVIFGFGFGITVETVVLRSVHL CIKFEKLIVSREVIAEYCNYSSVCVHEALDENRKFSAFEGKATTGEGLEWGVIFGFGFGITVETVVLRSVHL CIKFEKLIVSREVIAEYCNYSSVCVHEALDENRKFSAFEGKATTGEGLEWGVIFGFGFGITVETVVLRSVPL CIKFEKLIVSREVIAEYCNYSSVCVHEALDENRKFSAFEGKATTGEGLEWGVIFGFGFGITVETVVLRSVPL CIKFEKLIVSREVIAEYCNYSSVCVHEALDENRKFSAFEGKATTGEGLEWGVIFGFGFGITVETVULRSVPL CIKFEKLISSREVIAEYCNYSSVCVHEALDENRKFSAKEGKATTGEGLEWGVIFGFGFGITVETVILRSVPI CIKFEKLISSREVIAEYCNYSSVCVHEALDENRKFSAKEGKATTGEGLEWGVIFGFGFGTVETVILRSVPI CIKFEKLISSREVIAEYCNYSSVCVHEALDENRKFSAKEGKATTGEGLEWGVIFGFGFGTVETVILRSVPI CIKFEKLISSREVIAEYCNYSSVCVHEALDENRKFSAKEGKATTGEGLEWGVIFGFGFGTVETVILRSVPI CIKFEKLSSSREVIAEYCNYSSVCVHEALDENRKFSAKEGKATTGEGLEWGVIFGFGFGTITVETVILRSVPI CIKFEKLSVSREVIAEYCNYSSVCVHEALDENRKFSAKEGKATTGEGLEWGVIFGFGFGTITVETVILRSVPI CIKFEKLSVSREVIAEYCNYSSVCVHEALDENRKFSAKEGKATTGEGLEWGVIFGFGFGTITVETVILRSVPI CIKFEKLSVSREVIAEYCNYSSVCVHEALDENRKFSAKEGKATTGEGLEWGVIFGFGFGTITVETVILRSVPI CIKFEKLSVSREVIAEYCNYSSVCVHEALDENRKFSAKEGKATTGEGLEWGVIFGFGFGTITVETVILRSVPI CIKFEKLSVSREVIAEYCNYSSVCVHEALDENRKFSANEGKATTGEGLEWGVIFGFGFGTITETVULRSVPI CIKFEKLSVSREVIAEYCNYSSVCVHEALDENRKFSANEGKATTGEGLEWGVIFGFGFGTITETVULRSVPI CIKFEKLSVSREVIAEYCNYSSVCVHEALDENRKFSANEGKATTGEGLEWGVIFGFGFGTITETVULRSVPI CIKFEKLSVSREVIAEYCNYSSVCVHEALDENRKFSANEGKATTGEGLEWGVIFGFGFGTITETVULRSVPI NIKFEKMFATEDVISNYCNYSSACVFFTALDENRKFSANEGKATTGEGLEWGVIFGFGFGTITETVULRSVPI NIKFEKKFTFTYINGNYSACVFTTUTTVINGNYSACVFTTUTTTETVINGNYFT	390 390 390 390 390 390 390 390 390 389

Figure S2. Multiple alignment of DoBBSs and reported BBS, STS from plants. C164-H303-N336 are the conserved catalytic triad motif in PKSs.

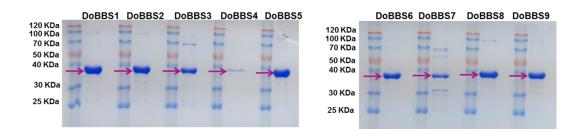


Figure S3. SDS-PAGE analysis of purified proteins of DoBBSs.

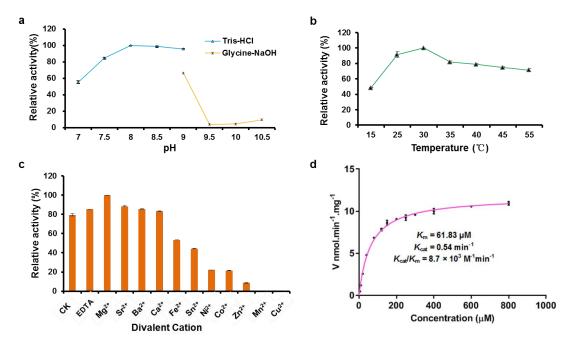


Figure S4. Biochemical characterization of DoBBS8. Effects of (a) pH of buffers, (b) temperature, (c) divalet metal ions on enzyme activity of DoBBS8 with *p*-hydroxyphenylpropionyl-CoA as the starter unit and malonyl-CoA as the extender unit. (d) Kinetic analysis of DoBBS8 towards *p*-hydroxyphenylpropionyl-CoA. The error bars show the SD (n = 2).

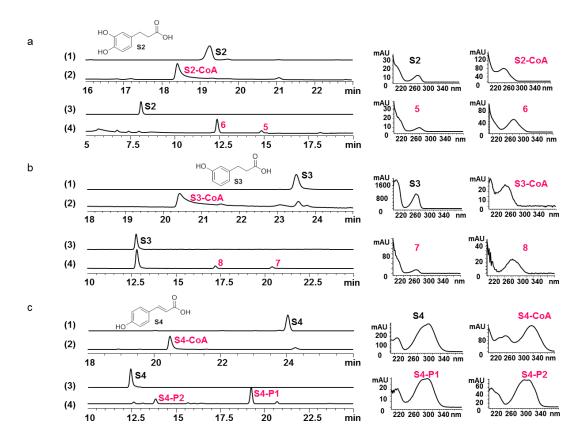
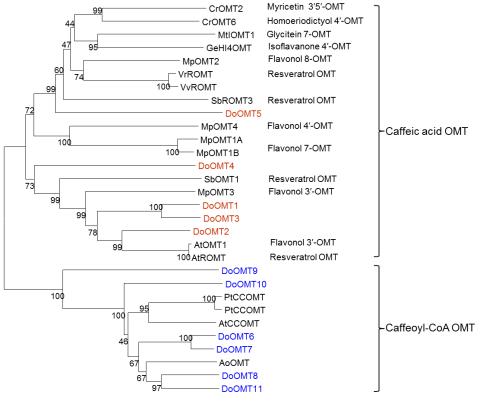


Figure S5. Substrate promiscuity of the purified DoBBS8. HPLC analysis of the enzymatic reactions with the substrate of S2 (a)/S3 (b)/S4 (c); HPLC analysis ($\lambda = 254$ nm) of (1) the standards S2–S4, (2) the enzymatic reactions catalyzed by the purified At4CL1 with CoA and S2–S4 as substrates on the Tosoh TSK gel ODS column; HPLC analysis ($\lambda = 280$ nm) of (3) the standards S2–S4, (4) the casade reactions catalyzed by the purified At4CL2, AAE13 and DoBBS8, with malonic acid, CoA, and S2–S4 as substrates on the Shiseido Capcell Pak C18 MGIII column.



0.05

Figure S6. Phylogenetic analysis of DoOMTs with plant OMTs. The results were calculated using the MEGA version 6 software. Method: Neighbor-joining, Bootstrap: 1000. The branch lengths represent relative genetic distances. The protein sequences and corresponding accession numbers that were used for this comparasion are as follows: AtOMT1 (U70424); CrOMT2 (AY127568); CrOMT6 (AY343490); MpOMT1A (AY337457); MpOMT1B (AY337458); MpOMT2 (AY337459); MpOMT3 (AY337460); MpOMT4 (AY337461); MtIOMT1 (AY942159); GeHI4'OMT (AB091684); AtROMT (AY062837); VrROMT (JX673941); SbOMT1 (EF189707); SbROMT3 (JX673942); VvROMT (NM_001281115); AoOMT (XP_020252875); PtCCOMT (XP_002312473); AtCCOMT (NP_564916); PtCCOMT (AFZ78549).

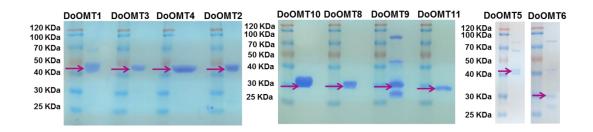


Figure S7. SDS-PAGE analysis of purified proteins of DoOMTs.

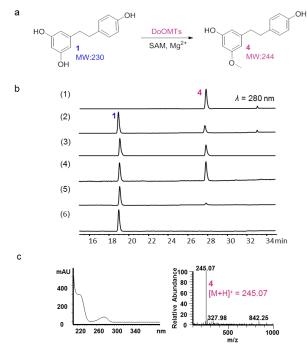


Figure S8. Functional characterization of DoOMTs. (a) Enzymatic reaction catalyzed by DoOMTs; (b) HPLC analysis ($\lambda = 280$ nm) of the reactions with (1) DoOMT1, (2) DoOMT2, (3) DoOMT3, (4) DoOMT4, (5) DoOMT5, (6) boiled DoOMT1; (c) UV and MS spectra of product **4** at positive mode.

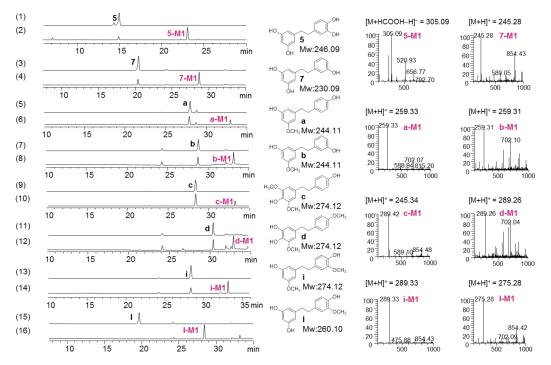


Figure S9. Substrate promiscuity analysis of the purified DoOMT1. HPLC-MS analysis ($\lambda = 280 \text{ nm}$) of the standard substrates of (1) 5, (3) 7, (5) a, (7) b, (9) c, (11) d, (13) i, (15) l, and the reactions catalyzed by DoOMT1 with substrates of (2) 5, (4) 7, (6) a, (8) b, (10) c, (12) d, (14) i, (16) l.

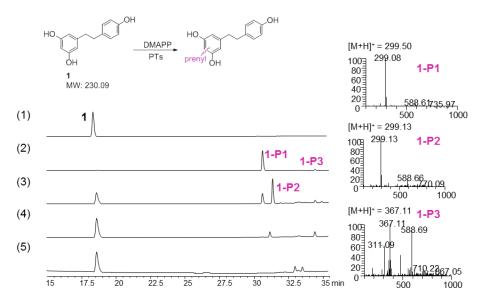


Figure S10. Screening for bibenzyl prenyltransferases. HPLC-MS analysis ($\lambda = 280$ nm) of the standard substrate of (1) **1**, and the reactions catalyzed by (2) PsPT1, (3) ScPT1, (4) AtaPT⁷, (5) PsPT2.

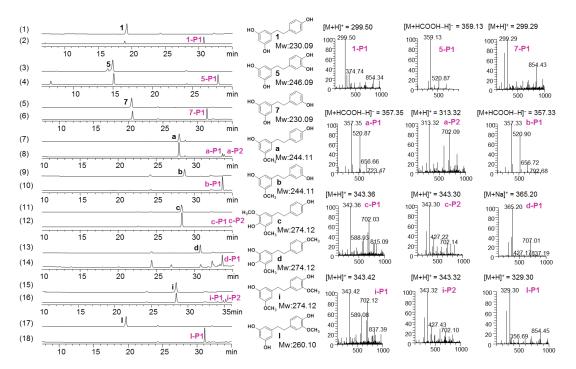


Figure S11. Substrate promiscuity analysis of the purified PsPT1. HPLC-MS analysis ($\lambda = 280$ nm) of the standard substrates of (1) **1**, (3) **5**, (5) **7**, (7) **a**, (9) **b**, (11) **c**, (13) **d**, (15) **i**, (17) **l**, and the reactions catalyzed by PsPT1 with substrates of (2) **1**, (4) **5**, (6) **7**, (8) **a**, (10) **b**, (12) **c**, (14) **d**, (16) **i**, (18) **l**.

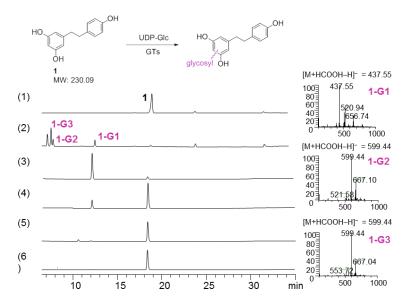


Figure S12. Screening for bibenzyl glycosyltransferases. HPLC-MS analysis ($\lambda = 280$ nm) of the standard substrate of (1) **1**, and the reactions catalyzed by (2) UGT71E5², (3) MiCGT⁸, (4) UGT73AE1⁹, (5) UGT88B2¹⁰, (6) MiCGTb^{11,12}.

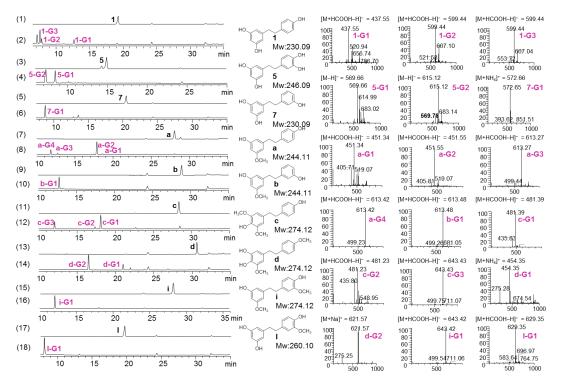


Figure S13. Substrate promiscuity analysis of the purified UGT71E5. HPLC-MS analysis (λ = 280 nm) of the standard substrates of (1) **1**, (3) **5**, (5) **7**, (7) **a**, (9) **b**, (11) **c**, (13) **d**, (15) **i**, (17) **l**, and the reactions catalyzed by UGT71E5 with substrates of (2) **1**, (4) **5**, (6) **7**, (8) **a**, (10) **b**, (12) **c**, (14) **d**, (16) **i**, (18) **l**.

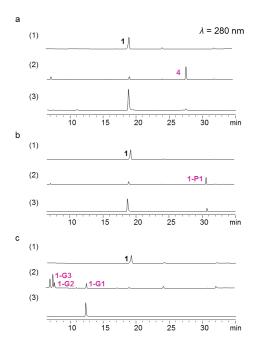


Figure S14. Functional identification of the modular post-modifying strains. HPLC analysis ($\lambda = 280 \text{ nm}$) of (1) the standard substrate of 1, (2) the enzymatic reactions catalyzed by a) DoOMT1, b) PsPT1, c) UGT71E5, (3) the whole-cell reactions catalyzed by a) the methylation strain *E-DoOMT1*, b) the prenylation strain *E-PsPT1*, c) the glycosylation strain *E-UGT71E5*, with substrate 1 as the starting material.

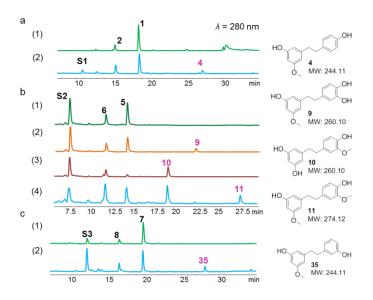


Figure S15. The whole-cell synthesis of methylated bibenzyl derivatives. HPLC analysis (λ = 280 nm) of the reactions with malonic acid and (a) S1, (b) S2, (c) S3 as the starting materials; The whole-cell reactions catalyzed by (1) *E-DoBBS8*, (2) the co-culture of *E-DoBBS8* and the methylation strain *E-DoOMT1*, (3) the co-culture of *E-DoBBS8* and the methylation strain *E-DoOMT6*, (4) the co-culture of *E-DoBBS8* and the methylation strains *E-DoOMT6*, (4) the co-culture of *E-DoBBS8* and the methylation strains *E-DoOMT6*.

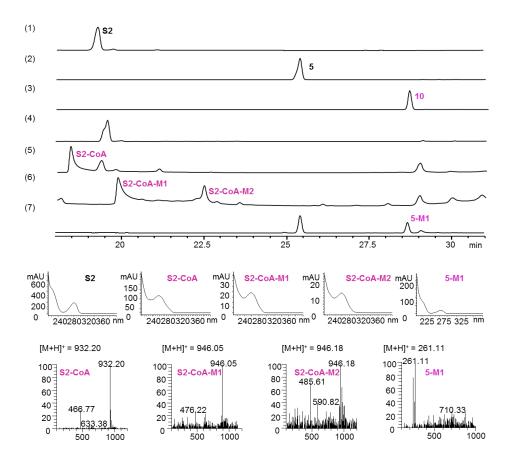


Figure S16. Functional identification of the enzyme activity of the purified DoOMT6. HPLC analysis ($\lambda = 280$ nm) of the standard substrates of (1) S2; (2) 5; and (3) 10; (4) HPLC analysis ($\lambda = 254$ nm) of the enzymatic reaction catalyzed by DoOMT6, with S2 and SAM as substrates; (5) HPLC analysis ($\lambda = 254$ nm) of the enzymatic reaction catalyzed by At4CL1, with S2 and CoA as substrates; (6) HPLC analysis ($\lambda = 254$ nm) of the cascade reaction catalyzed by At4CL1 and DoOMT6, with S2, CoA and SAM as substrates; (7) HPLC analysis ($\lambda = 254$ nm) of the enzymatic reaction catalyzed by At4CL1 and DoOMT6, with S2, CoA and SAM as substrates; (7) HPLC analysis ($\lambda = 254$ nm) of the enzymatic reaction catalyzed by DoOMT6, with 5 and SAM as substrates.

