Supporting information

Identification of yeast *α*-glucosidase inhibitors from *Pueraria lobata* by ligand fishing based on magnetic mesoporous silicon combined with knock-out/knock-in technology

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Contents

Fig. 1S. Standard curve of Allura red (peak area-concentration)

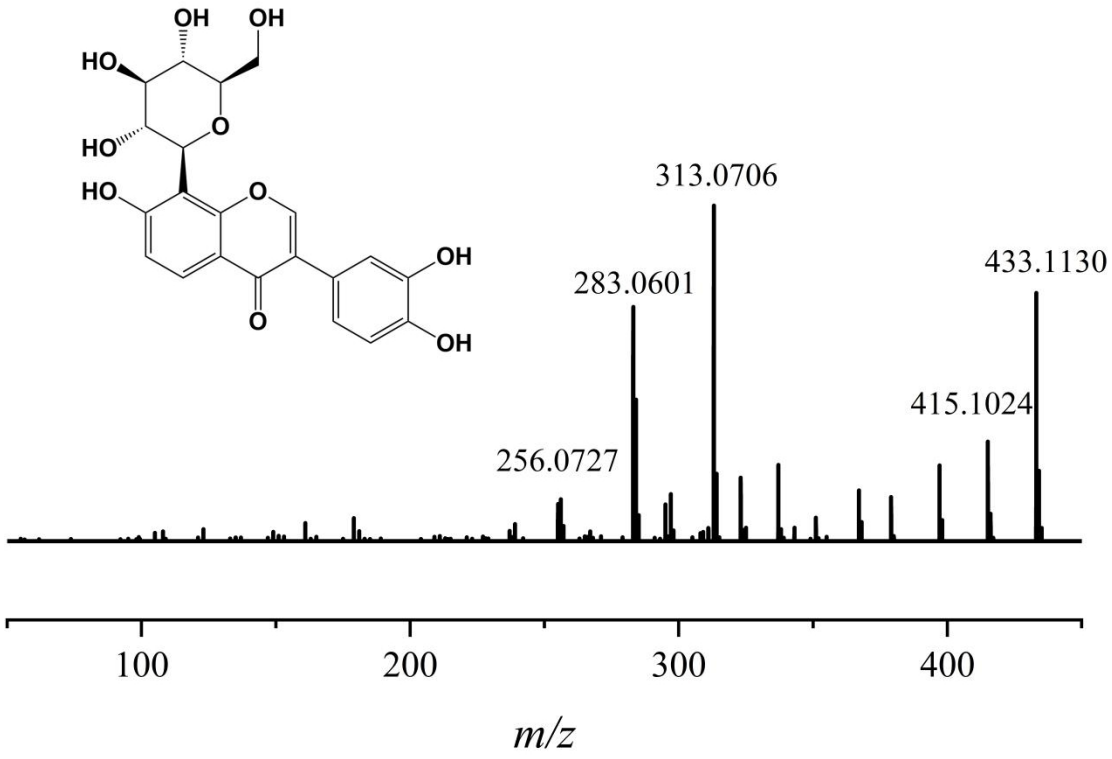

Fig. 2S. Mass spectrometry of compound **1**

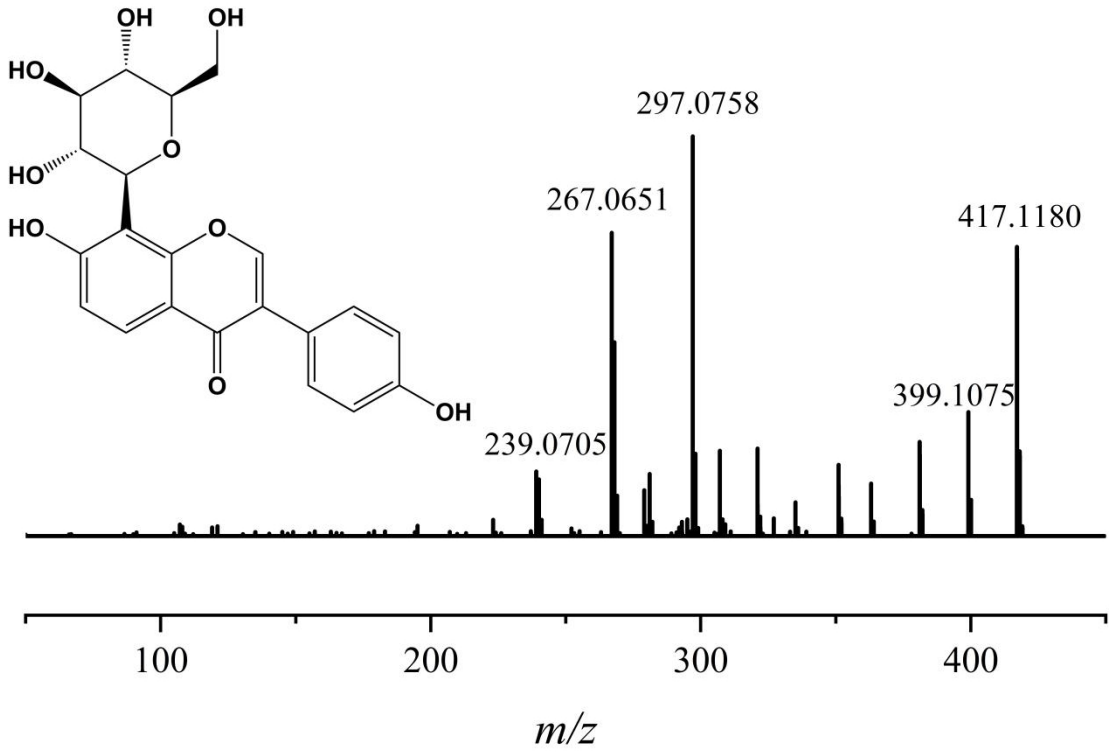

Fig. 3S. Mass spectrometry of compound **2**

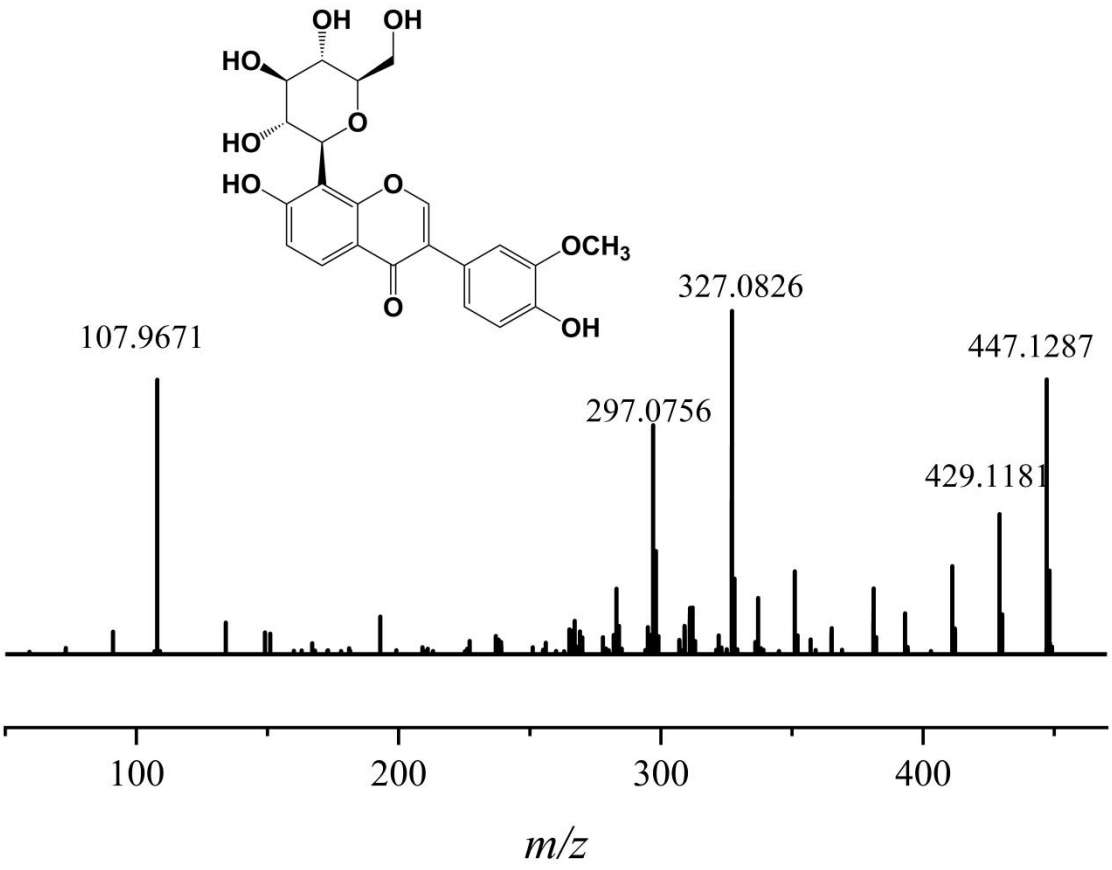

