

Supplementary material

Contents

1. Supplementary Figure

Fig. S1. Inhibitory effect of stigmasterol glucoside (A), campesterol glucoside (B), daucosterol (C) and acarbose (D) on alpha-amylase.

Fig. S2. Sequence alignment of the amino acid residue between alpha-amylase (GenBank: NP_999360.1) and 3L2M_A from pig pancreatic.

Fig. S3. ^1H NMR (A), ^{13}C NMR (B), DEPT 135 (C), HMQC (D), HMBC (E) and COSY (F) spectra of Compounds 1 (600 MHz, Pyridine- d_5).

Fig. S4. ^1H NMR (A), ^{13}C NMR (B), DEPT 135 (C), HMQC (D), HMBC (E) and COSY (F) spectra of Compounds 2 (600 MHz, Pyridine- d_5).

Fig. S5. ^1H NMR (A), ^{13}C NMR (B), DEPT 135 (C), HMQC (D), HMBC (E) and COSY (F) spectra of Compounds 3 (600 MHz, Pyridine- d_5).

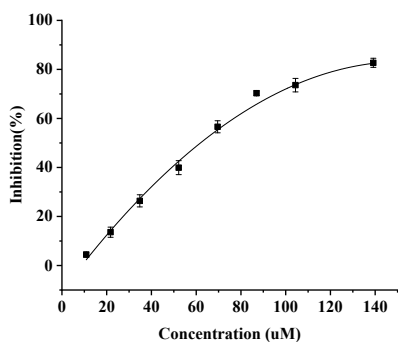
2. Supplementary Tables

Table S1. ^1H NMR Chemical Shifts for Compounds 1-3 (600 MHz, Pyridine- d_5).

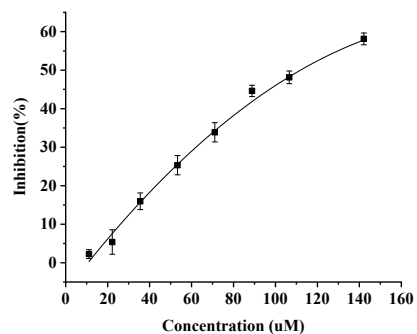
Table S2. ^{13}C NMR Chemical Shifts for Compounds 1-3 (600 MHz, Pyridine- d_5).