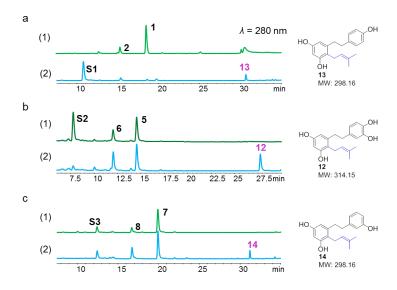


Figure S17. The whole-cell synthesis of prenylated bibenzyl derivatives. HPLC analysis (λ = 280 nm) of the reactions with malonic acid and (a) **S1**, (b) **S2**, (c) **S3** as the starting materials; The whole-cell reactions catalyzed by (1) *E-DoBBS8*, (2) the co-culture of *E-DoBBS8* and the prenylation strain *E-PsPT1*.

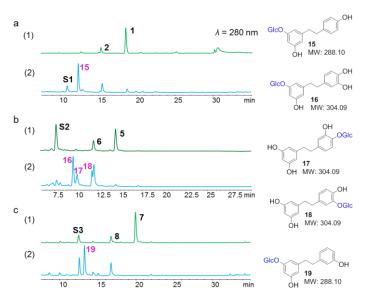


Figure S18. The whole-cell synthesis of glycosylated bibenzyl derivatives. HPLC analysis (λ = 280 nm) of the reactions with malonic acid and (a) **S1**, (b) **S2**, (c) **S3** as the starting materials; The whole-cell reactions catalyzed by (1) *E-DoBBS8*, (2) the co-culture of *E-DoBBS8* and the glycosylation strain *E-UGT71E5*.

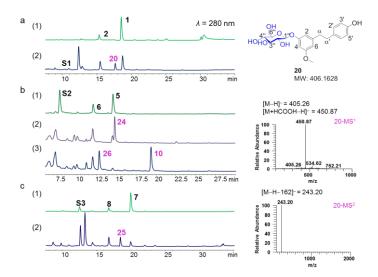


Figure S19. The whole-cell synthesis of methylated and glycosylated bibenzyl derivatives. HPLC-MS analysis ($\lambda = 280$ nm) of the reactions with malonic acid and (a) S1, (b) S2, (c) S3 as the starting materials; The whole-cell reactions catalyzed by (1) *E-DoBBS8*, (2) the co-culture of *E-DoBBS8*, the glycosylation strain *E-UGT71E5* and the methylation strain *E-DoOMT1*, (3) the co-culture of *E-DoBBS8*, the glycosylation strain *E-UGT71E5* and the methylation strain *E-DoOMT6*.

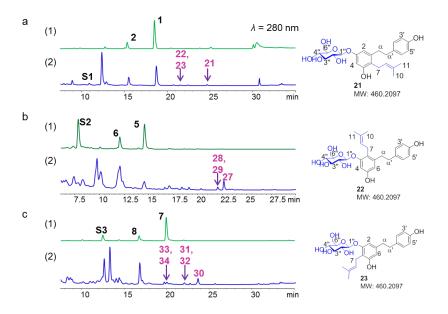


Figure S20. The whole-cell synthesis of prenylated and glycosylated bibenzyl derivatives. HPLC analysis ($\lambda = 280$ nm) of the reactions with malonic acid and (a) S1, (b) S2, (c) S3 as the starting materials; The whole-cell reactions catalyzed by (1) *E-DoBBS8*, (2) the co-culture of *E-DoBBS8* and the glycosylation strain *E-UGT71E5* and the prenylation strain *E-PsPT1*.

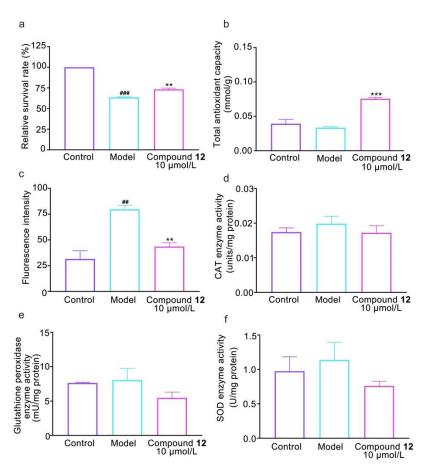


Figure S21. Effects of compound 12 on cell survival and the levels of ROS, total antioxidant capacity, CAT, GSH-Px and SOD in SK-N-SH cells after glutamate injury. (a) Relative survival rate after glutamate injury (n = 3). (b) The level of total antioxidant capacity after glutamate injury (n = 3). (c) The level of ROS after glutamate injury (n = 3). (d) The level of CAT after glutamate injury (n = 6). (e) The level of GSH-Px after glutamate injury (n = 3). (f) The level of SOD after glutamate injury (n = 3). Data were shown as mean \pm SEM, ^{##}P<0.01, ^{###}P<0.001 vs the control group, ^{*}P<0.05, ^{**}P<0.01 and ^{***}P<0.001 vs the model group.

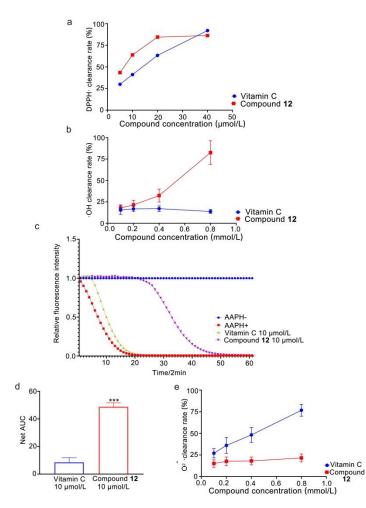


Figure S22. Scavenging effects of compound 12 on free radicals *in vitro*. The clearance rate of compound 12 and vitamin C for DPPH \cdot (a), OH (b), oxidative radical (c–d), and $O_2^- \cdot$ (e), Data were shown as mean \pm SEM, *** *P*<0.001 *vs* the vitamin C, *n* = 3.

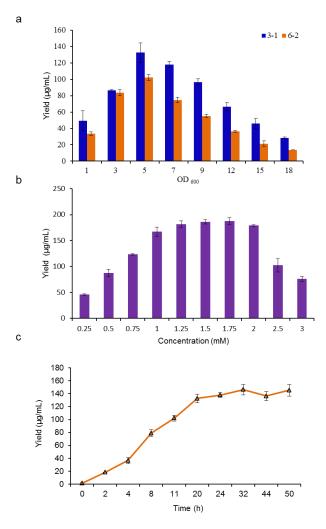


Figure S23. Optimizing the reaction conditions of whole-cell system of *E-DoBBS8*. (a). Effects of OD_{600} on the yield of product 1. 3-1 means that the final concentration of malonic acid was at 3 mmol/L, S1 was at 1 mmol/L. 6-2 means that the final concentration of malonic acid was at 6 mmol/L, S1 was at 2 mmol/L. (b). Effects of the S1 concentration on the yield of product 1. The concentration of malonic acid was kept at three times of S1. (c) The time course for whole-cell reaction of *E-DoBBS8*. The error bars show the SD (n = 2).

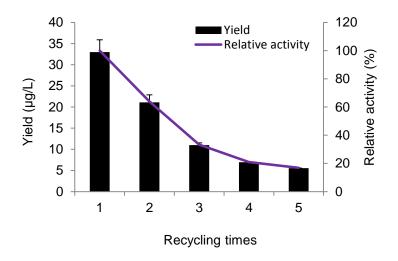


Figure S24. Recycling biosynthesis of compound 12. The error bars show the SD (n = 3).

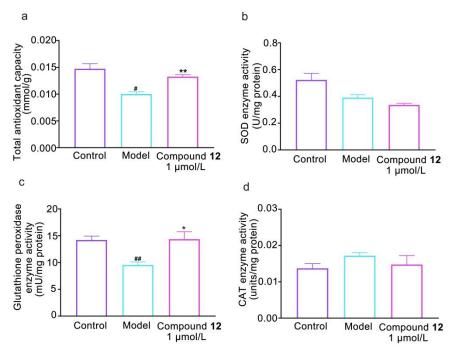


Figure S25. The effects of compound 12 on damaged cells induced by OGD/R. (a) The level of total antioxidant capacity after OGD/R injury. (b) The activities of SOD after OGD/R injury. (c) The activities of GSH-Px after OGD/R injury. (d) The activities of CAT after OGD/R injury. Data were shown as mean \pm SEM, ${}^{\#}P < 0.05$, ${}^{\#\#}P < 0.01$ vs the control group, ${}^{*}P < 0.05$ and ${}^{**}P < 0.01$ vs the model group, n = 3.

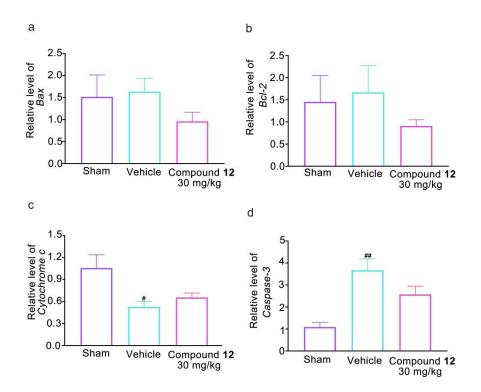
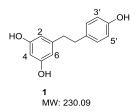
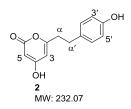


Figure S26. Compound 12 had no effect on apoptosis-related genes expressions. (a) The level of *Bax* mRNA. (b) The level of *Bcl-2* mRNA. (c) The level of *Cytochrome c* mRNA. (d) The level of *Caspase-3* mRNA. Data were shown as mean \pm SEM, $^{\#}P < 0.05$, $^{\#\#}P < 0.001$ vs the sham group, n = 5.

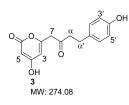
Supplementary spectroscopic data of bibenzyl derivatives (1-23).



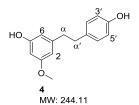
3,4',5-Trihydroxybibenzyl (**1**): $C_{14}H_{14}O_3$, ESI-MS *m/z* 231.05 [M+H]⁺; ¹H NMR (DMSO-*d*₆, 400 MHz): δ_H 9.13 (s, 4'-OH), 9.04 (s, 2H, 3, 5-OH), 6.98 (d, *J* = 8.4 Hz, 2H, H-2', 6'), 6.64 (d, *J* = 8.4 Hz, 2H, H-3', 5'), 6.05 (d, *J* = 2.1 Hz, 2H, H-2, 6), 6.01 (t, *J* = 2.1 Hz, H-4), 2.63 (m, overlapped, 4H, H- α , α'); ¹³C NMR (DMSO-*d*₆, 100 MHz): δ_C 158.2 (C-3, 5), 155.3 (C-4'), 143.6 (C-1), 131.7 (C-1'), 129.1 (C-2', 6'), 115.0 (C-3', 5'), 106.4 (C-2, 6), 100.1 (C-4), 37.6 (C- α), 36.1 (C- α').¹³



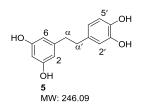
Dihydrobisnoryangonin (2): $C_{13}H_{12}O_4$, ESI-MS *m/z* 232.96 [M+H]⁺; ¹H NMR (DMSO-*d*₆, 400 MHz): δ_H 7.00 (d, *J* = 8.40 Hz, 2H, H-2', 6'), 6.65 (d, *J* = 8.36 Hz, 2H, H-3', 5'), 5.76 (d, *J* = 2.00 Hz, H-3), 5.00 (d, *J* = 2.08 Hz, H-5), 2.74 (t, *J* = 8.08 Hz, 2H, H- α), 2.62 (t, *J* = 8.08 Hz, 2H, H- α '); ¹³C NMR (DMSO-*d*₆, 100 MHz): δ_C 167.8 (C-4), 164.6 (C-2), 164.4 (C-6), 155.6 (C-4'), 130.3 (C-1'), 129.1 (C-2', 6'), 115.1 (C-3', 5'), 101.6 (C-3), 87.7 (C-5), 34.9 (C- α), 31.4 (C- α ').¹⁴



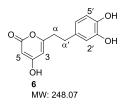
4-Hydroxy-6-[4-(4-hydroxyphenyl)-2-oxobutyl]-2*H***-pyran-2-one (3): C₁₅H₁₄O₅, ESI-MS** *m***/***z* **275.06 [M+H]⁺; ¹H NMR (DMSO-***d***₆, 400 MHz): \delta_{\rm H} 6.97 (d,** *J* **= 8.4 Hz, 2H, H-2', 6'), 6.64 (d,** *J* **= 8.4 Hz, 2H, H-3', 5'), 5.68 (s, H-3), 4.71 (s, H-5), 3.56 (s, H-7), 2.74 (t,** *J* **= 7.2 Hz, 2H, H-α), 2.66 (t,** *J* **= 7.2 Hz, 2H, H-α').^{15,16}**



3-Methoxy-4',5-dihydroxybibenzyl (4): $C_{15}H_{16}O_3$, ESI-MS *m/z* 245.07 [M+H]⁺; ¹H NMR (DMSO-*d*₆, 400 MHz): δ_H 9.26 (s, 5-OH), 9.13 (s, 4'-OH), 7.00 (d, *J* = 8.4 Hz, 2H, H-2', 6'), 6.65 (d, *J* = 8.4 Hz, 2H, H-3', 5'), 6.21 (d, *J* = 2.2 Hz, 2H, H-2, 6), 6.14 (t, *J* = 2.2 Hz, H-4), 3.65 (s, 3H, 3-OMe), 2.68 (m, overlapped, 4H, H- α , α '); ¹³C NMR (DMSO-*d*₆, 100 MHz): δ_C 160.3 (C-3), 158.3 (C-5), 155.3 (C-4'), 143.8 (C-1), 131.6 (C-1'), 129.1 (C-2', 6'), 115.0 (C-3', 5'), 107.9 (C-2), 104.9 (C-6), 98.7 (C-4), 54.8 (3-OMe), 37.7 (C- α), 36.0 (C- α ').¹⁷

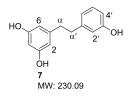


3,3',4',5-Tetrahydroxybibenzyl (5): $C_{14}H_{14}O_4$, ESI-MS m/z 290.91 [M+HCOOH–H]⁻; ¹H NMR (DMSO- d_6 , 400 MHz): δ_H 9.01 (s, 2H, 3, 5-OH), 8.66 (s, 3'-OH), 8.59 (s, 4'-OH), 6.60 (d, J = 8.0 Hz, H-5'), 6.58 (d, J = 1.8 Hz, H-2'), 6.44 (dd, J = 1.8, 8.0 Hz, H-6'), 6.05 (d, J = 1.9 Hz, 2H, H-2, 6), 6.01 (t, J = 1.9 Hz, H-4), 2.59 (m, overlapped, 4H, H- α , α'); ¹³C NMR (DMSO- d_6 , 100 MHz): δ_C 158.2 (C-3, 5), 144.9 (C-3'), 143.7 (C-4'), 143.2 (C-1), 132.5 (C-1'), 118.8 (C-6'), 115.7 (C-5'), 115.4 (C-2'), 106.4 (C-2, 6), 100.1 (C-4), 37.6 (C- α), 36.3 (C- α').¹⁸

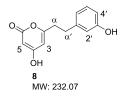


6-(3,4-Dihydroxyphenethyl)-4-hydroxy-2*H*-pyran-2-one (6): $C_{13}H_{12}O_5$, ESI-MS *m/z* 248.89 [M+H]⁺; ¹H NMR (DMSO-*d*₆, 400 MHz): δ_H 6.61 (d, *J* = 8.0 Hz, H-5'), 6.57 (d, *J* = 2.0 Hz, H-2'), 6.44 (dd, *J* = 2.0, 8.0 Hz, H-6'), 5.88 (d, *J* = 2.0 Hz, H-3),

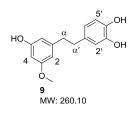
5.20 (d, J = 2.0 Hz, H-5), 2.67 (m, overlapped, 4H, H- α , α'); ¹³C NMR (DMSO- d_6 , 100 MHz): δ_C 170.8 (C-4), 166.2 (C-2), 164.4 (C-6), 145.5 (C-3'), 144.0 (C-4'), 131.3 (C-1'), 119.3 (C-6'), 116.1 (C-5'), 115.9 (C-2'), 100.5 (C-3), 88.9 (C-5), 35.3 (C- α), 31.9 (C- α').¹⁹



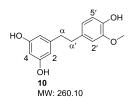
3,3',5-Trihydroxybibenzyl (7): $C_{14}H_{14}O_3$, ESI-MS *m/z* 231.06 [M+H]⁺; ¹H NMR (DMSO-*d*₆, 400 MHz): δ_H 9.28 (s, 3'-OH), 9.08 (s, 2H, 3, 5-OH), 7.04 (t, *J* = 7.7 Hz, H-5'), 6.63 (m, overlapped, 2H, H-2', 4'), 6.56 (dd, *J* = 1.7, 8.0 Hz, H-6'), 6.07 (d, *J* = 2.0 Hz, 2H, H-2, 6), 6.02 (t, *J* = 2.0 Hz, H-4), 2.66 (m, overlapped, 4H, H- α , α'); ¹³C NMR (DMSO-*d*₆, 100 MHz): δ_C 158.2 (C-3, 5), 157.3 (C-3'), 143.5 (C-1), 143.1 (C-1'), 129.1 (C-5'), 118.9 (C-6'), 115.2 (C-2'), 112.7 (C-4'), 106.3 (C-2, 6), 100.2 (C-4), 37.1 (C- α), 36.8 (C- α').²⁰



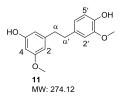
4-Hydroxy-6-(3-hydroxyphenethyl)-2H-pyran-2-one (**8**): C₁₃H₁₂O₄, ESI-MS *m/z* 232.96 [M+H]⁺; ¹H NMR (DMSO-*d*₆, 400 MHz): $\delta_{\rm H}$ 7.06 (t, *J* = 8.0 Hz, H-5'), 6.64-6.57 (m, overlapped, 3H, H-2', 4', 6'), 5.85 (d, *J* = 1.8 Hz, H-3), 5.11 (d, *J* = 1.8 Hz, H-5), 2.73 (m, overlapped, 4H, H-α, α'); ¹³C NMR (DMSO-*d*₆, 100 MHz): $\delta_{\rm C}$ 171.6 (C-4), 164.9 (C-2), 164.2 (C-6), 157.3 (C-3'), 141.6 (C-1'), 129.3 (C-5'), 118.9 (C-6'), 115.2 (C-2'), 113.1 (C-4'), 100.9 (C-3), 88.0 (C-5), 34.4 (C-α), 32.1 (C-α').²¹