Fig. 4S. Mass spectrometry of compound **3**

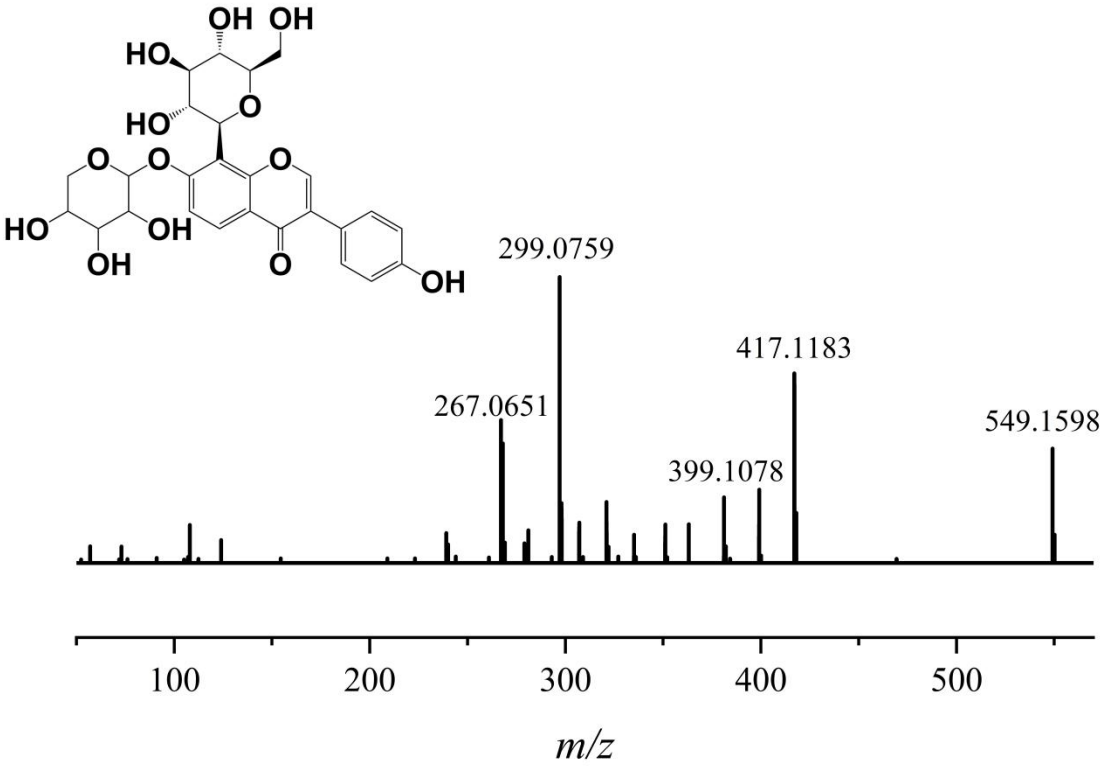

Fig. 5S. Mass spectrometry of compound **4**

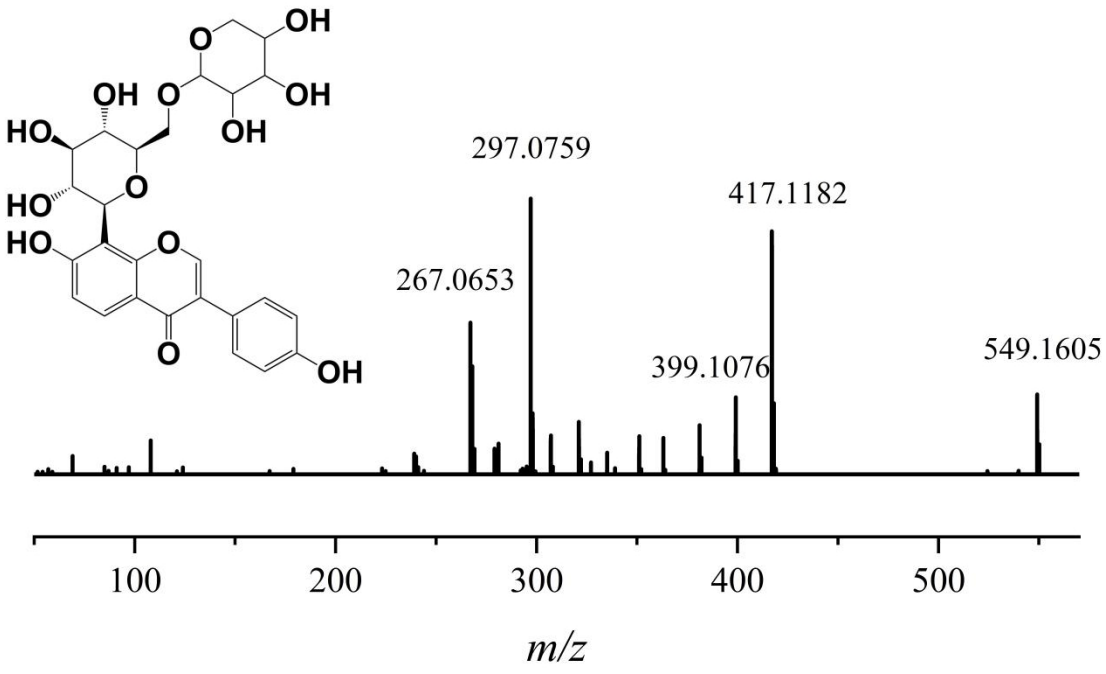

Fig. 6S. Mass spectrometry of compound **5**

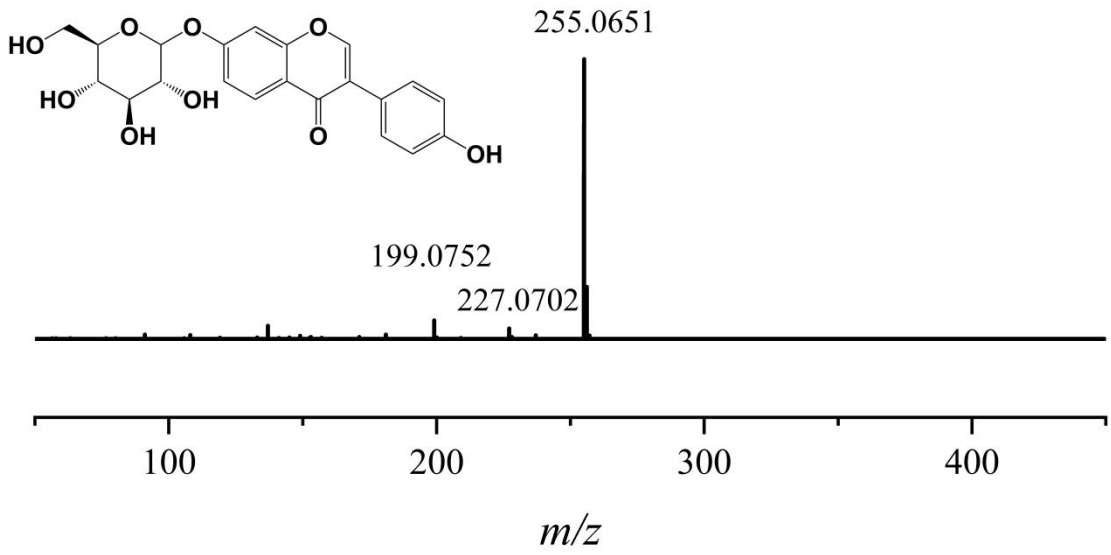

