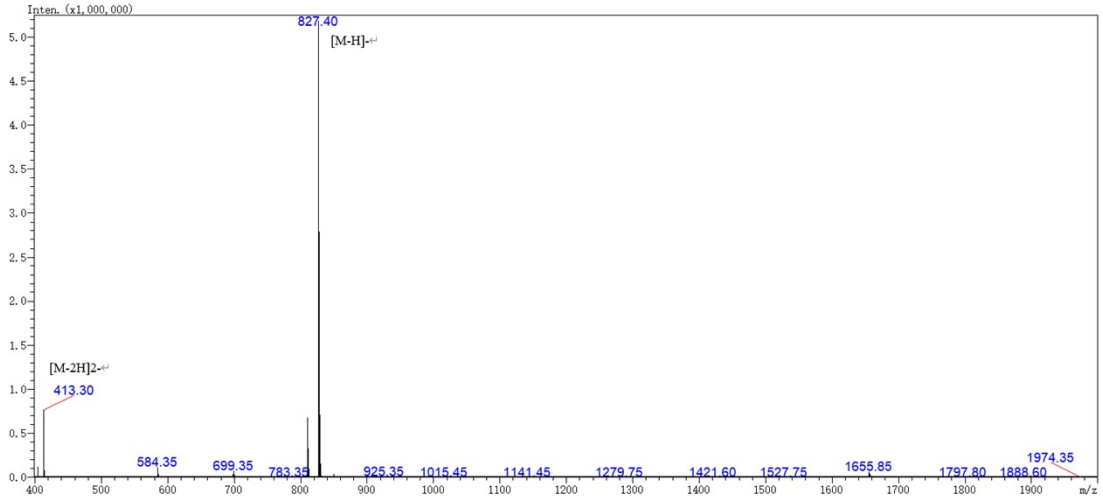
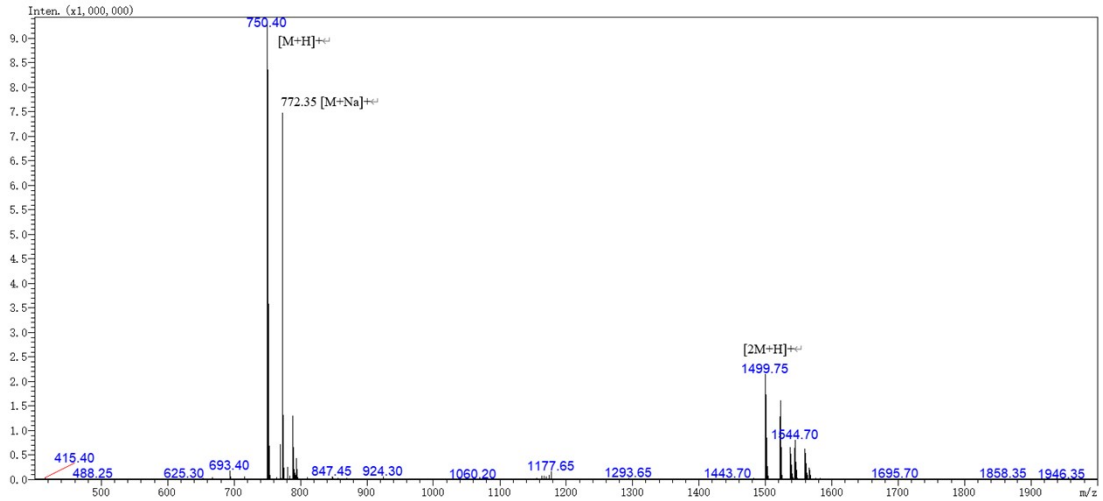
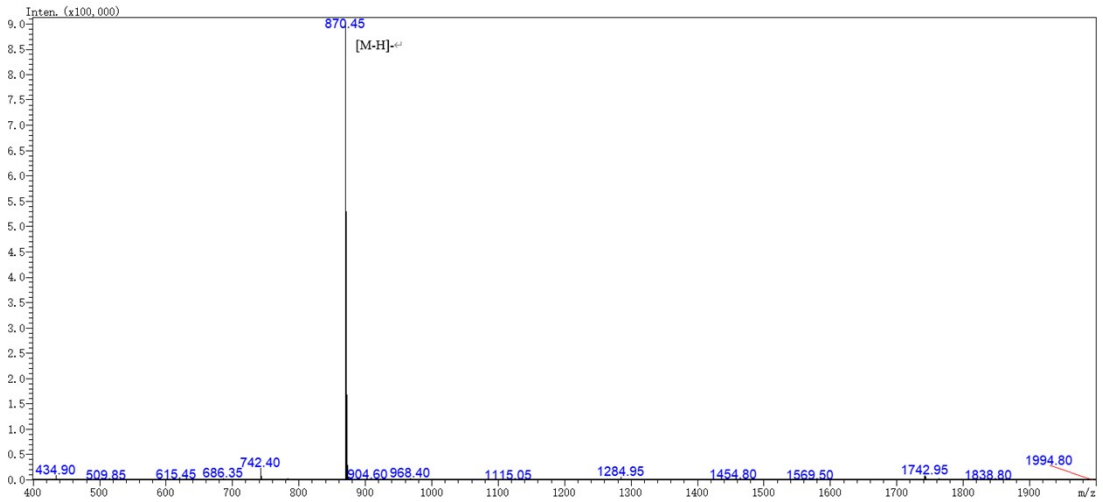
Electronic Supplementary Material (ESI) for Food & Function.