3-Methoxy-3',4',5-trihydroxybibenzyl (9): $C_{15}H_{16}O_4$, ESI-MS *m/z* 259.21 [M–H]⁻; ¹H NMR (DMSO-*d*₆, 600 MHz): δ_H 6.61 (d, *J* = 8.0 Hz, H-5'), 6.59 (d, *J* = 2.0 Hz, H-2'), 6.44 (dd, *J* = 2.0, 8.0 Hz, H-6'), 6.21 (t, *J* = 2.0 Hz, 2H, H-2, 6), 6.13 (t, *J* = 2.0 Hz, H-4), 3.65 (s, 3H, 3-OMe), 2.64 (s, 4H, H- α , α'); ¹³C NMR (DMSO-*d*₆, 100 MHz): δ_C 160.3 (C-3), 158.3 (C-5), 145.0 (C-3'), 143.9 (C-4'), 143.3 (C-1), 132.4 (C-1'), 118.8 (C-6'), 115.8 (C-5'), 115.5 (C-2'), 107.9 (C-6), 104.8 (C-2), 98.7 (C-4), 54.8 (C-3-OMe), 37.6 (C- α), 36.3 (C- α').²²

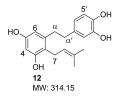


3'-Methoxy-3,4',5-trihydroxybibenzyl (**10**): $C_{15}H_{16}O_4$, ESI-MS *m/z* 261.11 $[M+H]^+$; ¹H NMR (DMSO-*d*₆, 600 MHz): δ_H 9.03 (s, 2H, 3,5-OH), 8.64 (s, 3'-OH), 6.75 (d, *J* = 2.0 Hz, H-2'), 6.65 (d, *J* = 8.0 Hz, H-5'), 6.58 (dd, *J* = 2.0, 8.0 Hz, H-6'), 6.06 (d, *J* = 2.1 Hz, 2H, H-2, 6), 6.02 (t, *J* = 2.1 Hz, H-4), 3.72 (s, 3H, 3'-OMe), 2.65 (m, overlapped, 4H, H- α , α'); ¹³C NMR (DMSO-*d*₆, 100 MHz): δ_C 158.2 (C-3, 5), 147.3 (C-3'), 144.5 (C-4'), 143.7 (C-1), 132.5 (C-1'), 120.4 (C-6'), 115.2 (C-5'), 112.6 (C-2'), 106.4 (C-2, 6), 100.1 (C-4), 55.5 (C-3'-OMe), 37.6 (C- α), 36.6 (C- α').²³

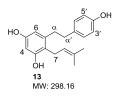


3,3'-Dimethoxy-4',5-dihydroxybibenzyl (**11**): C₁₆H₁₈O₄, ESI-MS *m/z* 275.02 $[M+H]^+$; ¹H NMR (DMSO-*d*₆, 400 MHz): $\delta_{\rm H}$ 6.76 (d, *J* = 1.9 Hz, H-2'), 6.65 (d, *J* = 7.9 Hz, H-5'), 6.59 (dd, *J* = 1.9, 7.9 Hz, H-6'), 6.21-6.23 (m, overlapped, 2H, H-2, 6), 6.14 (t, *J* = 2.2 Hz, H-4), 3.72 (s, 3H, 3'-OMe), 3.66 (s, 3H, 3-OMe), 2.70 (m, overlapped, 4H, H- α , α'); ¹³C NMR (DMSO-*d*₆, 100 MHz): $\delta_{\rm C}$ 160.3 (C-3), 158.3 (C-5), 147.3 (C-3'), 144.5 (C-4'), 143.9 (C-1), 132.4 (C-1'), 120.4 (C-6'), 115.2 (C-5'), 112.6 (C-2'), 108.0 (C-6), 104.9 (C-2), 98.7 (C-4), 55.5 (C-3'-OMe), 54.8

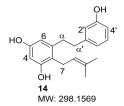
(C-3-OMe), 37.7 (C-α), 36.6 (C-α').²⁴



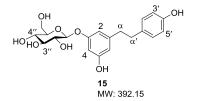
2-Isopentenyl-3,3',4',5-tetrahydroxybibenzyl (12): $C_{19}H_{22}O_4$, ESI-MS *m/z* 313.17 [M-H]⁻; ¹H NMR (DMSO-*d*₆, 400 MHz): δ_H 6.62 (d, *J* = 8.0 Hz, H-5'), 6.58 (d, *J* = 2.0 Hz, H-2'), 6.44 (dd, *J* = 2.0, 8.0 Hz, H-6'), 6.14 (d, *J* = 2.4 Hz, H-4), 6.06 (d, *J* = 2.4 Hz, H-6), 5.00 (t, *J* = 5.4 Hz, H-8), 3.14 (d, *J* = 6.4 Hz, H-7), 2.56 (m, overlapped, 4H, H- α , α'), 1.67 (s, 3H, H-10), 1.61 (s, 3H, H-11); ¹³C NMR (DMSO-*d*₆, 100 MHz): δ_C 156.2 (C-3, 5), 145.5 (C-3'), 143.7 (C-4'), 142.0 (C-1), 133.3 (C-1'), 129.3 (C-9), 125.2 (C-8), 119.1 (C-6'), 116.7 (C-2'), 116.1 (C-2), 115.9 (C-5'), 107.4 (C-6), 100.7 (C-4), 37.0 (C- α), 36.7 (C- α'), 26.0 (C-11), 24.4 (C-7), 18.3 (C-10).^{25,26}



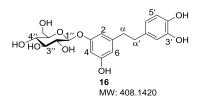
2-Isopentenyl-3,4',5-trihydroxybibenzyl (13): $C_{19}H_{22}O_3$, ESI-MS *m/z* 298.99 [M+H]⁺; ¹H NMR: (DMSO-*d*₆, 400 MHz): δ_H 9.15 (s, 3-OH), 8.98 (s, 5-OH), 8.83 (s, 4'-OH), 6.98 (d, *J* = 8.4 Hz, 2H, H-2', 6'), 6.66 (d, *J* = 8.4 Hz, 2H, H-3', 5'), 6.14 (d, *J* = 2.3 Hz, 2H, H-2, 6), 6.07 (d, *J* = 2.3 Hz, H-4), 4.99 (t, *J* = 6.6 Hz, H-8), 3.13 (d, *J* = 6.6 Hz, H-7), 2.60 (s, 4H, H- α , α '), 1.66 (s, 3H, H-10), 1.60 (s, 3H, H-11); ¹³C NMR (DMSO-*d*₆, 100 MHz): δ_C 156.7 (C-3), 156.5 (C-5), 156.3 (C-4'), 141.4 (C-1), 132.0 (C-1'), 129.0 (C-2', 6'), 128.8 (C-9), 124.7 (C-8), 116.3 (C-2), 115.0 (C-3', 5'), 106.9 (C-6), 100.3 (C-4), 37.6 (C- α), 36.1 (C- α '), 25.5 (C-11), 23.9 (C-7), 17.7 (C-10).²⁷



2-Isopentenyl-3,3',5-trihydroxybibenzyl (14): $C_{19}H_{22}O_4$, HR-ESI-MS: *m/z* 297.1492 [M–H]⁻; ¹H NMR (DMSO-*d*₆, 400 MHz): δ_H 7.06 (dd, *J* = 7.7 Hz, H-5'), 6.64–6.60 (m, overlapped, 2H, H-6', 2'), 6.57 (ddd, *J* = 0.9, 2.4, 7.7 Hz, H-5'), 6.14 (d, *J* = 2.4 Hz, H-4), 6.08 (d, *J* = 2.4 Hz, H-6), 5.00 (t, *J* = 6.6 Hz, H-8), 3.14 (d, *J* = 6.6 Hz, H-7), 2.63 (s, 4H, H- α , α'), 1.67 (s, 3H, H-10), 1.61 (s, 3H, H-11); ¹³C NMR (DMSO-*d*₆, 100 MHz): δ_C 157.4 (C-3'), 155.8 (C-3), 155.6 (C-5), 143.5 (C-1'), 141.4 (C-1), 129.3 (C-9), 128.9 (C-5'), 124.8 (C-8), 118.7 (C-6'), 115.0 (C-2'), 116.3 (C-2), 112.8 (C-4'), 106.9 (C-6), 100.4 (C-4), 37.0 (C- α '), 34.7 (C- α), 25.5 (C-11), 23.8 (C-7), 17.8 (C-10).

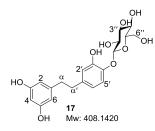


3-*O*-*β*-**D**-glucosyl-3',5-dihydroxybibenzyl (15): C₂₀H₂₄O₈, ESI-MS *m/z* 391.20 [M–H]⁻; ¹H NMR (DMSO-*d*₆, 400 MHz): $\delta_{\rm H}$ 7.00 (d, *J* = 8.4 Hz, 2H, H-2', 6'), 6.65 (d, *J* = 8.4 Hz, 2H, H-3', 5'), 6.25 (m, overlapped, 2H, H-2, 6), 6.34 (t, *J* = 1.7 Hz, H-4), 4.73 (d, *J* = 7.6 Hz, H-1"), 3.68 (dd, *J* = 2.0, 11.8 Hz, H-6"a), 3.47 (dd, *J* = 5.40 Hz, 11.8 Hz, H-6"b), 3.25–3.13 (m, overlapped, 4H, H-2"-5"), 2.68 (m, overlapped, 4H, H-α, α'); ¹³C NMR (DMSO- *d*₆, 100 MHz): $\delta_{\rm C}$ 158.5 (C-3), 158.1 (C-5), 156.4 (C-4'), 143.7 (C-1), 131.6 (C-1'), 129.1 (C-2', 6'), 115.0 (C-3', 5'), 109.1 (C-6), 107.2 (C-2), 101.1 (C-4), 100.4 (C-1"), 77.0 (C-3"), 76.7 (C-5"), 73.2 (C-2"), 69.7 (C-4"), 60.6 (C-6"), 37.6 (C-α), 36.0 (C-α').²⁸

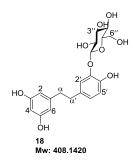


3-*O*-*β*-**D**-glucosyl-3',4',5-trihydroxybibenzyl (16): C₂₀H₂₄O₉, HR-ESI-MS: m/z 407.1343 [M–H]⁻; ESI-MS m/z 407.50 [M–H]⁻; ¹H NMR (DMSO- d_6 , 400 MHz): $\delta_{\rm H}$

6.60 (d, J = 8.0 Hz, H-5'), 6.59 (d, J = 2.0 Hz, H-2'), 6.44 (dd, J = 2.0, 8.0 Hz, H-6'), 6.34 (dd, J = 1.7, 1.7 Hz, H-6), 6.26–6.25 (m, overlapped, 2H, H-2, 4), 4.74 (d, J =7.7 Hz, H-1"), 3.68 (dd, J = 2.0, 12.0 Hz, H-6"a), 3.48 (dd, J = 5.4, 12.0 Hz, H-6"b), 3.25–3.16 (m, overlapped, 4H, H-2"–5"), 2.64 (s, 4H, H-α, α'); ¹³C NMR (DMSO- d_6 , 100 MHz): δ_C 158.5 (C-3), 158.1 (C-5), 145.1 (C-3'), 143.7 (C-1), 143.3 (C-4'), 132.4 (C-1'), 118.8 (C-6'), 115.9 (C-2'), 115.4 (C-5'), 109.1 (C-2), 107.2 (C-6), 101.1 (C-4), 100.4 (C-1"), 77.0 (C-3"), 76.2 (C-5"), 73.2 (C-2"), 69.7 (C-4"), 60.6 (C-6"), 37.6 (C-α), 36.2 (C-α').

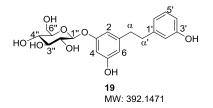


4'-O-β-D-glucosyl-3,3',5-trihydroxybibenzyl (**17**): C₂₀H₂₄O₉, HR-ESI-MS: m/z 407.1342 [M–H]⁻; ESI-MS m/z 407.65 [M–H]⁻; ¹H NMR (DMSO- d_6 , 400 MHz): $\delta_{\rm H}$ 6.99 (d, J = 8.2 Hz, H-5'), 6.66 (d, J = 2.0 Hz, H-2'), 6.56 (dd, J = 2.0, 8.2 Hz, H-6'), 6.06 (d, J = 2.2 Hz, 2H, H-2, 6), 6.01 (dd, J = 2.2, 2.2 Hz, H-4), 4.61 (d, J = 7.6 Hz, H-1"), 3.72 (dd, J = 2.1, 11.8 Hz, H-6"a), 3.47 (dd, J = 5.8, 11.8 Hz, H-6"b), 3.27–3.15 (m, overlapped, 4H, H-2"–5"), 2.66 (s, 4H, H- α , α '); ¹³C NMR (DMSO- d_6 , 100 MHz): $\delta_{\rm C}$ 158.3 (C-3, 5), 146.8 (C-3'), 143.6 (C-4'), 143.5 (C-1), 136.6 (C-1'), 119.0 (C-6'), 116.9 (C-5'), 116.0 (C-2'), 106.3 (C-2, 6), 102.9 (C-1"), 100.2 (C-4), 77.1 (C-3"), 75.9 (C-5"), 73.3 (C-2"), 69.8 (C-4"), 60.8 (C-6"), 37.3 (C- α), 36.2 (C- α ').

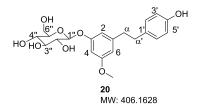


3'-O-β-D-glucosyl-3,4',5-trihydroxybibenzyl (18): C₂₀H₂₄O₉, HR-ESI-MS: m/z 407.1343 [M–H]⁻; ESI-MS m/z 407.56 [M–H]⁻; ¹H NMR (DMSO- d_6 , 400 MHz): $\delta_{\rm H}$ 7.00 (d, J = 1.5 Hz, H-2'), 6.72–6.67 (m, overlapped, 2H, H-5', 6'), 6.06 (d, J = 2.2 Hz,

2H, H-2, 6), 6.01 (dd, J = 2.2, 2.2 Hz, H-4), 4.61 (d, J = 7.5 Hz, H-1"), 3.72 (dd, J = 2.1, 11.8 Hz, H-6"a), 3.49 (dd, J = 5.7, 11.8 Hz, H-6"b), 3.29–3.16 (m, overlapped, 4H, H-2"–5"), 2.66 (m, overlapped, 4H, H- α , α'); ¹³C NMR (DMSO- d_6 , 100 MHz): δ_C 158.6 (C-3, 5), 145.1 (C-3'), 144.8 (C-4'), 143.6 (C-1), 132.7 (C-1'), 122.5 (C-6'), 115.5 (C-5'), 117.1 (C-2'), 106.3 (C-2, 6), 102.7 (C-1"), 100.2 (C-4), 77.1 (C-3"), 75.9 (C-5"), 73.4 (C-2"), 69.8 (C-4"), 60.7 (C-6"), 37.3 (C- α), 36.3 (C- α').

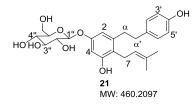


3-*O*-*β***-D**-glucosyl-3',5-dihydroxybibenzyl (19): C₂₀H₂₄O₈, HR-ESI-MS: *m/z* 391.1394 [M–H]⁻; ¹H NMR (DMSO-*d*₆, 400 MHz): $\delta_{\rm H}$ 7.04 (t, *J* = 7.7 Hz, H-5'), 6.65–6.60 (m, overlapped, 2H, H-6', 2'), 6.56 (ddd, *J* = 1.0, 2.5, 7.7 Hz, H-4'), 6.36 (t, *J* = 1.8 Hz, H-6), 6.27 (d, *J* = 1.8 Hz, 2H, H-2, 4), 4.73 (d, *J* = 7.6 Hz, H-1"), 3.68 (dd, *J* = 2.0, 11.8 Hz, H-6"a), 3.48 (dd, *J* = 5.4, 11.8 Hz, H-6"b), 3.25–3.15 (m, overlapped, 4H, H-2"–5"), 2.71 (m, overlapped, 4H, H-α, α'); ¹³C NMR (DMSO-*d*₆, 100 MHz): $\delta_{\rm C}$ 158.9 (C-3), 158.6 (C-5), 157.7 (C-3'), 144.0 (C-1), 143.5 (C-1'), 129.6 (C-5'), 119.4 (C-6'), 115.6 (C-2'), 113.2 (C-4'), 109.5 (C-2), 107.7 (C-6), 101.6 (C-4), 100.9 (C-1"), 77.5 (C-3"), 77.2 (C-5"), 73.7 (C-2"), 70.1 (C-4"), 61.0 (C-6"), 37.5 (C-α), 37.2 (C-α').