Fig. 7S. Mass spectrometry of compound **6**

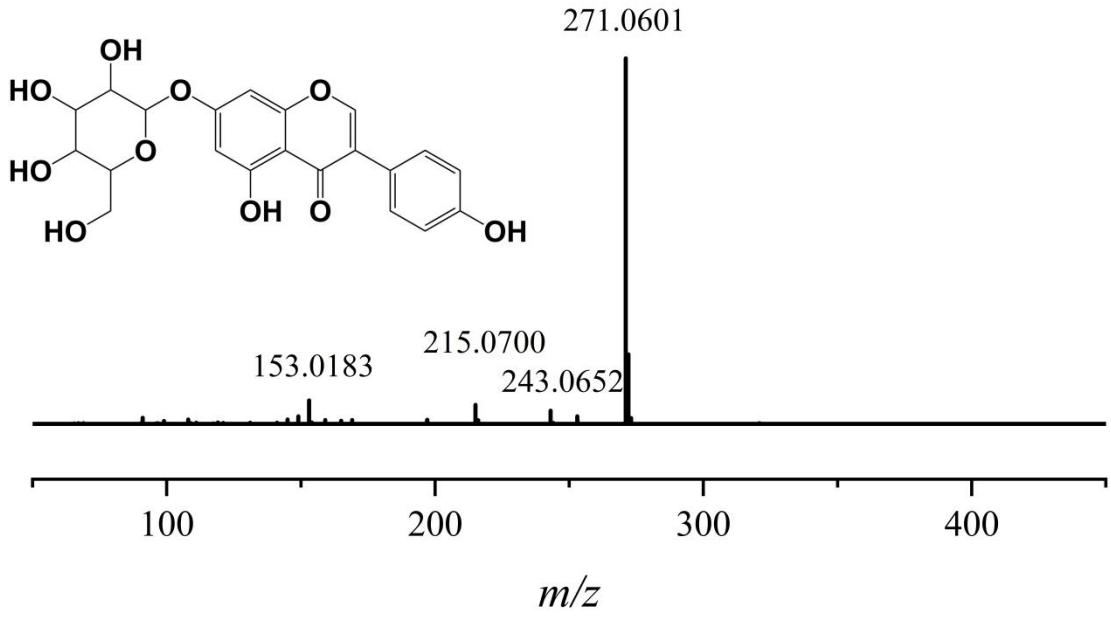

Fig. 8S. Mass spectrometry of compound **7**

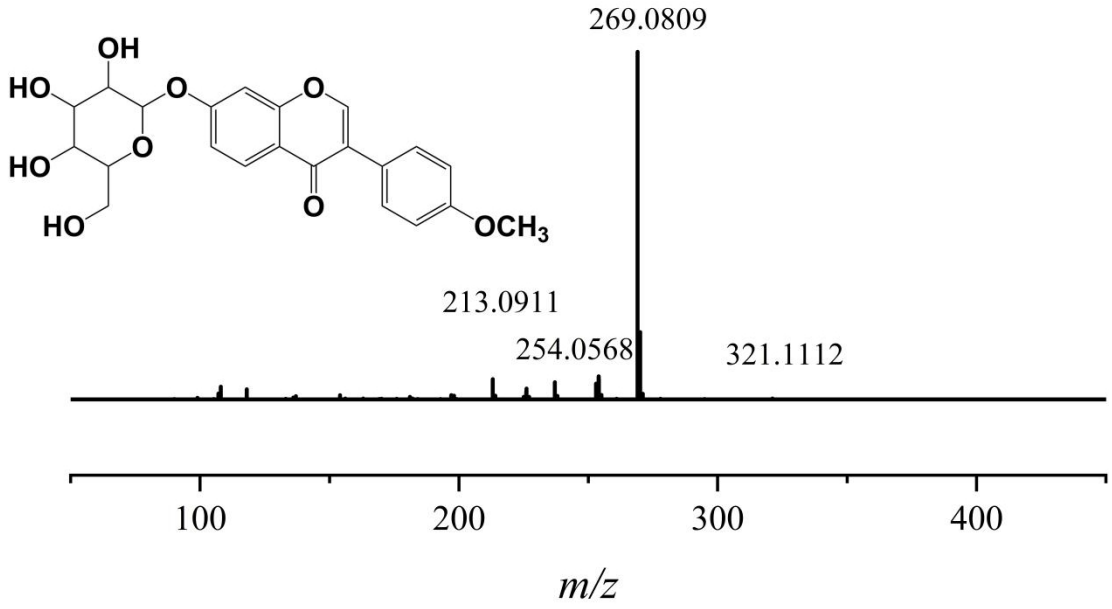

Fig. 9S. Mass spectrometry of compound **8**

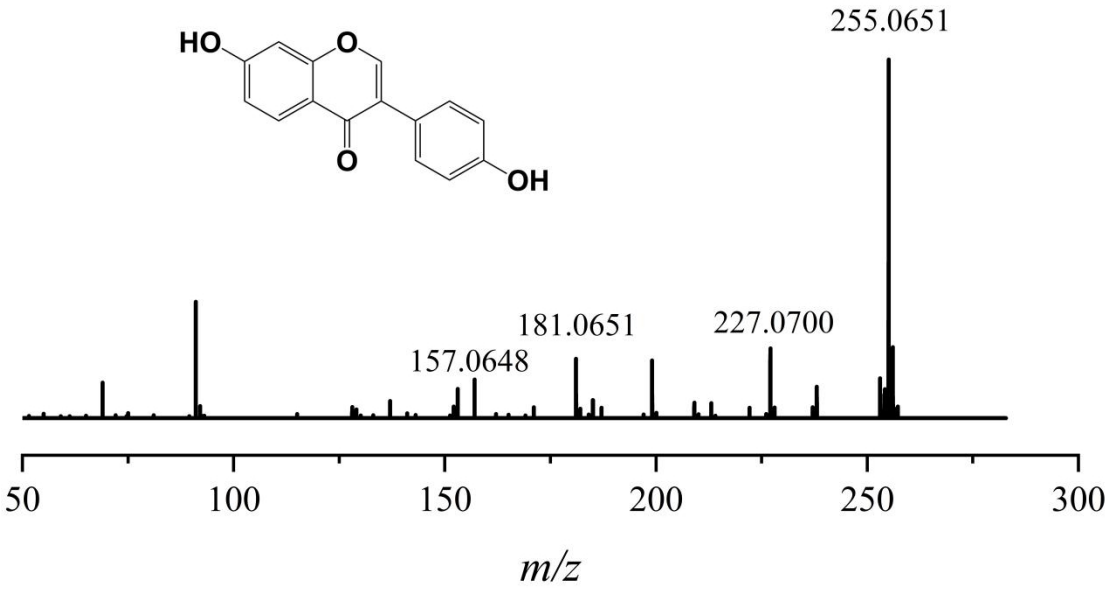