1. Supplementary Figure

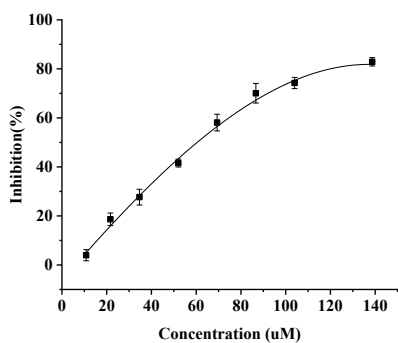
A



B



C



D

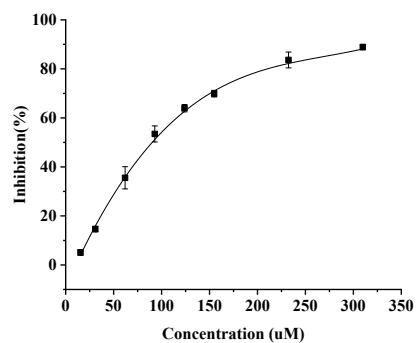
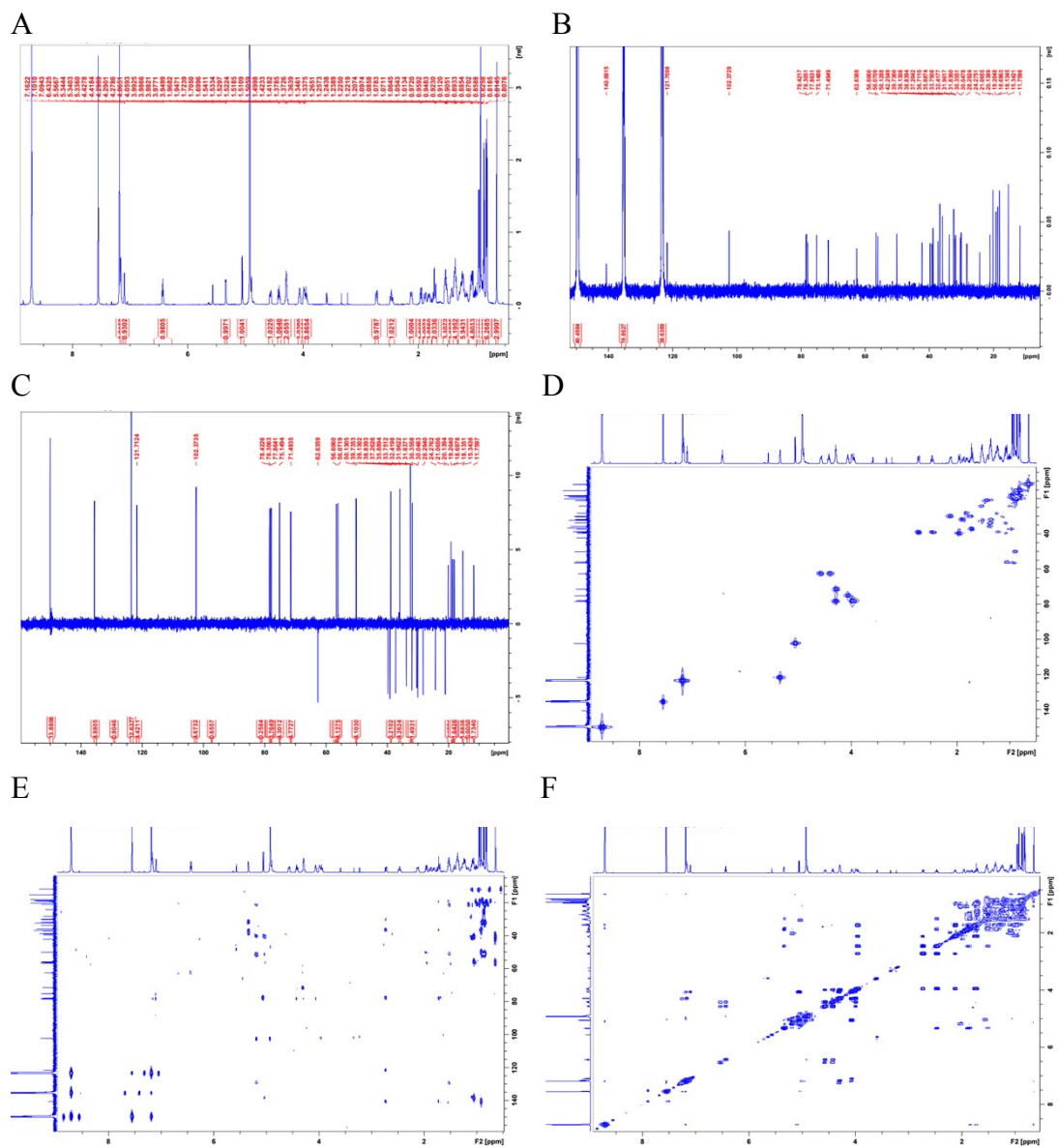


Fig S1. Inhibitory effect of stigmasterol glucoside (A), campesterol glucoside (B), daucosterol (C) and acarbose (D) on alpha-amylase.