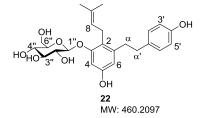


3-*O*-*β*-**D**-glucosyl-5-methoxy-4'-hydroxybibenzyl (20): $C_{21}H_{26}O_8$, HR-ESI-MS: *m/z* 405.1552 [M–H]⁻; ¹H NMR (DMSO-*d*₆, 400 MHz): δ_H 7.01 (*d*, *J* = 8.5 Hz, 2H, H-2', 6'), 6.65 (d, *J* = 8.5 Hz, 2H, H-3', 5'), 6.49 (dd, *J* = 2.1, 2.1 Hz, H-2), 6.43 (dd, *J* = 2.1, 2.1 Hz, H-4), 6.41 (dd, *J* = 2.1, 2.1 Hz, H-6), 4.79 (d, *J* = 7.6 Hz, H-1"), 3.70 (m, overlapped, H-6"a), 3.69 (s, 3H, 5-OMe), 3.45 (dd, *J* = 5.7, 11.7 Hz, H-6"b), 3.31–3.14 (m, overlapped, 4H, H-2"–5"), 2.73 (s, 4H, H-α, α'); ¹³C NMR (DMSO-*d*₆, 100 MHz): δ_C 160.1 (C-5), 158.6 (C-3), 155.4 (C-4'), 144.1 (C-1), 131.6 (C-1'), 129.2

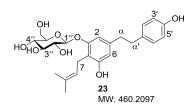
(C-2', 6'), 115.0 (C-3', 5'), 108.6 (C-2), 107.6 (C-6), 100.4 (C-1"), 99.6 (C-4), 77.2 (C-3"), 76.8 (C-5"), 73.3 (C-2"), 69.7 (C-4"), 60.6 (C-6"), 55.0 (5-OMe), 37.7 (C-α), 35.9 (C-α').



3-*O*-*β*-**D**-glucosyl-6-isopentenyl-4',5-dihydroxybibenzyl (21): C₂₅H₃₂O₈, HR-ESI-MS: *m*/*z* 459.2021 [M–H]⁻; ¹H NMR (DMSO-*d*₆, 400 MHz): $\delta_{\rm H}$ 9.22 (s, 5-OH), 9.14 (s, 4'-OH), 6.99 (d, *J* = 8.5 Hz, 2H, H-2', 6'), 6.66 (d, *J* = 8.5 Hz, 2H, H-3', 5'), 6.38 (d, *J* = 2.4 Hz, H-2), 6.37 (d, *J* = 2.4 Hz, H-4), 5.24 (d, *J* = 5.1 Hz, 2"-OH), 5.06 (d, *J* = 4.6 Hz, 3"-OH), 4.99 (m, overlapped, 2H, 4"-OH, H-8), 4.69 (d, *J* = 7.6 Hz, H-1"), 4.53 (t, *J* = 5.8 Hz, 6"-OH), 3.69 (dd, *J* = 1.8, 11.7 Hz, H-6"a), 3.49 (dd, *J* = 5.2, 11.7 Hz, H-6"b), 3.23–3.17 (m, overlapped, 4H, H-2"–5"), 2.65 (s, 4H, H-α, α'), 1.67 (s, 3H, H-10), 1.61 (s, 3H, H-11); ¹³C NMR (DMSO-*d*₆, 100 MHz): $\delta_{\rm C}$ 155.9 (C-3), 155.6 (C-5), 155.4 (C-4'), 141.5 (C-1), 131.9 (C-1'), 129.3 (C-9), 129.0 (C-2', 6'), 124.3 (C-8), 119.4 (C-6), 115.0 (C-3', 5'), 107.8 (C-2), 100.6 (C-4), 100.5 (C-1"), 77.0 (C-3"), 76.9 (C-5"), 73.5 (C-2"), 69.6 (C-4"), 60.7 (C-6"), 36.1 (C-α'), 35.1 (C-α), 25.5 (C-11), 24.2 (C-7), 17.8 (C-10).



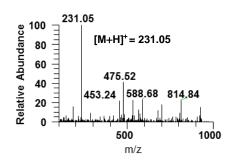
2-Isopentenyl-3-*O*-*β*-**D**-glucosyl-4',5-dihydroxybibenzyl (22): $C_{25}H_{32}O_8$, HR-ESI-MS: *m/z* 459.2020 [M–H]⁻; ¹H NMR (DMSO-*d*₆, 400 MHz): δ_H 6.99 (d, *J* = 8.4 Hz, 2H, H-2', 6'), 6.66 (d, *J* = 8.4 Hz, 2H, H-3', 5'), 6.40 (d, *J* = 2.3 Hz, H-4), 6.28 (d, *J* = 2.3 Hz, H-6), 5.03 (t, *J* = 5.6 Hz, H-8), 4.68 (d, *J* = 7.2 Hz, H-1"), 3.70 (dd, *J* = 1.8, 11.7 Hz, H-6"a), 3.50 (dd, *J* = 5.0, 11.7 Hz, H-6"b), 3.24–3.17 (m, overlapped, 4H, H-2"–5"), 2.64 (m, overlapped, 4H, H-α, α'), 1.68 (s, 3H, H-10), 1.60 (s, 3H, H-11); ¹³C NMR (DMSO-*d*₆, 100 MHz): δ_C 156.5 (C-3), 155.8 (C-5), 155.4 (C-4'), 141.3 (C-1), 131.9 (C-1'), 129.0 (C-2', 6'), 128.8 (C-9), 124.7 (C-8), 118.9 (C-2), 115.0 (C-3', 5'), 109.5 (C-6), 101.6 (C-1"), 100.8 (C-4), 77.0 (C-3"), 76.9 (C-5"), 73.5 (C-2"), 69.6 (C-4"), 60.7 (C-6"), 36.2 (C-α'), 35.1 (C-α), 25.5 (C-11), 23.9 (C-7), 17.8 (C-10).

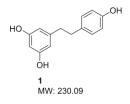


3-*O*-*β*-**D**-glucosyl-4-isopentenyl-4',5-dihydroxybibenzyl (23): $C_{25}H_{32}O_8$, HR-ESI-MS: *m/z* 459.2020 [M–H]⁻; ¹H NMR (DMSO-*d*₆, 400 MHz): δ_H 7.11 (d, *J* = 8.7 Hz, 2H, H-2', 6'), 6.94 (d, *J* = 8.7 Hz, 2H, H-3', 5'), 6.15 (d, *J* = 2.4 Hz, H-2), 6.08 (d, *J* = 2.4 Hz, H-6), 5.03 (t, *J* = 5.6 Hz, H-8), 4.80 (d, *J* = 7.4 Hz, H-1"), 3.69 (dd, *J* = 1.8, 11.8 Hz, H-6"a), 3.50 (dd, *J* = 5.0, 11.8 Hz, H-6"b), 3.24–3.17 (m, overlapped, 4H, H-2"–5"), 2.64 (m, overlapped, 4H, H- α , α '), 1.67 (s, 3H, H-10), 1.60 (s, 3H, H-11); ¹³C NMR (DMSO-*d*₆, 100 MHz): δ_C 155.7 (C-5, 3), 155.6 (C-4'), 141.3 (C-1), 135.2 (C-1'), 129.0 (C-2', 6'), 128.9 (C-9), 124.8 (C-8), 116.3 (C-4), 116.1 (C-3', 5'), 107.0 (C-6), 100.6 (C-1"), 100.4 (C-2), 76.6 (C-3", 5"), 73.3 (C-2"), 69.7 (C-4"), 60.7 (C-6"), 36.2 (C- α '), 35.1 (C- α), 25.5 (C-11), 23.9 (C-7), 17.8 (C-10).

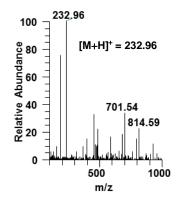
Supplementary spectra

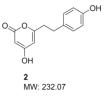
Supplementary MS spectra of products (1–34)



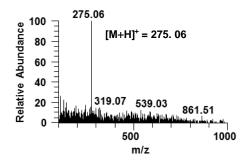


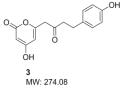
Spectrum S1. The ESI-MS spectrum of 1.



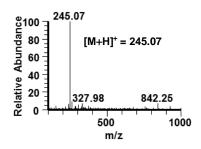


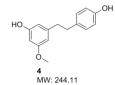
Spectrum S2. The ESI-MS spectrum of 2.



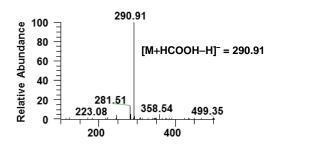


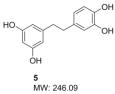
Spectrum S3. The ESI-MS spectrum of 3.



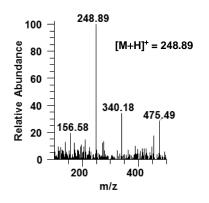


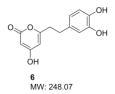
Spectrum S4. The ESI-MS spectrum of 4.



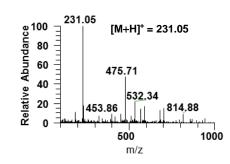


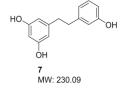
Spectrum S5. The ESI-MS spectrum of 5.



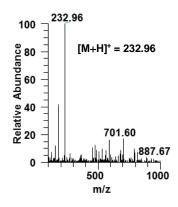


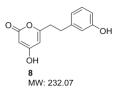
Spectrum S6. The ESI-MS spectrum of **6**.



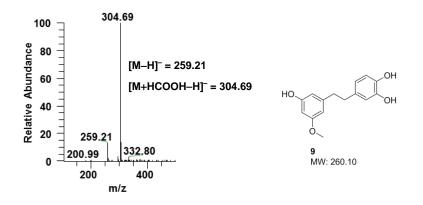


Spectrum S7. The ESI-MS spectrum of 7.

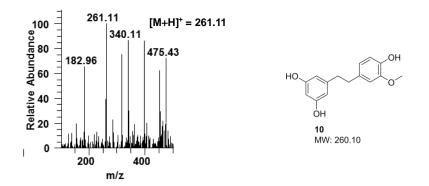




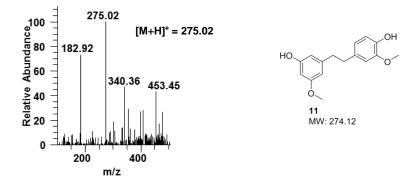
Spectrum S8. The ESI-MS spectrum of 8.



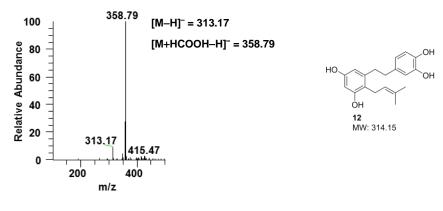
Spectrum S9. The ESI-MS spectrum of 9.



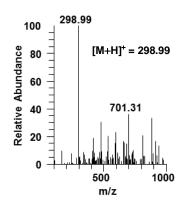
Spectrum S10. The ESI-MS spectrum of 10.

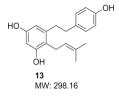


Spectrum S11. The ESI-MS spectrum of 11.

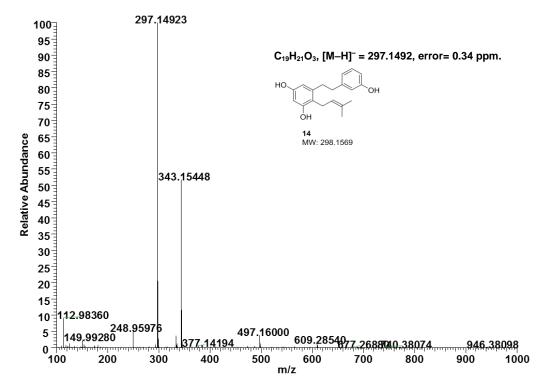


Spectrum S12. The ESI-MS spectrum of 12.

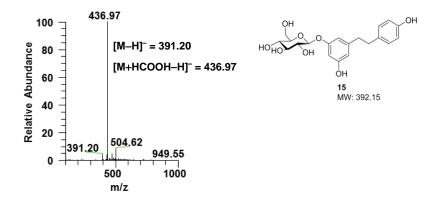




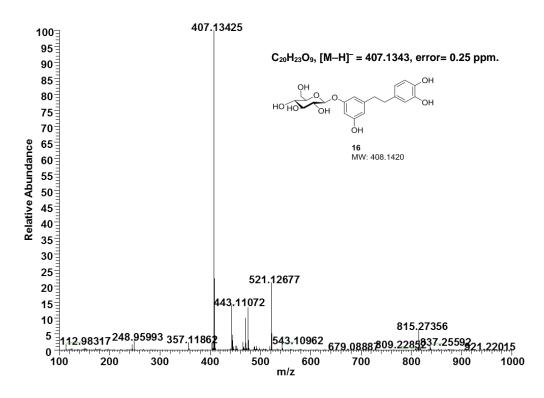
Spectrum S13. The ESI-MS spectrum of 13.



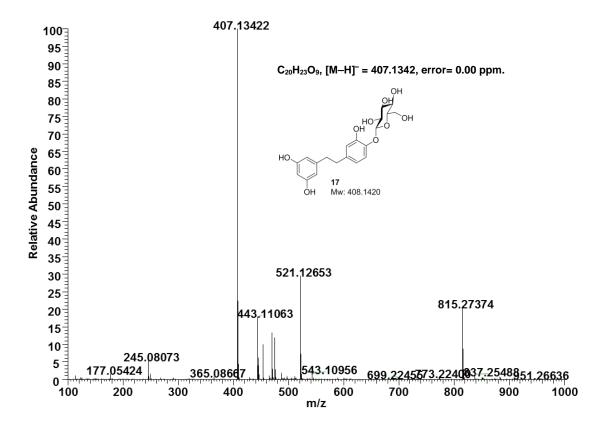
Spectrum S14. The HR-ESI-MS spectrum of 14.



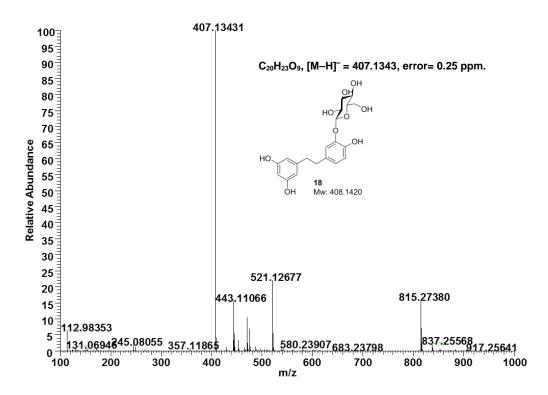
Spectrum S15. The ESI-MS spectrum of 15.



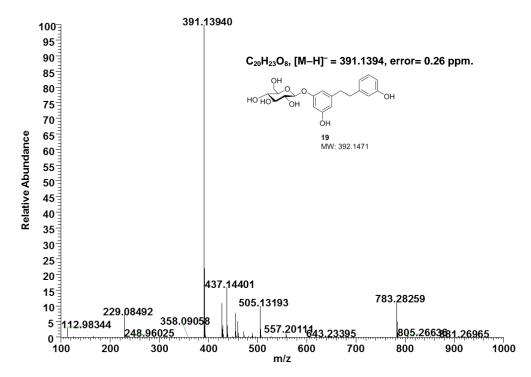
Spectrum S16. The HR-ESI-MS spectrum of 16.



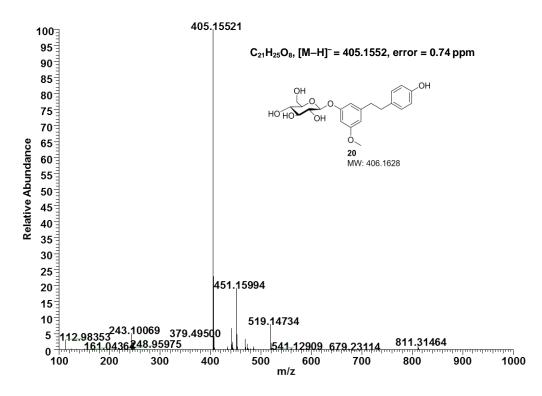
Spectrum S17. The HR-ESI-MS spectrum of 17.



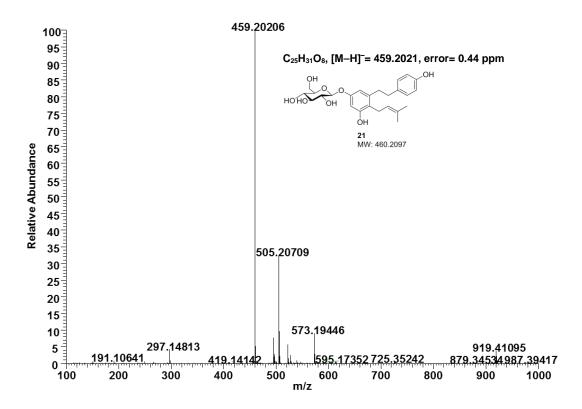
Spectrum S18. The HR-ESI-MS spectrum of 18.



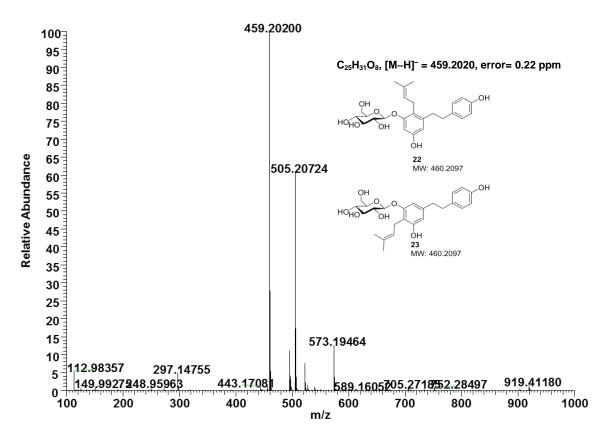
Spectrum S19. The HR-ESI-MS spectrum of 19.



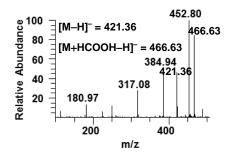
Spectrum S20. The HR-ESI-MS spectrum of 20.

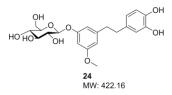


Spectrum S21. The HR-ESI-MS spectrum of 21.

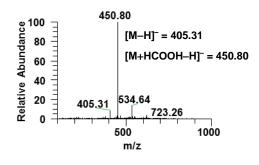


Spectrum S22. The HR-ESI-MS spectrum of 22 and 23.





Spectrum S23. The ESI-MS spectrum of 24.