Fig. 10S. Mass spectrometry of compound **9**

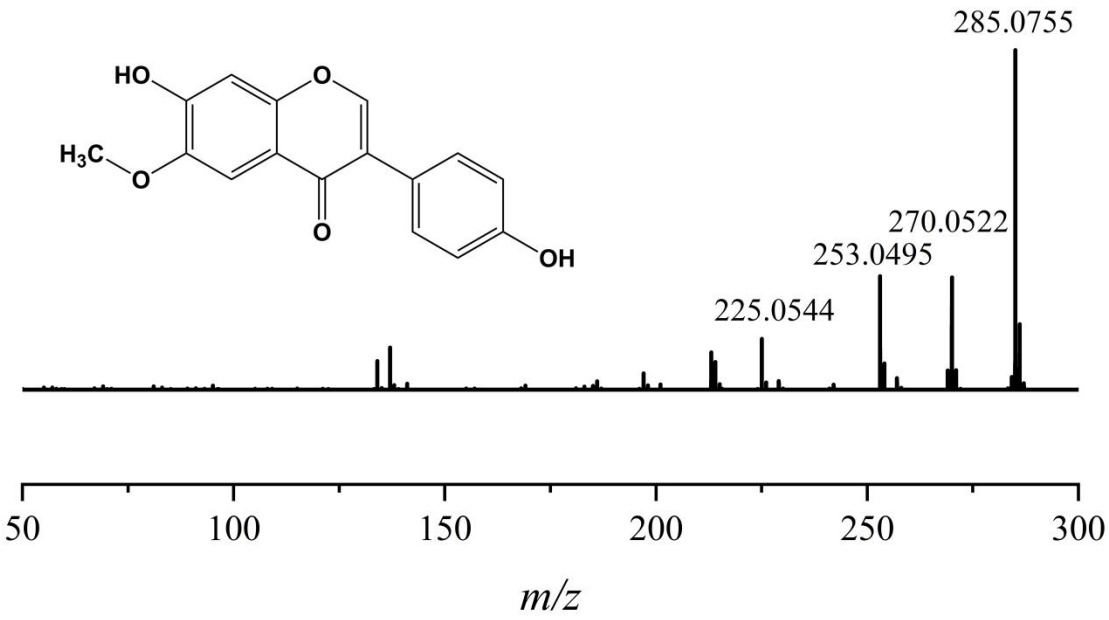

Fig. 11S. Mass spectrometry of compound **10**

Table. 1S. Molecular docking analysis of the 10 ligands with α-glucosidase

Compound number	Total Score	Hydrogen bonding associated amino acid residues
1	5.3938	Asp307 Gln279 Tyr158 Asp352 Asp215 Asp213
2	5.8709	Asp307 Gln279 Ser241 Lys156 Glu411 Asr442
3	3.5659	Asp307 Ser311 Arg315 Lys156 Ser241 Asp242 His280 Glu277
4	4.5122	Asp307 Glu279 Asp215 Arg442
5	4.4246	Arg315 Ser241 Glu411 Arg442 Asp352 His112 Asp69
6	7.7858	Asp307 Arg442 Asp325 Gln279 Glu277
7	7.3186	Glu411 Pro312 Asp242 Gln279 Asp215
8	6.6854	Arg213 Glu277 Gln279 His351 Asp352 Arg442
9	5.3531	Asp307 Thr310 Arg315 Ser241 Lys156
10	5.4960	Asp307 Gln353 Arg442 Asp215