Score	Expect	Method	Identities	Positives	Gaps
1023 bits (2646)	0.0	Compositional matrix adjust.	494/495 (99%)	494/495 (99%)	0/495 (0%)
NP_999360.1	MKLFLLLSAFGFCWAQ	YAPCTQSGRTSIVHLFEWRWVDIALECERYLGPKGGVQVSPNENIIVVTNPSRPWWERYQPV			80
pdb 3L2M A	YAPCTQSGRTSIVHLFEWRWVDIALECERYLGPKGGVQVSPNENIIVVTNPSRPWWERYQPV			65
Consensus		yapqtqsgrtsivhlfewrwwdialecerylgpkggvqvspneniivvtnpsrppwweryqpv			
NP_999360.1	SYKLCTRSGNENEFRCMVTFCNNVGVRIYVDVINHMCGSGAAAGTGTTCGSYCNFGNREFPAVFYSAWDFNDGKCKTAS				160
pdb 3L2M A		SYKLCTRSGNENEFRCMVTFCNNVGVRIYVDVINHMCGSGAAAGTGTTCGSYCNFGNREFPAVFYSAWDFNDGKCKTAS			145
Consensus		syklctrsgnenefrdrvtrcnnvgvriyvdavinhmcgsgaaagtgttcgsychnfgnrefpavfysawdfndgkcktas			
NP_999360.1	GGIESYNDPYQVRDQQLVGLLDLALEKDYVRSMIADYLNKLIIDIGVAGFRIDASKHMWPGDIKAVLDKLNHNLNTNWFPAQ				240
pdb 3L2M A		GGIESYNDPYQVRDQQLVGLLDLALEKDYVRSMIADYLNKLIIDIGVAGFRIDASKHMWPGDIKAVLDKLNHNLNTNWFPAQ			225
Consensus		ggiesyndpyqvrqcqlvglldlalekdyvrsmiadylnkllidigvagfridaskhmrwpgdikavldklhnlntnwfpaq			
NP_999360.1	SRPFIHQEVIDIGGEAIGSSEYFGNGRVTEFKYGAKLCTVVRKWSGEEKMSYLNKMWGEWGFMPDRALVFVDNHDNQRGH				320
pdb 3L2M A		SRPFIHQEVIDIGGEAIGSSEYFGNGRVTEFKYGAKLCTVVRKWSGEEKMSYLNKMWGEWGFMPDRALVFVDNHDNQRGH			305
Consensus		srpfihqevidlggeaigsseyfnggrvtefkygaklctvvrkwsgeekmsylknwgegwgfmpsdralvfvdnhdnqrgh			
NP_999360.1	GAGGASILTFWDARLYKVAVGFMLAHPYCFTRVMSYRWARNFVNGQEVNDWIGPPNNGV I KEVTINADTTCCNDWVCE				400
pdb 3L2M A		GAGGASILTFWDARLYKVAVGFMLAHPYCFTRVMSYRWARNFVNGQEVNDWIGPPNNGV I KEVTINADTTCCNDWVCE			385
Consensus		gaggasiltfwdarlykvavgfmlahpycftrvmsyrwarnfvngqevndwigppnngvikevtinadtccndwvce			
NP_999360.1	HRWRQIRNMVWFRNVVDGQFFANWMDNGSNQVAFGRGNRGFIVFNNDLWQLSSTLQITGLPGGTYCDVISGDKVGNSTGT				480
pdb 3L2M A		HRWRQIRNMVWFRNVVDGQFFANWMDNGSNQVAFGRGNRGFIVFNNDLWQLSSTLQITGLPGGTYCDVISGDKVGNSTGT			465
Consensus		hrwrqirnmvwfrnvvdgqffanwmdngsnqvafgrgnrgfivfnndlwqlsstlqitglpggtycdvisgdkvgnstgti			
NP_999360.1	KVYVSSDGTACFSISNSAEDFFIAIHAESK				510
pdb 3L2M A		KVYVSSDGTACFSISNSAEDFFIAIHAESK			495
Consensus		kvyvssdgtacfsisnsaedffiaihaesk			

Fig S2. Sequence alignment of the amino acid residue between alpha-amylase (GenBank: NP_999360.1) and 3L2M_A from pig pancreatic. ■: Identical sequence (homology=100%); ■: similar sequence (homology≥50%); □: different sequence (homology=0%).