25 MW: 406.16

о́н **26** MW: 422.16

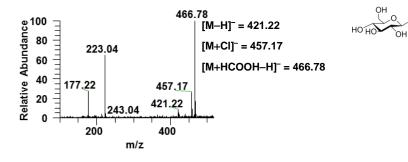
Οŀ

HOLO

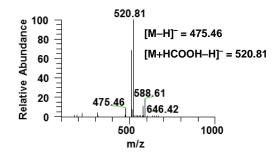
ОН

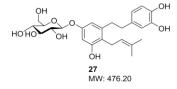
ОН

Spectrum S24. The ESI-MS spectrum of 25.

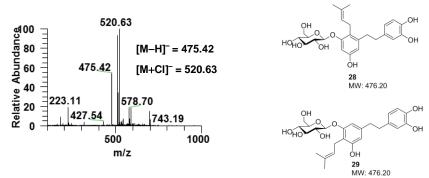


Spectrum S25. The ESI-MS spectrum of 26.

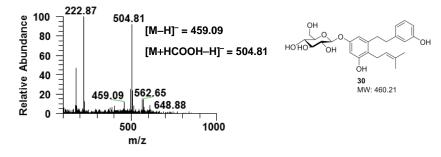




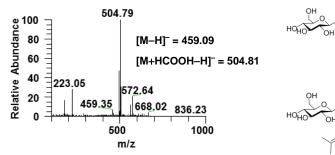
Spectrum S26. The ESI-MS spectrum of 27.

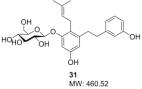


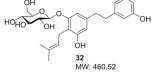
Spectrum S27. The ESI-MS spectrum of 28 and 29.



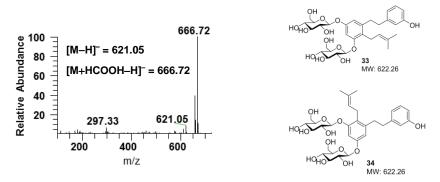
Spectrum S28. The ESI-MS spectrum of 30.



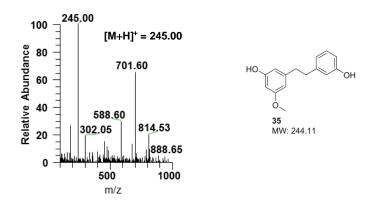




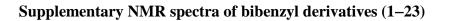
Spectrum S29. The ESI-MS spectrum of 31 and 32.

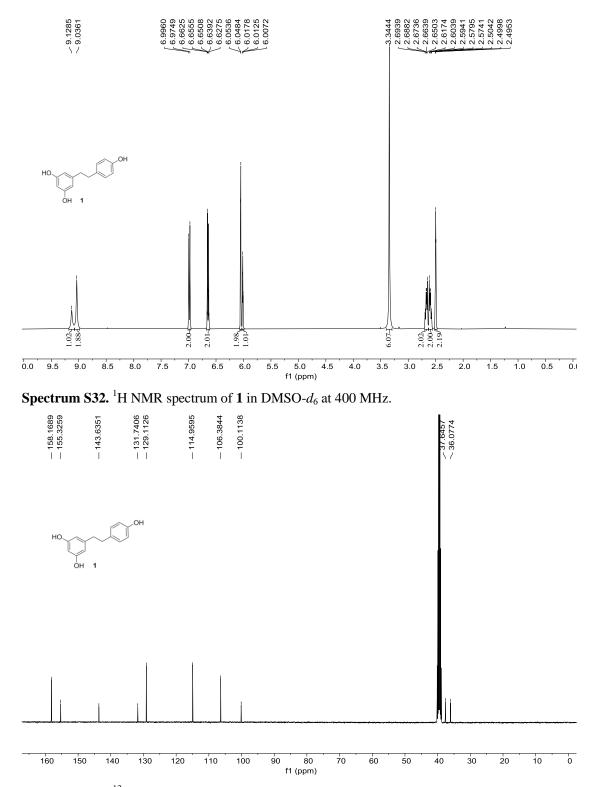


Spectrum S30. The ESI-MS spectrum of 33 and 34.

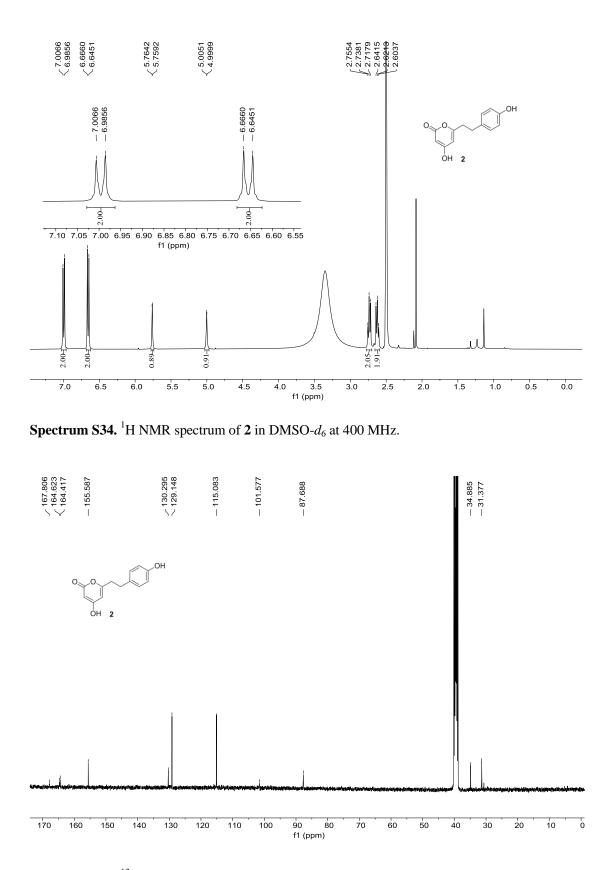


Spectrum S31. The ESI-MS spectrum of 35.

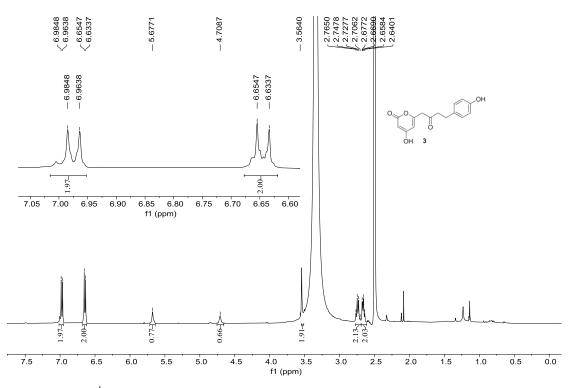




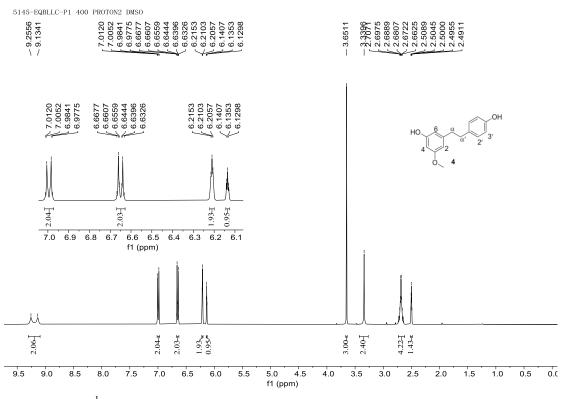
Spectrum S33. ¹³C NMR spectrum of **1** in DMSO- d_6 at 100 MHz.



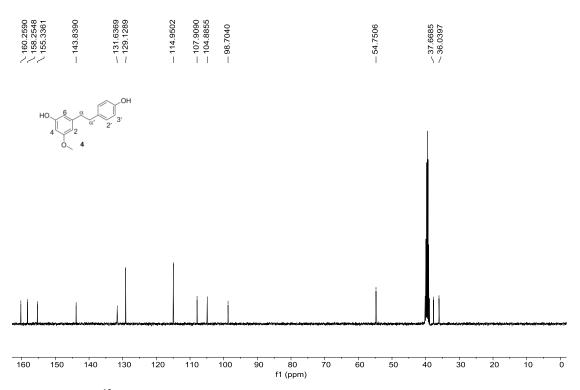
Spectrum S35. ¹³C NMR spectrum of **2** in DMSO- d_6 at 100 MHz.



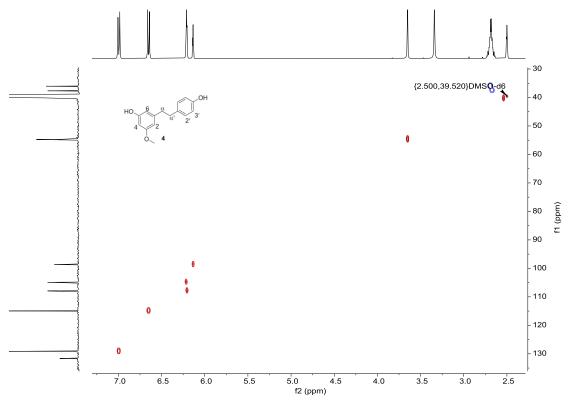
Spectrum S36. ¹H NMR spectrum of **3** in DMSO-*d*₆ at 400 MHz.



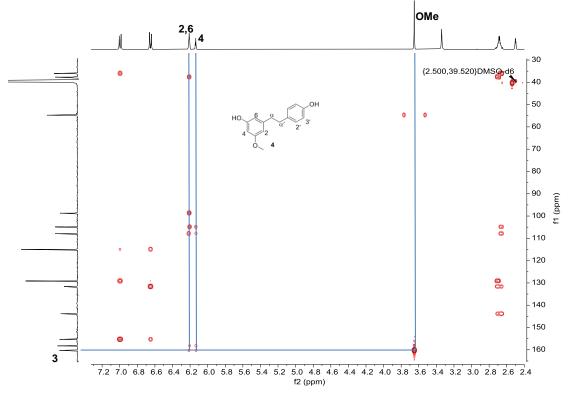
Spectrum S37. ¹H NMR spectrum of **4** in DMSO- d_6 at 400 MHz.



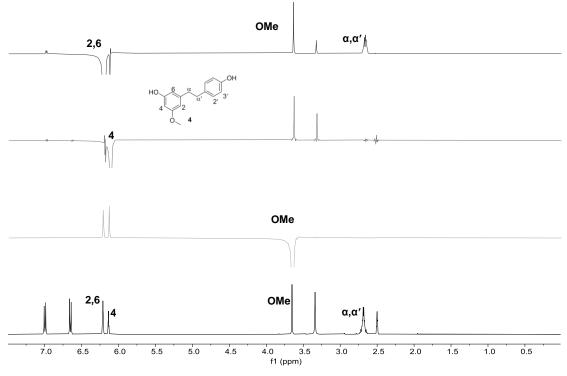
Spectrum S38. ¹³C NMR spectrum of **4** in DMSO- d_6 at 100 MHz.



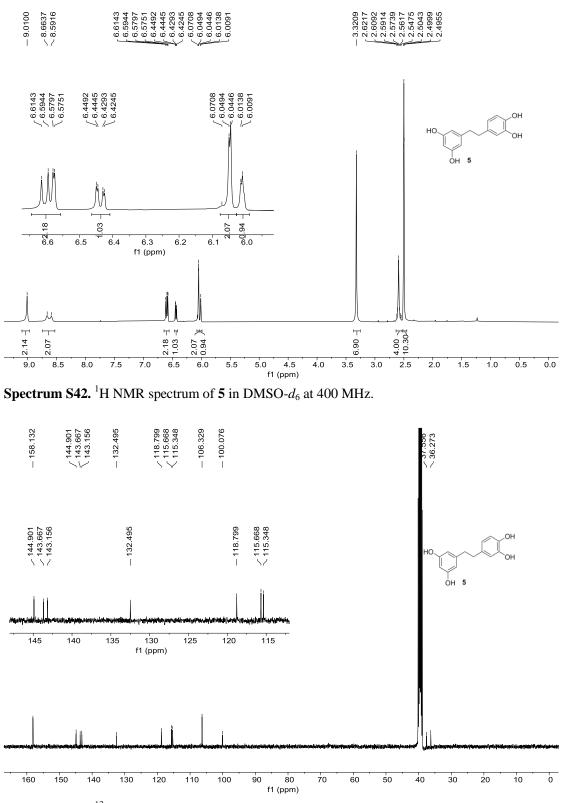
Spectrum S39. HSQC spectrum of 4 in DMSO-*d*₆.



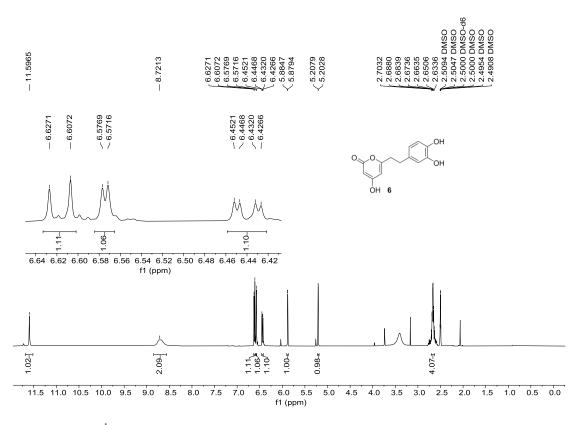
Spectrum S40. HMBC spectrum of 4 in DMSO-*d*₆.



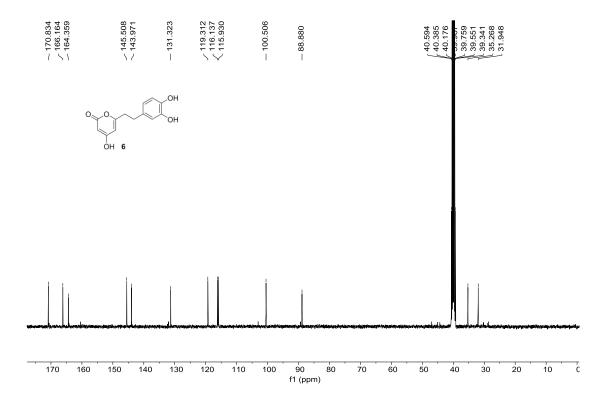
Spectrum S41. NOESY spectrum of 4 in DMSO-*d*₆.



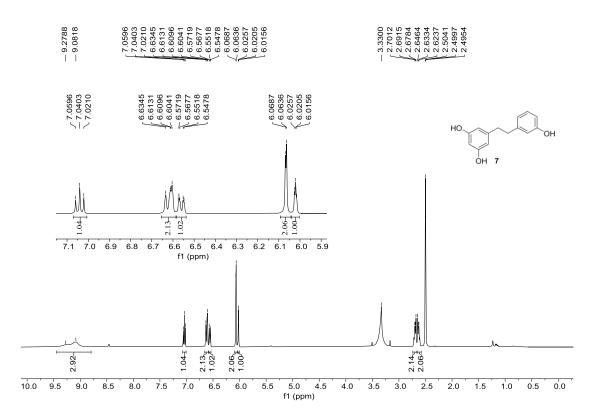
Spectrum S43. ¹³C NMR spectrum of **5** in DMSO- d_6 at 100 MHz.



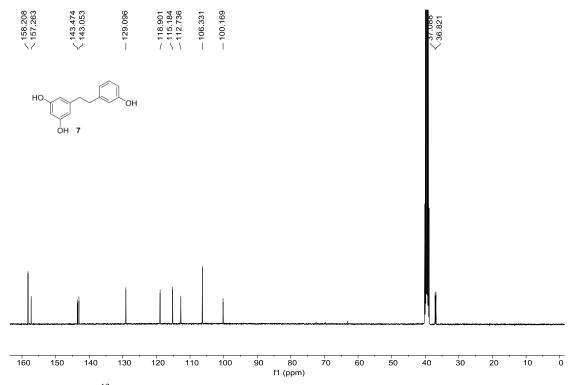
Spectrum S44. ¹H NMR spectrum of **6** in DMSO- d_6 at 400 MHz.



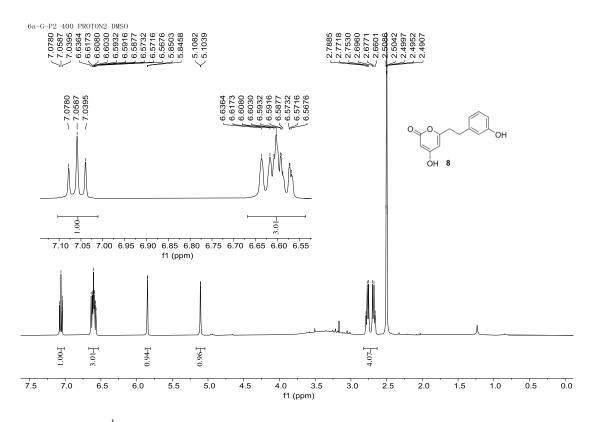
Spectrum S45. ¹³C NMR spectrum of **6** in DMSO- d_6 at 100 MHz.



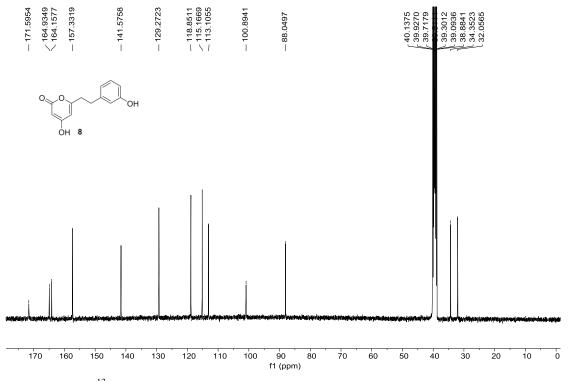
Spectrum S46. ¹H NMR spectrum of **7** in DMSO- d_6 at 400 MHz.



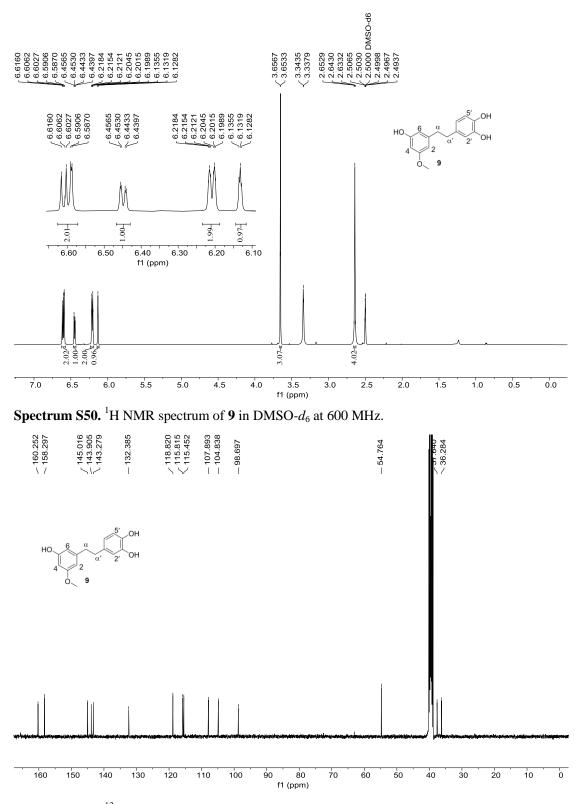
Spectrum S47. ¹³C NMR spectrum of **7** in DMSO- d_6 at 100 MHz.



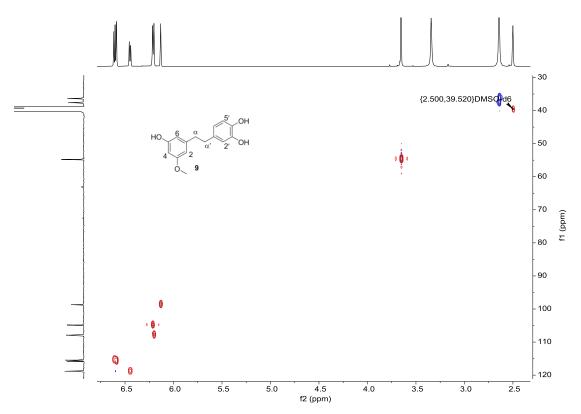
Spectrum S48. ¹H NMR spectrum of **8** in DMSO- d_6 at 400 MHz.



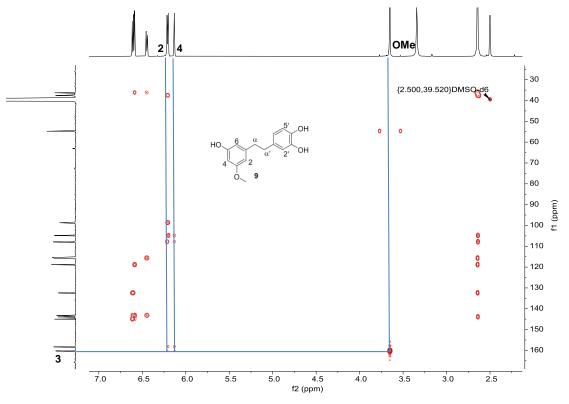
Spectrum S49. ¹³C NMR spectrum of **8** in DMSO- d_6 at 100 MHz.



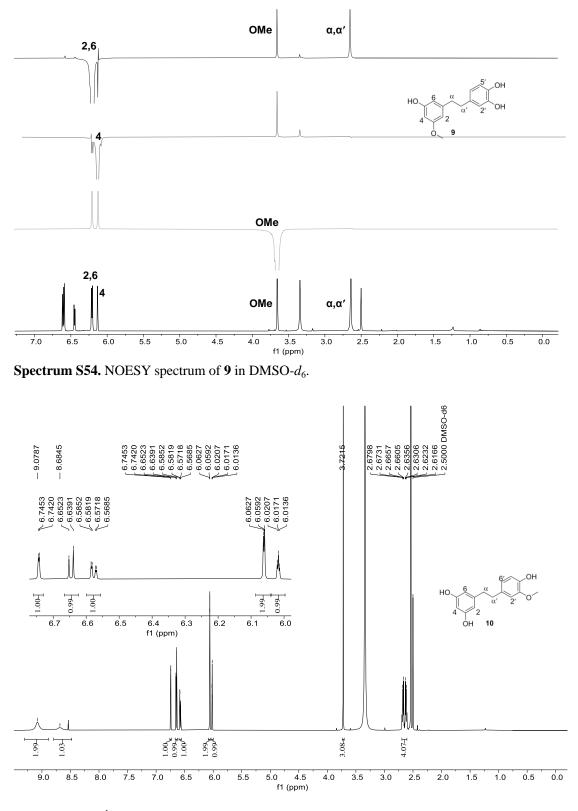
Spectrum S51. ¹³C NMR spectrum of **9** in DMSO- d_6 at 100 MHz.



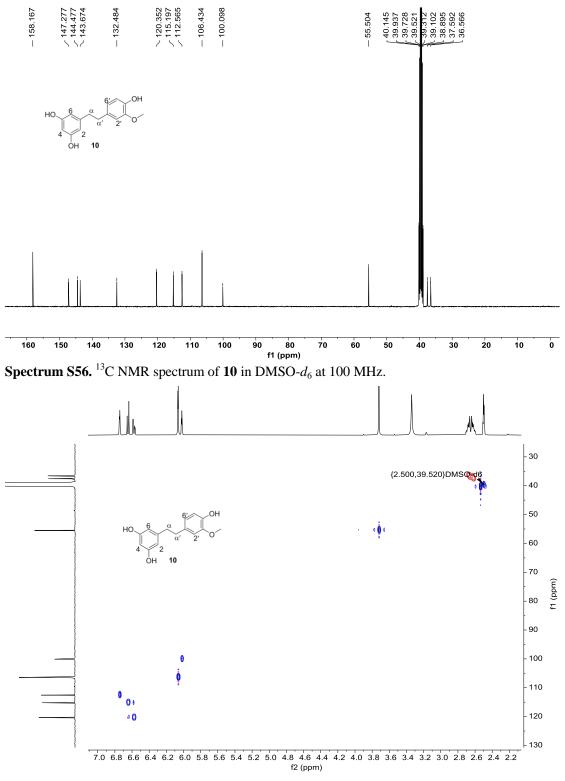
Spectrum S52. HSQC spectrum of 9 in DMSO-*d*₆.



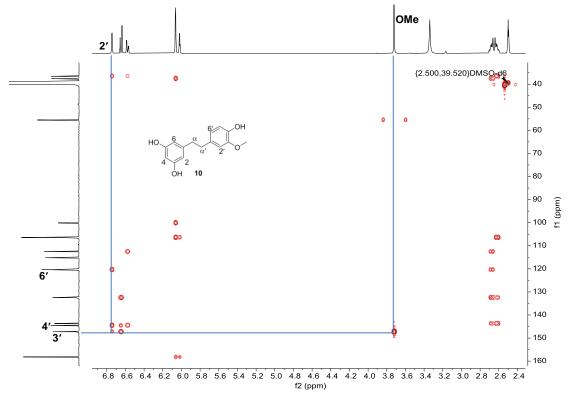
Spectrum S53. HMBC spectrum of 9 in DMSO-*d*₆.



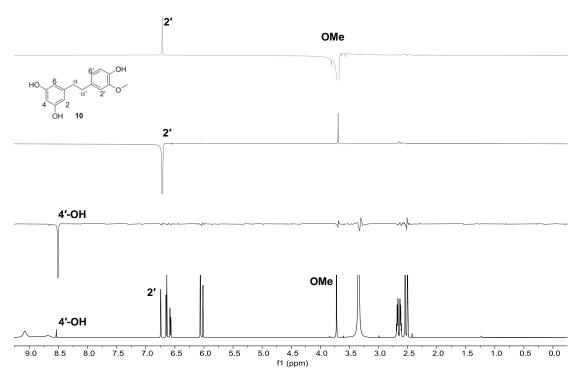
Spectrum S55. ¹H NMR spectrum of **10** in DMSO-*d*₆ at 600 MHz.



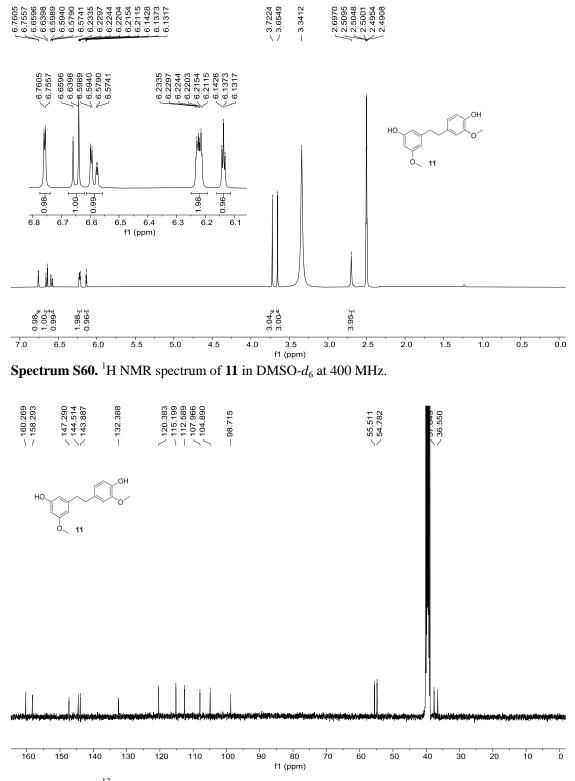
Spectrum S57. HSQC spectrum of 10 in DMSO-*d*₆.



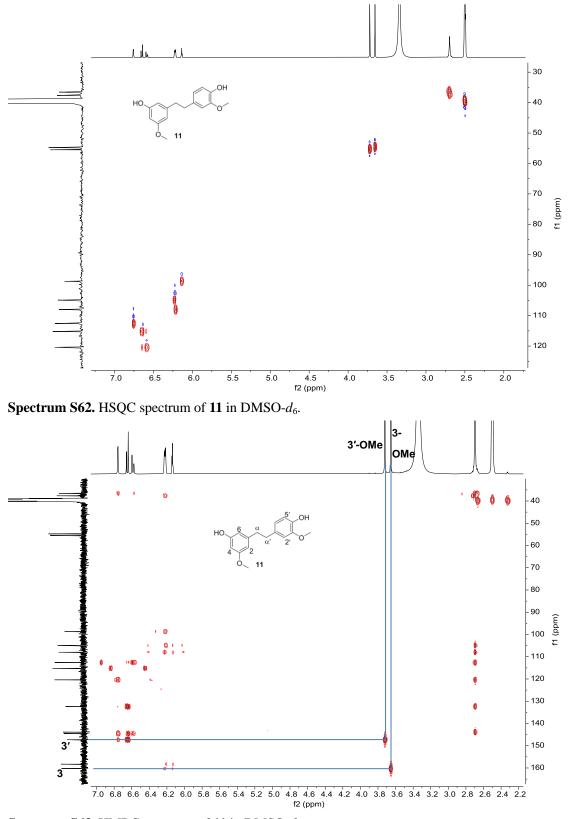
Spectrum S58. HMBC spectrum of 10 in DMSO-*d*₆.



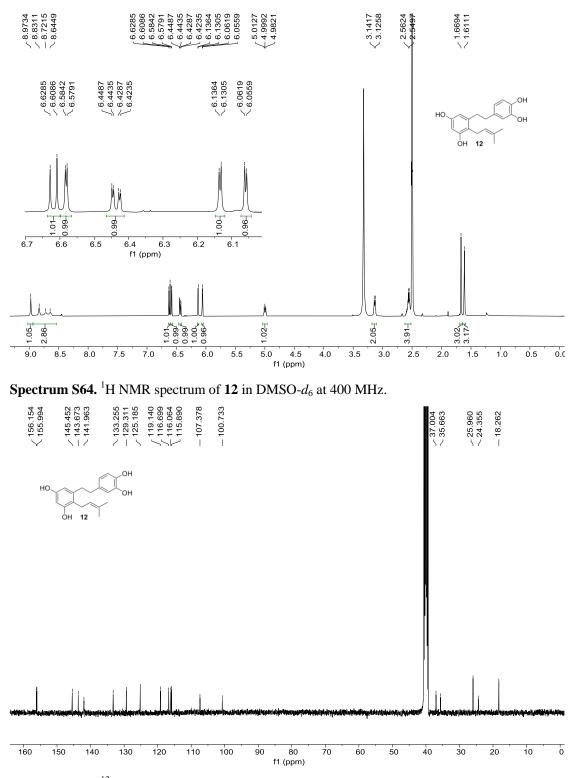
Spectrum S59. NOESY spectrum of 10 in DMSO-*d*₆.



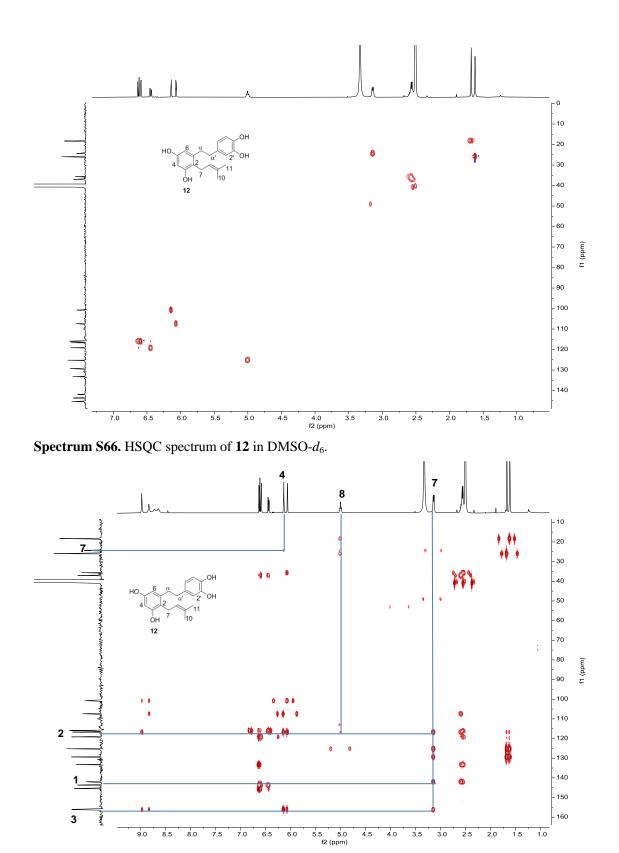
Spectrum S61. ¹³C NMR spectrum of **11** in DMSO- d_6 at 100 MHz.



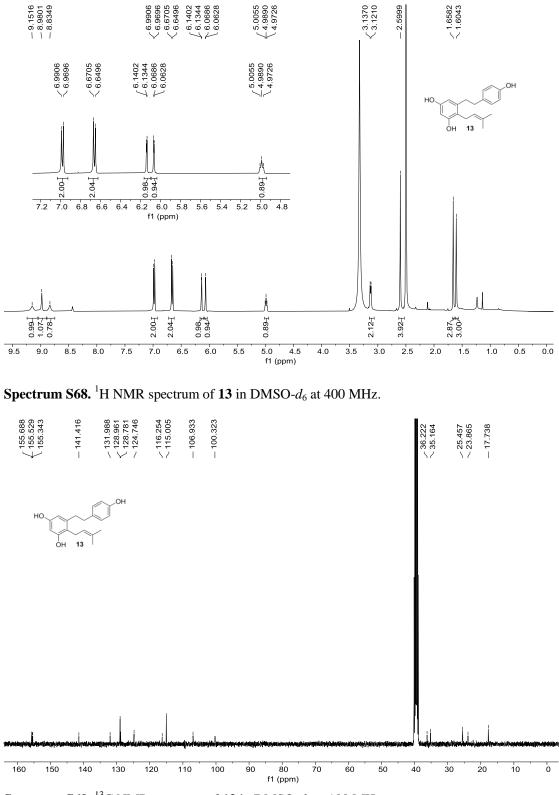
Spectrum S63. HMBC spectrum of 11 in DMSO-d₆.



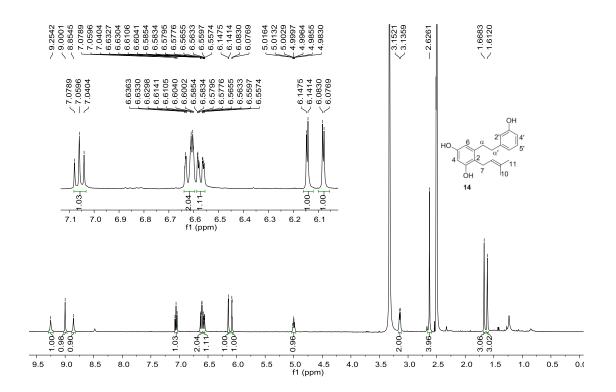
Spectrum S65. ¹³C NMR spectrum of **12** in DMSO-*d*₆ at 100 MHz.



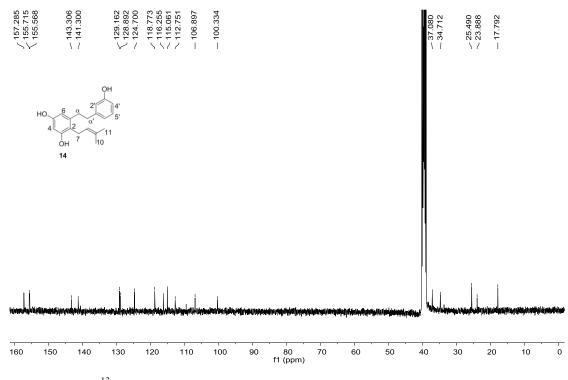
Spectrum S67. HMBC spectrum of **12** in DMSO-*d*₆.