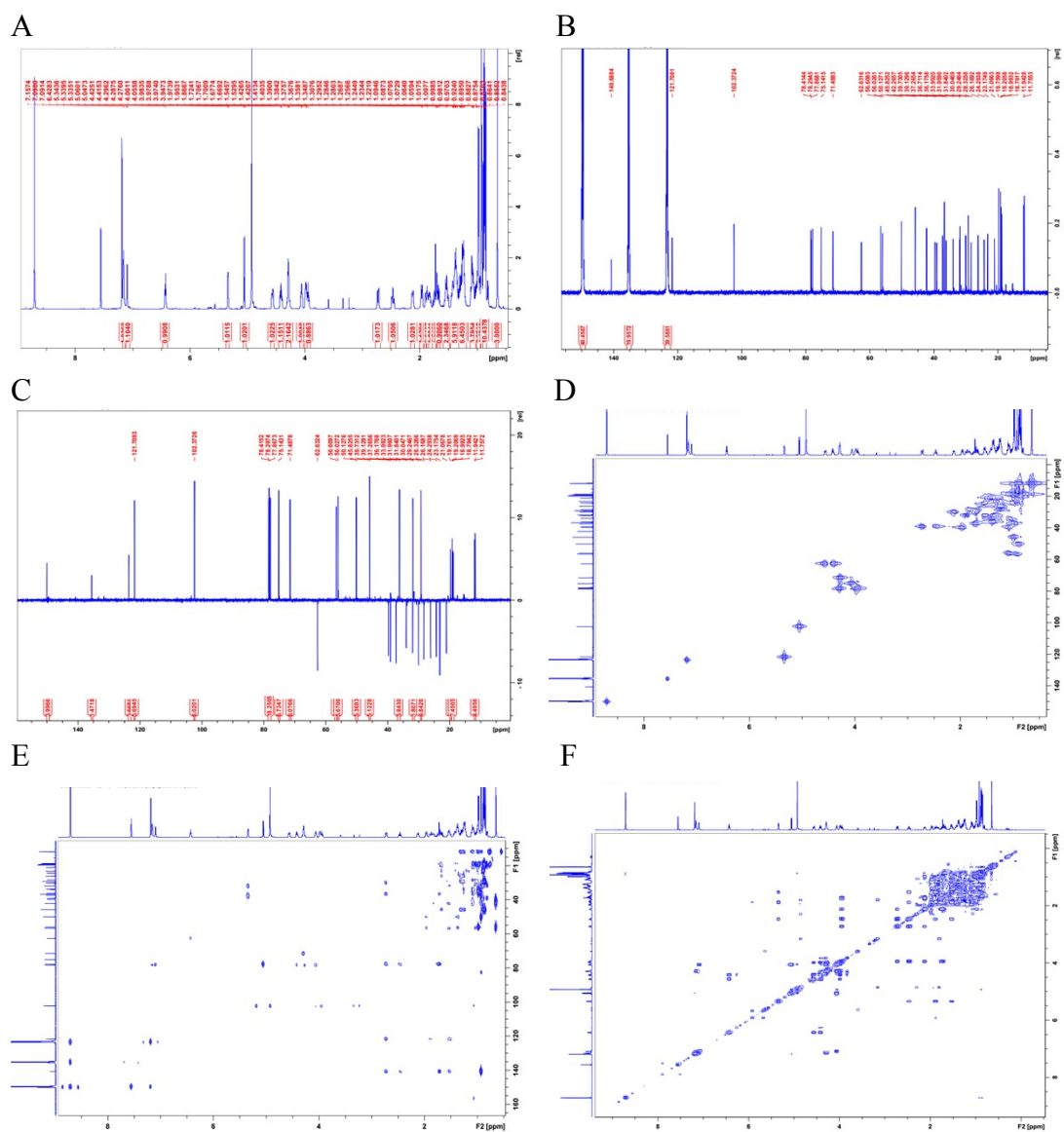


Fig S5. ¹H NMR (A), ¹³C NMR (B), DEPT 135 (C), HMQC (D), HMBC (E) and COSY (F) spectra of Compounds 3 (600 MHz, Pyridine-*d*₅)