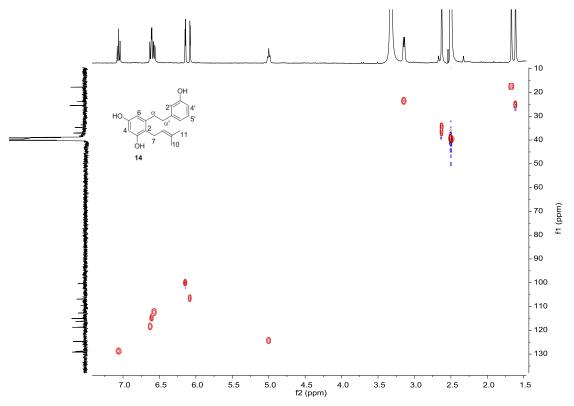
Spectrum S69. ¹³C NMR spectrum of **13** in DMSO- d_6 at 100 MHz.



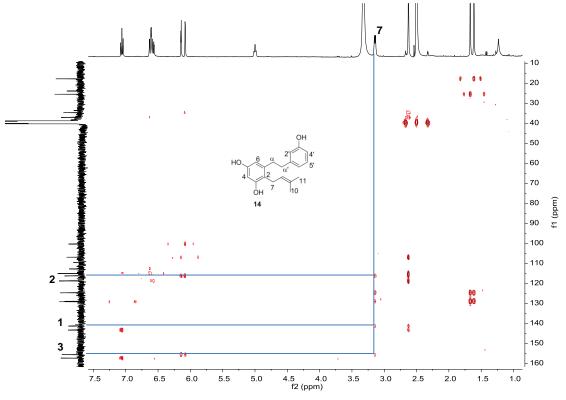
Spectrum S70. ¹H NMR spectrum of **14** in DMSO- d_6 at 400 MHz.



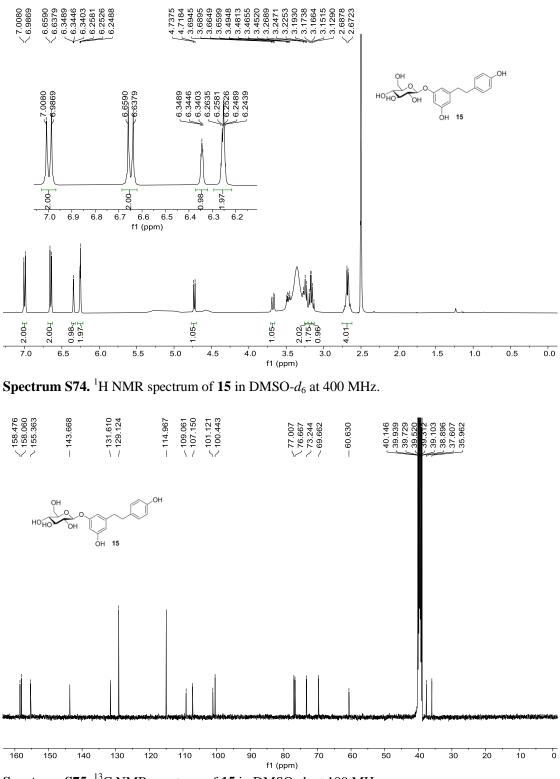
Spectrum S71. ¹³C NMR spectrum of **14** in DMSO- d_6 at 100 MHz.



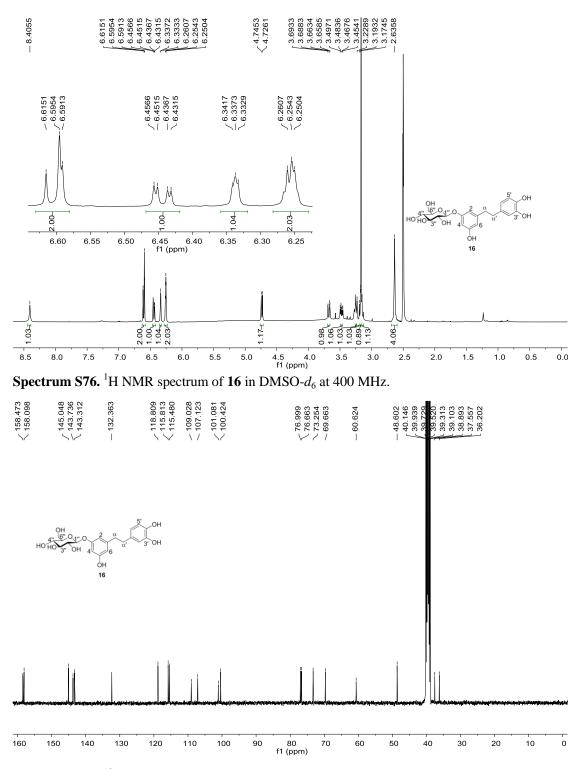
Spectrum S72. HSQC spectrum of 14 in DMSO-d₆.



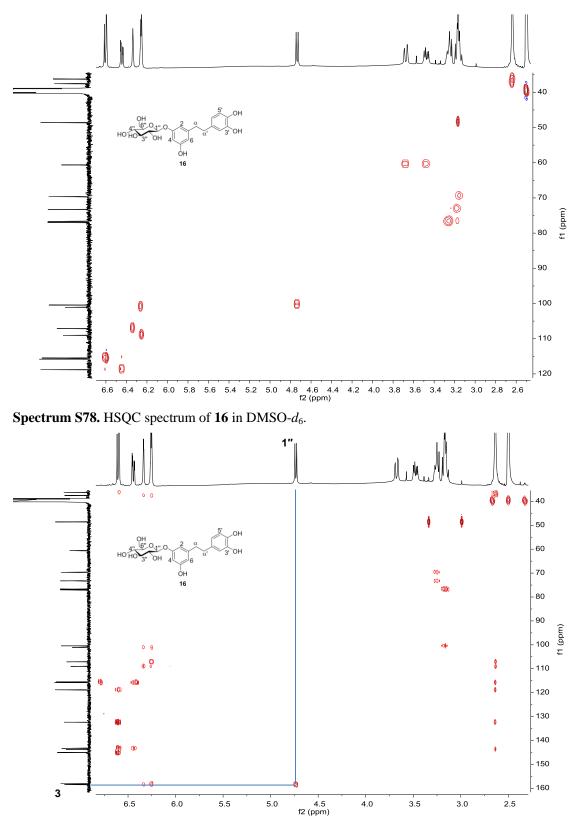
Spectrum S73. HMBC spectrum of 14 in DMSO-*d*₆.



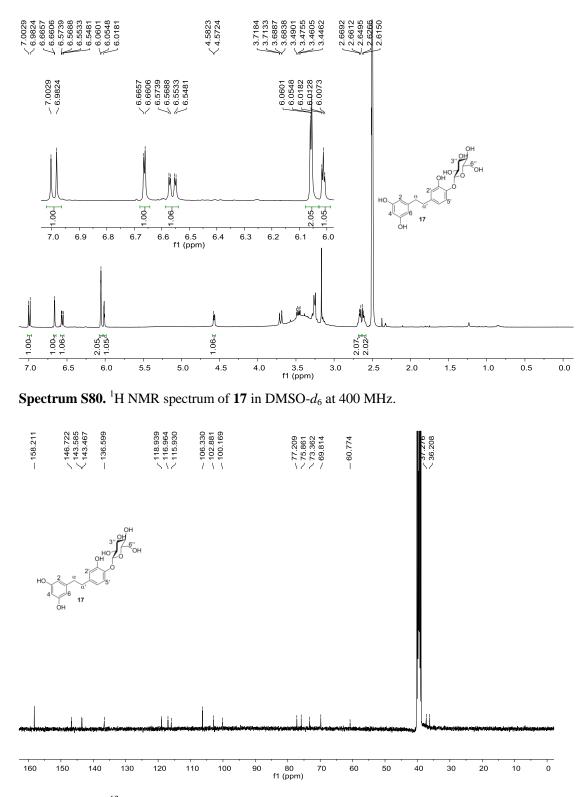
Spectrum S75. ¹³C NMR spectrum of **15** in DMSO-*d*₆ at 100 MHz.



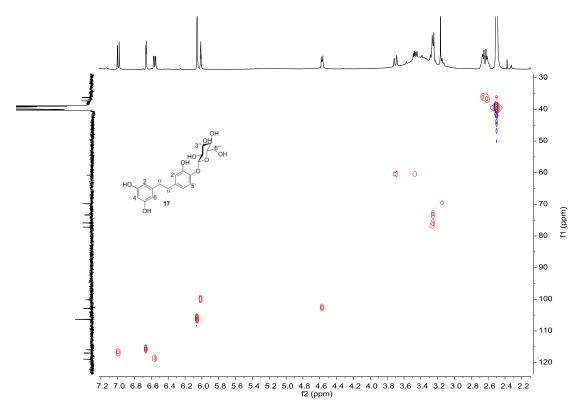
Spectrum S77. ¹³C NMR spectrum of **16** in DMSO- d_6 at 100 MHz.



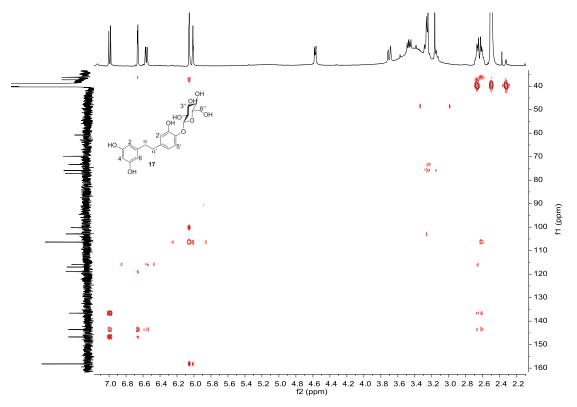
Spectrum S79. HMBC spectrum of 16 in DMSO-*d*₆.



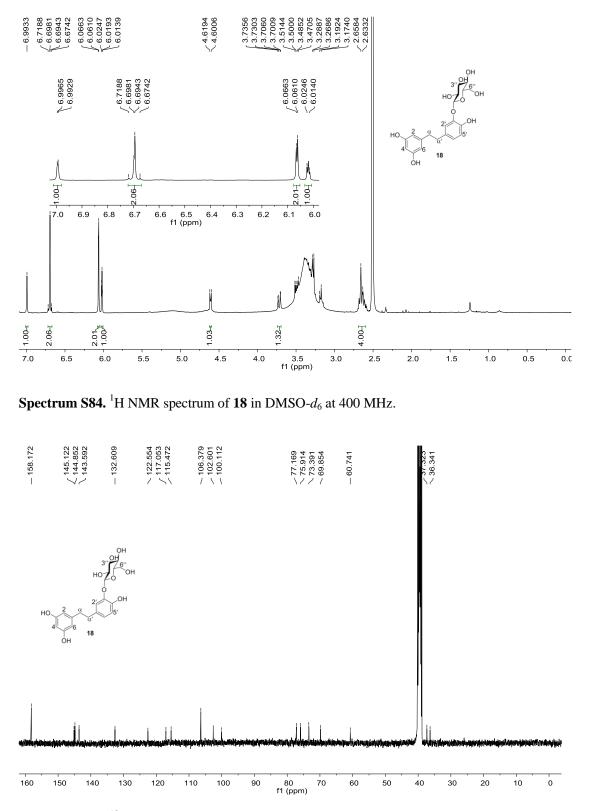
Spectrum S81. ¹³C NMR spectrum of **17** in DMSO- d_6 at 100 MHz.



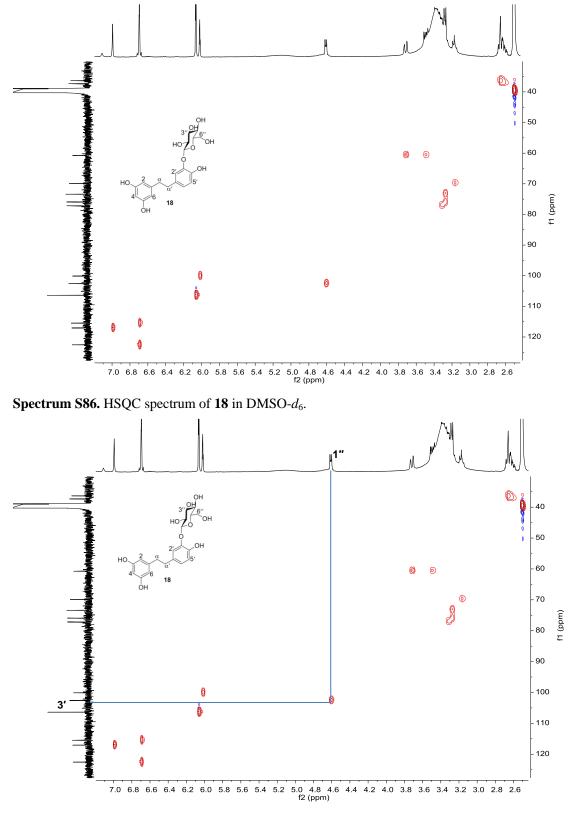
Spectrum S82. HSQC spectrum of 17 in DMSO-*d*₆.



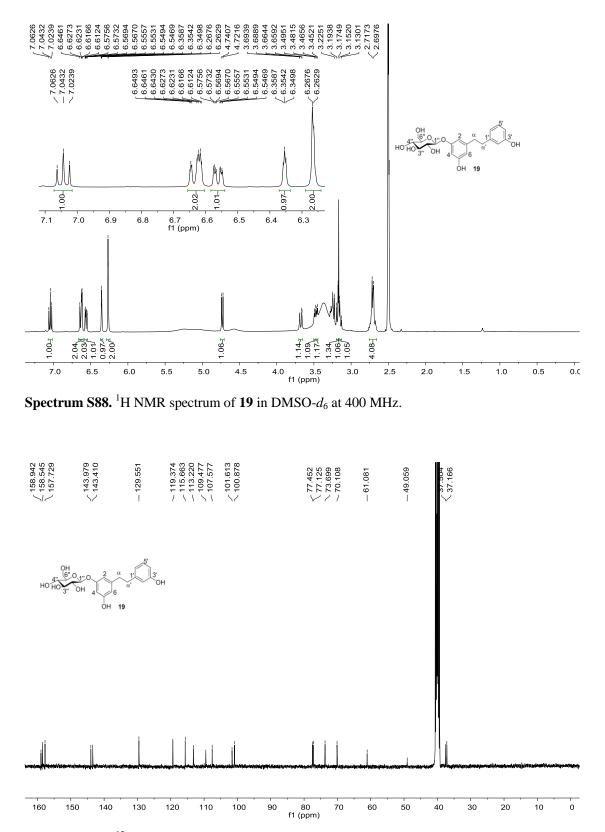
Spectrum S83. HMBC spectrum of 17 in DMSO-*d*₆.



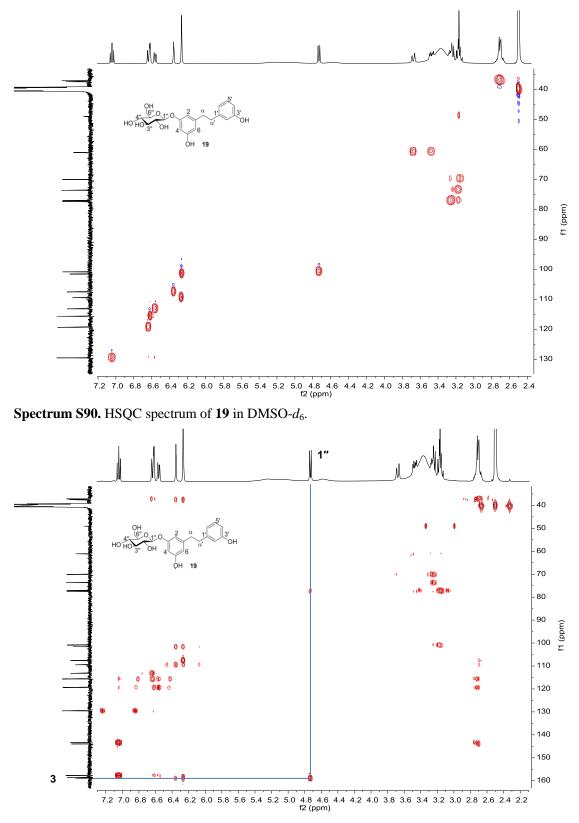
Spectrum S85. ¹³C NMR spectrum of **18** in DMSO-*d*₆ at 100 MHz.



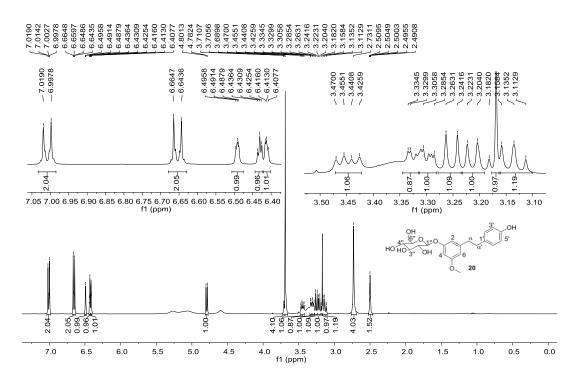
Spectrum S87. HMBC spectrum of 18 in DMSO-*d*₆.



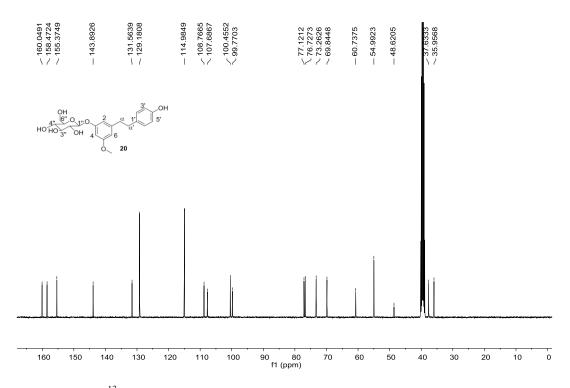
Spectrum S89. ¹³C NMR spectrum of **19** in DMSO- d_6 at 100 MHz.