2. Supplementary Tables

Table S1. ¹H NMR Chemical Shifts for Compounds 1-3 (600 MHz, Pyridine-*d*₅)

Proto n	Compounds (δ in ppm)		
	1 (<i>J</i> in Hz)	2 (<i>J</i> in Hz)	3 (<i>J</i> in Hz)
1a	1.70 (m)	1.71 (m)	1.70 (m)
1b	0.95 (m)	0.97 (m)	0.95 (m)
2a	2.12 (m)	2.12 (m)	2.11 (m)
2b	1.73 (overlapped)	1.73 (overlapped)	1.73 (overlapped)
3	3.96 (m)	3.98 (m)	3.98 (m)
4a	2.72 (ddd, 13.4, 4.8, 2.3)	2.73 (ddd, 13.4, 4.8, 2.3)	2.72 (ddd, 13.4, 4.8, 2.3)
4b	2.47 (m)	2.47 (m)	2.47 (m)
6	5.34 (dd, 4.8, 2.1)	5.34 (dd, 4.8, 2.1)	5.34 (dd, 4.8, 2.1)
7a	1.86 (m)	1.87 (m)	1.86 (m)
7b	1.36 (overlapped)	1.36 (overlapped)	1.36 (overlapped)
8	1.52 (m)	1.51 (m)	1.52 (m)
9	0.89 (overlapped)	0.89 (m)	0.89 (overlapped)
11a	1.47 (m)	1.44 (m)	1.46 (m)
11b	1.42 (m)	1.42 (m)	1.42 (m)
12a	1.91 (dd, 12.5, 3.5)	1.96 (dd, 12.7, 3.3)	1.96 (dd, 12.5, 3.5)
12b	1.08 (overlapped)	1.09 (overlapped)	1.09 (overlapped)
14	1.09 (overlapped)	1.07 (overlapped)	1.08 (overlapped)
15a	1.48 (m)	1.54 (m)	1.54 (m)
15b	0.92 (overlapped)	1.00 (overlapped)	1.00 (overlapped)
16a	1.73 (overlapped)	1.84 (m)	1.83 (m)
16b	1.24 (m)	1.25 (m)	1.26 (overlapped)
17	0.94 (overlapped)	0.93 (overlapped)	0.93 (overlapped)
18	0.65 (s)	0.65 (s)	0.65 (s)
19	0.92 (s)	0.92 (s)	0.92 (s)
20	2.02 (m)	1.38 (overlapped)	1.37 (overlapped)
21	0.84 (d, 6.6)	0.95 (d, 6.5)	0.97 (d, 6.5)
22a	5.19 (dd, 15.2, 8.8)	1.38 (overlapped)	1.38 (overlapped)
22b	-	1.08 (overlapped)	1.04 (overlapped)
23a	5.06 (overlapped)	1.16 (overlapped)	1.25 (overlapped)
23b	-	1.15 (overlapped)	1.24 (overlapped)
24	1.56 (m)	1.22 (m)	0.99 (overlapped)
25	1.53 (m)	1.90 (m)	1.68 (m)
26	0.89 (d, 6.6)	0.82 (d, 6.8)	0.85 (d, 6.8)
27	1.05 (d, 6.6)	0.87 (d, 6.8)	0.87 (d, 6.8)
28a	1.42 (m)	0.81 (d, 6.5)	1.31 (m)
28b	1.20 (m)	-	1.27 (m)
29	0.86 (t, 7.4)	-	0.88 (t, 7.4)
Glc			
1'	5.07 (overlapped)	5.06 (d, 7.7)	5.05 (d, 7.7)
2'	4.07 (dd, 8.1, 3.5)	4.06 (dd, 8.5, 3.8)	4.06 (dd, 8.0, 3.6)
3'	4.30 (overlapped)	4.29 (overlapped)	4.29 (overlapped)
4'	4.29 (overlapped)	4.28 (overlapped)	4.28 (overlapped)
5'	3.95 (m)	3.95 (m)	3.94 (m)
6'a	4.58 (ddd, 11.8, 5.7, 2.5)	4.56 (ddd, 11.8, 5.6, 2.5)	4.56 (ddd, 11.8, 5.6, 2.5)
6'b	4.43 (m)	4.42 (m)	4.42 (m)