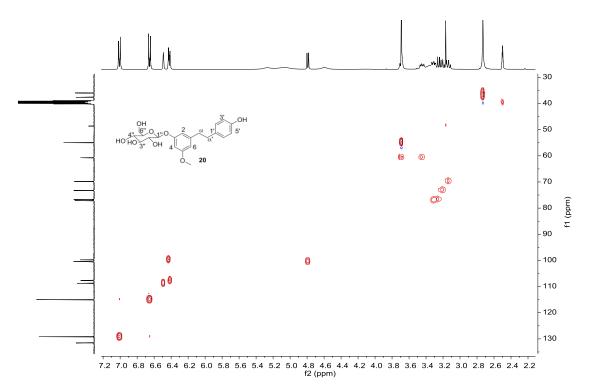
Spectrum S91. HMBC spectrum of 19 in DMSO-d₆.



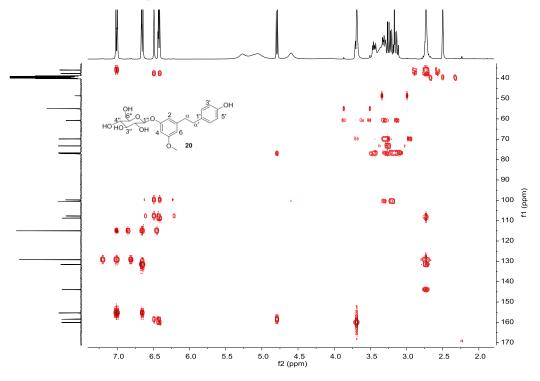
Spectrum S92. ¹H NMR spectrum of **20** in DMSO-*d*₆ at 400 MHz.



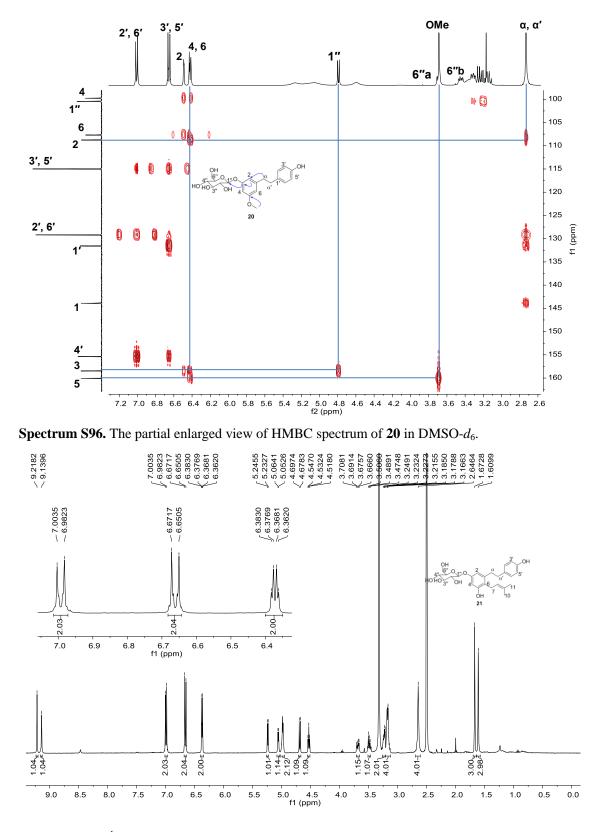
Spectrum S93. ¹³C NMR spectrum of **20** in DMSO- d_6 at 100 MHz.



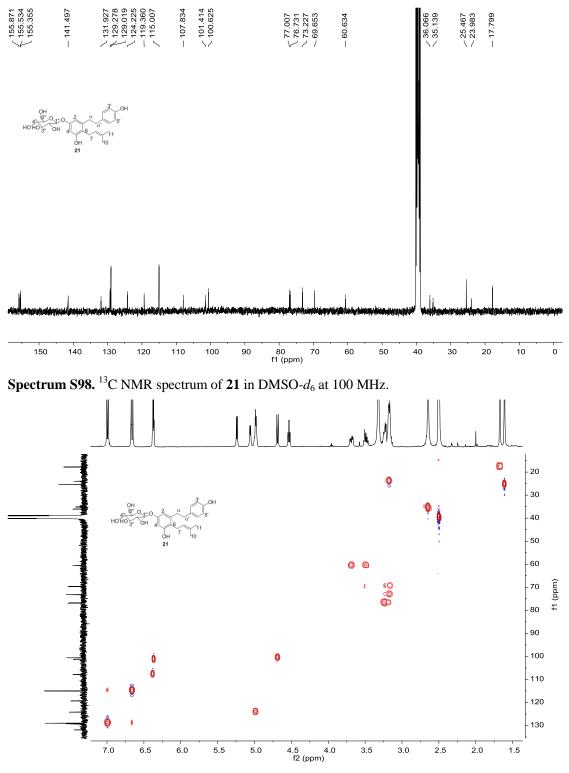
Spectrum S94. HSQC spectrum of 20 in DMSO-d₆.



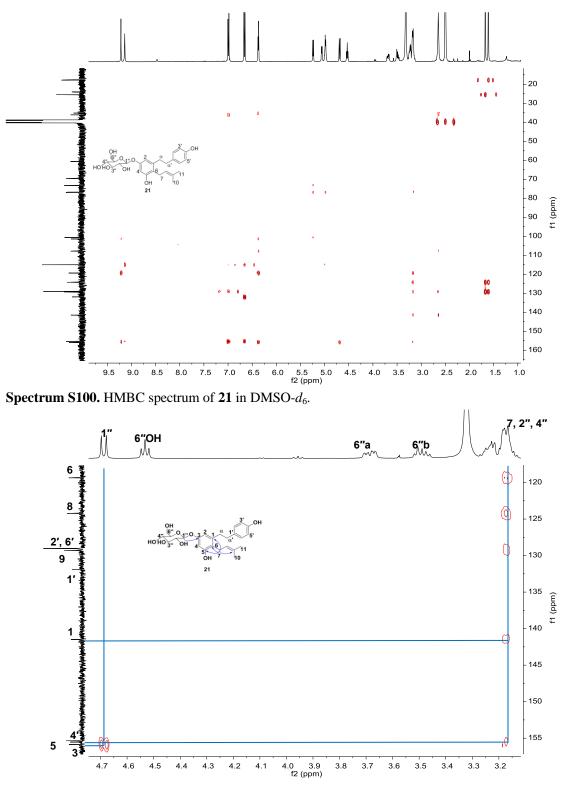
Spectrum S95. HMBC spectrum of 20 in DMSO-d₆.



Spectrum S97. ¹H NMR spectrum of **21** in DMSO- d_6 at 400 MHz.

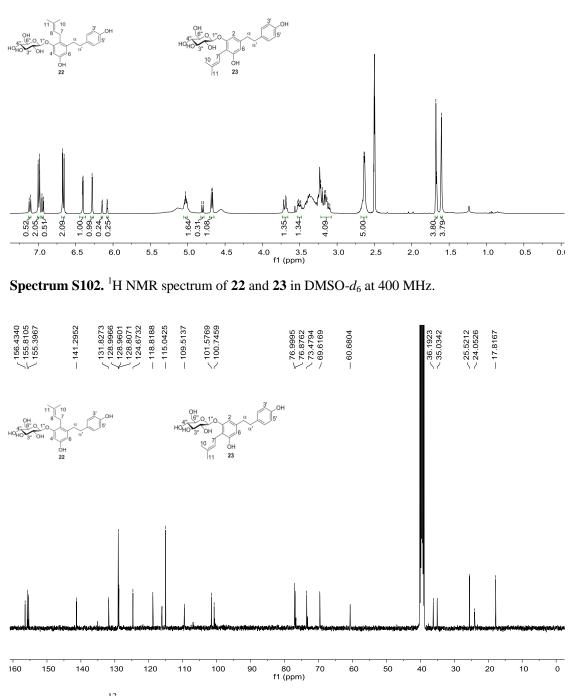


Spectrum S99. HSQC spectrum of 21 in DMSO-d₆.

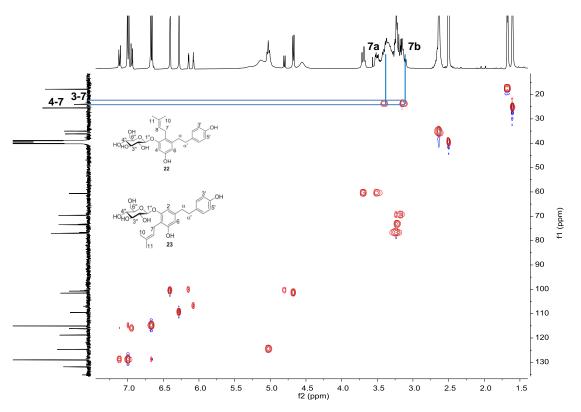


Spectrum S101. The partial enlarged view of HMBC spectrum of **21** in DMSO-*d*₆.

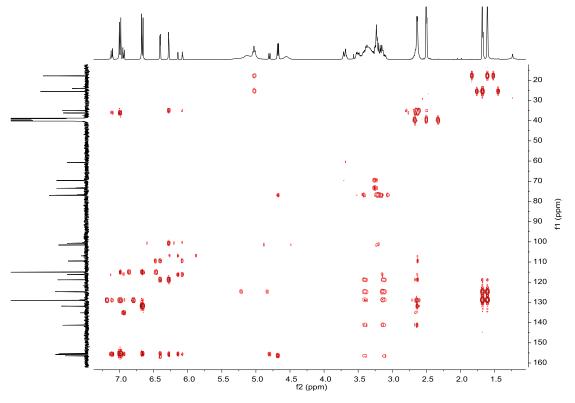
7.1238 7.1021 6.69836 6.9820 6.69826 6.9820 6.69830 6.69704 6.65753 6.61427 6.61477 6.61477 6.61477 6.61477 6.61477 6.61477 6.61477 6.61477 6.61477 6.61477 6.61477 6.61477 6.61477 6.61477 6.61477 6.61477 6.61477 6.614776 6.61476 6.61476



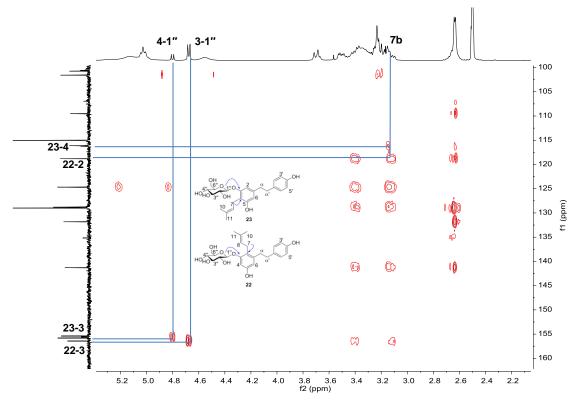
Spectrum S103. ¹³C NMR spectrum of **22** and **23** in DMSO- d_6 at 100 MHz.



Specrtrum S104. HSQC spectrum of 22 and 23 in DMSO-d₆.



Spectrum S105. HMBC spectrum of 22 and 23 in DMSO-d₆.



Spectrum S106. The partial enlarged view of HMBC spectrum of 22 and 23 in DMSO- d_6 .

References

- Markham GD, DeParasis J, Gatmaitan J. The sequence of *metK*, the structural gene for *S*-adenosylmethionine synthetase in *Escherichia coli*. *J Biol Chem* 1984;259:14505–7.
- Xie K, Chen R, Chen D, Li J, Wang R, Yang L, et al. Enzymatic *N*-glycosylation of diverse arylamine aglycones by a promiscuous glycosyltransferase from *Carthamus tinctorius*. *Adv Synth Catal* 2017;**359**:603–8.
- Ehlting J, Büttner D, Wang Q, Douglas CJ, Somssich IE, Kombrink E. Three
 4-coumarate: coenzyme A ligases in *Arabidopsis thaliana* represent two evolutionarily divergent classes in angiosperms. *Plant J* 1999;19:9–20.
- Chen H, Kim HU, Weng H, Browse J. Malonyl-CoA synthetase, encoded by acyl activating enzyme 13, is essential for growth and development of *Arabidopsis*. *Plant Cell* 2011;23:2247–62.
- 5. An JH, Kim YS. A gene cluster encoding malonyl-CoA decarboxylase (MatA), malonyl-CoA synthetase (MatB) and a putative dicarboxylate carrier protein (MatC) in *Rhizobium trifolii*: cloning, sequencing, and expression of the enzymes in *Escherichia coli*. Eur J Biochem 1998;257:395–402.
- Wang J, Li S, Xiong Z, Wang Y. Pathway mining-based integration of critical enzyme parts for *de novo* biosynthesis of steviolglycosides sweetener in *Escherichia coli*. *Cell Res* 2016;26:258–61.

- Chen R, Gao B, Liu X, Ruan F, Zhang Y, Lou J, et al. Molecular insights into the enzyme promiscuity of an aromatic prenyltransferase. *Nat Chem Biol* 2017;13:226–34.
- Xie K, Chen R, Chen D, Li J, Wang R, Yang L, et al. Exploring the catalytic promiscuity of a new glycosyltransferase from *Carthamus tinctorius*. Org Lett 2014;16:4874–7.
- Chen D, Chen R, Wang R, Li J, Xie K, Bian C, et al. Probing the catalytic promiscuity of a regio- and stereospecific C-glycosyltransferase from Mangifera indica. Angew Chem Int Ed 2015;127:12869–73.
- Sui S, Guo R, Xie K, Yang L, Dai J. UGT88B2: A promiscuous
 O-glycosyltransferase from *Carthamus tinctorius*. *Chin Herb Med* 2020;12:440–5.
- Chen D, Fan, S., Chen, R., Xie, K., Yin, S., Sun, L., et al. Probing and engineering key residues for bis-C-glycosylation and promiscuity of a C-glycosyltransferase. ACS Catal 2018;8:4917–27.
- Chen D, Sun L, Chen R, Xie K, Yang L, Dai J. Enzymatic synthesis of acylphloroglucinol 3-C-glucosides from 2-O-glucosides using a C-glycosyltransferase from Mangifera indica. Chem Eur J 2016;22:5873–7.
- Adesanya SA, Ogundana SK, Roberts MF. Dihydrostilbene phytoalexins from Dioscorea bulbifera and D. dumentorum. Phytochemistry 1989,28:773–4.
- 14. Brand S, Hölscher D, Schierhorn A, Svatoš A, Schröder J, Schneider B. A type III polyketide synthase from *Wachendorfia thyrsiflora* and its role in diarylheptanoid S101

and phenylphenalenone biosynthesis. *Planta* 2006, **224**:413–28.

- 15. Mo T, Wang J, Gao B, Zhang L, Liu X, Wang X, et al. Combinatorial synthesis of flavonoids and 4-hydroxy-δ-lactones by plant-oringinated enzymes. *Chin J Org Chem* 2015,35:1052–9.
- Akiyama T, Shibuya M, Liu HM, Ebizuka Y. p-Coumaroyltriacetic acid synthase, a new homologue of chalcone synthase, from *Hydrangea macrophylla* var. *thunbergii. Eur J Biochem* 1999, 263:834–9.
- Kettenes-van den BJJ, Salemink CA. Cannabis XIX. Oxygenated
 1,2-Diphenylethanes from Marihuana. *Recueil des Travaux Chimiques des Pays-Bas* 1978,97:221–2.
- Hata K, Baba K, Kozawa M. Chemical studies on the heartwood of Cassia garrettiana Craib. II. Nonanthraquinonic constituents. *Chem pharm bull* 1979,27:984–9.
- Edwards RL, Lewis DG, Wilson DV. Constituents of the higher fungi. Part I. Hispidin, a new 4-hydroxy-6-styryl-2-pyrone from *Polyporus hispidus* (Bull.) Fr. *J Chem Soc* 1961:4995–5002.
- 20. Wang QH, Wang ML, He X, Wang Q. Structural elucidation of two new diphenylethanes from *Artemisia mongolica*. *Chem Nat Compd* 2021,**57**:448–50.
- Werner SR, Chen H, Jiang H, Morgan JA. Synthesis of non-natural flavones and dihydrochalcones in metabolically engineered yeast. J Mol Catal B Enzym 2020,66:257–63.
- 22. Wang J, Liu Y, Liu C, Shi Q. Characterization of the metabolites of gigantol in rat,

dog, monkey, and human hepatocytes using ultra-high-performance liquid chromatography coupled with high-resolution mass spectrometry. *Rapid Commun Mass Spectrom* 2020,**34**:e8810.

- Majumder PL, Pal S. Cumulatin and tristin, two bibenzyl derivatives from the orchids *Dendrobium cumulatum* and *Bulbophyllum triste*. *Phytochemistry* 1993,32:1561–5.
- Crombie L, Jamieson SV. Dihydrostilbenes of Cannabis. Synthesis of canniprene.
 J Chem Soc Perk T 1 1982:1467–75.
- 25. Yanagisawa T, Sato S, Maruno M, Nomura T. 5-Lipoxygenase and cyclooxygenase inhibitors for treatment of arachidonate metabolism disorders. Japan, JP07017859 A 1995-01-20.
- 26. Kyoshi K, Yuka O, Shunji S, Taro N. Cardiovascular agents containing gancaonins and glycerol as Na⁺-K⁺ ATPase inhibitors, canantagonists, and phosphodiesterase inhibitors. Japan, JP07017857 A 1995-01-20.
- 27. Zhou B, Wan C. Phenolic constituents from the aerial parts of *Glycyrrhiza inflata* and their antibacterial activities. *J Asian Nat Prod Res* 2015,**17**:256–61.
- Feng W, Cao X, Kuang H, Zheng X, A new stilbene glycoside from *Dryopteris* sublaeta. Acta Pharmaceutica Sinica 2005,40:1131–4.