Not: *J* values are given in parentheses. Overlapped signals are detected on HMQC experiment. Multiplicities: s = singlet, d = doublet, t = triplet, m = multiplet.

Table S2. ^{13}C NMR Chemical Shifts for Compounds 1-3 (600 MHz, Pyridine- d_5)

Carbon	Compounds (δ in ppm)		
	1	2	3
1	37.3 (CH ₂)	37.3 (CH ₂)	37.3 (CH ₂)
2	30.0 (CH ₂)	30.0 (CH ₂)	30.0 (CH ₂)
3	78.3 (CH)	78.3 (CH)	78.3 (CH)
4	39.1 (CH ₂)	39.1 (CH ₂)	39.1 (CH ₂)
5	140.7 (C)	140.7 (C)	140.7 (C)
6	121.7 (CH)	121.7 (CH)	121.7 (CH)
7	31.9 (CH ₂)	32.0 (CH ₂)	31.9 (CH ₂)
8	31.8 (CH)	31.8 (CH)	31.8 (CH)
9	50.1 (CH)	50.1 (CH)	50.1 (CH)
10	36.7 (C)	36.7 (C)	36.7 (C)
11	21.0 (CH ₂)	21.1 (CH ₂)	21.0 (CH ₂)
12	39.6 (CH ₂)	39.7 (CH ₂)	39.7 (CH ₂)
13	42.1 (C)	42.3 (C)	42.3 (C)
14	56.7 (CH)	56.6 (CH)	56.6 (CH)
15	24.3 (CH ₂)	24.2 (CH ₂)	24.2 (CH ₂)
16	29.1 (CH ₂)	28.3 (CH ₂)	28.3 (CH ₂)
17	55.8 (CH)	56.1 (CH)	56.0 (CH)
18	11.9 (CH ₃)	11.8 (CH ₃)	11.7 (CH ₃)
19	19.2 (CH ₃)	19.2 (CH ₃)	19.2 (CH ₃)
20	40.6 (CH)	35.9 (CH)	36.1 (CH)
21	19.0 (CH ₃)	18.7 (CH ₃)	18.9 (CH ₃)
22	138.6 (CH)	33.8 (CH ₂)	33.9 (CH ₂)
23	129.2 (CH)	30.4 (CH ₂)	26.1 (CH ₂)
24	51.2 (CH)	38.8 (CH)	45.3 (CH)
25	32.0 (CH)	32.4 (CH)	29.2 (CH)
26	21.1 (CH ₃)	18.1 (CH ₃)	18.7 (CH ₃)
27	21.3 (CH ₃)	20.1 (CH ₃)	19.7 (CH ₃)
28	25.5 (CH ₂)	15.3 (CH ₃)	23.1 (CH ₂)
29	12.3 (CH ₃)	-	11.9 (CH ₃)
Glc			
1'	102.3 (CH)	102.4 (CH)	102.4 (CH)
2'	75.1 (CH)	75.1 (CH)	75.1 (CH)
3'	78.4 (CH)	78.4 (CH)	78.4 (CH)
4'	71.5 (CH)	71.5 (CH)	71.5 (CH)
5'	77.8 (CH)	77.9 (CH)	77.9 (CH)
6'	62.6 (CH ₂)	62.6 (CH ₂)	62.6 (CH ₂)

Not: Multiplicities are decided on DEPT experiments