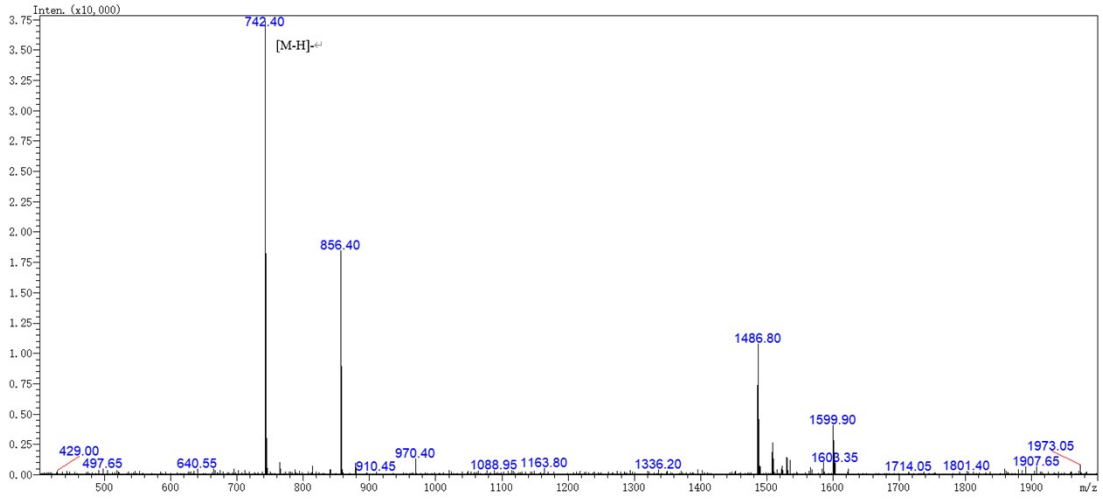
(A) QDPLFPL



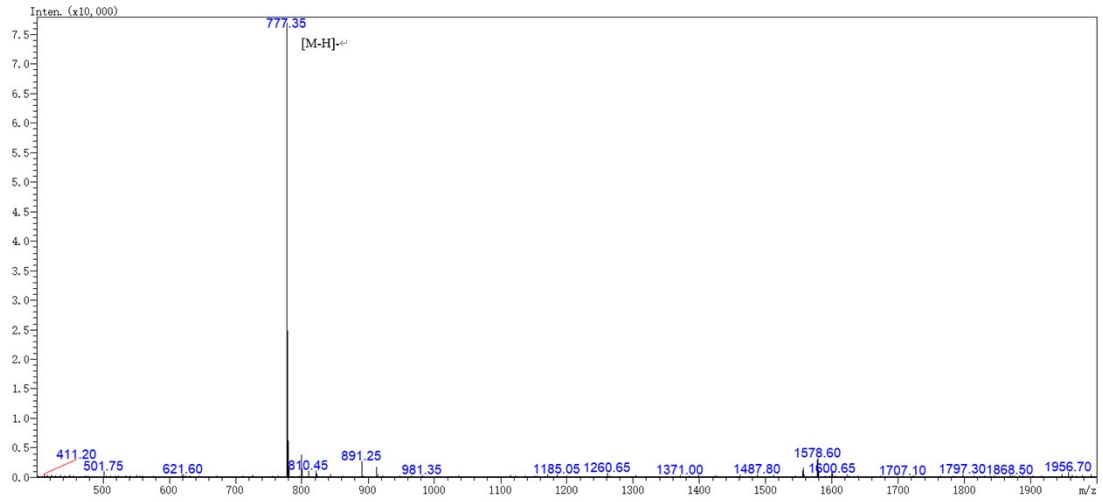
(B) FPGVSPF



(C) SPAQLLPF



(D) LVPYRP



(E) WYWPQ

Figure S1 Mass spectra of QDPLFPL (A), FPGVSPF (B), SPAQLLPF (C), LVPYRP (D) and WYWPQ (E) characterized by LC-MS/MS.

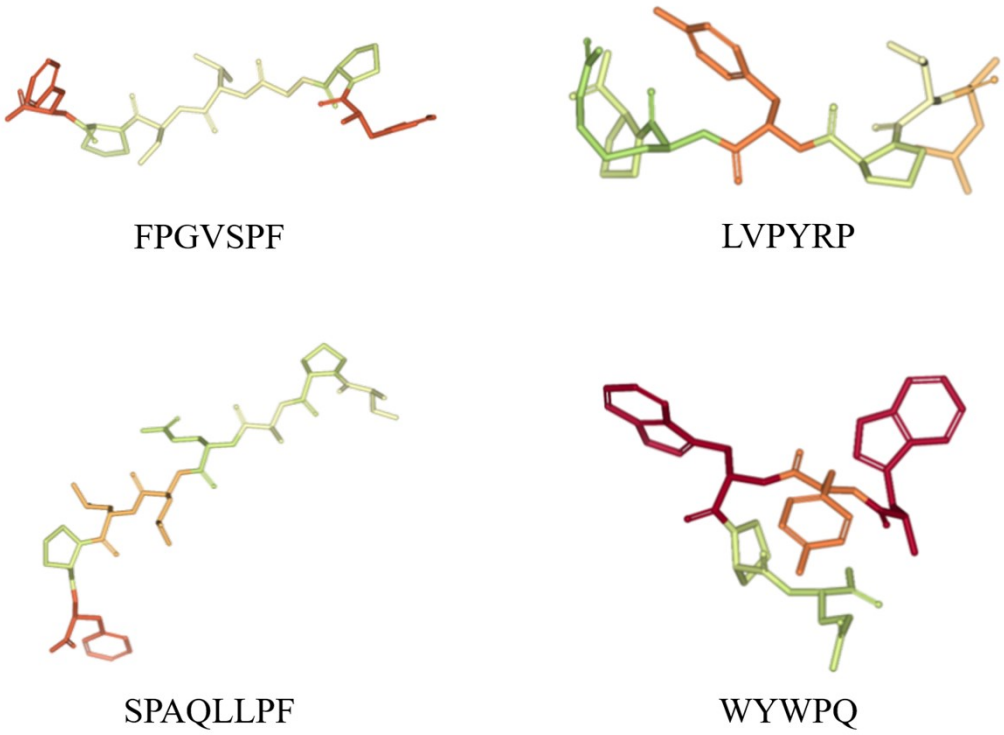


Figure S2 Structure of four ACE inhibitory peptides prepared by PyMOL software.

Table S1 ACE residues in coordination with Zn^{2+} and in the S_1, $S_1'$and S_2 pockets interacting with LVPYRP and WYWPQ.

ACE region	ACE key residue	LVPYRP	WYWPQ
Zinc ligand	His383	√	-
	His387	√	-
	Glu411	√	√
S_1 pocket	Ala354	√	-
	Glu384	√	-
	Tyr523	√	-
S_1' pocket	Glu162	√	-
S_2 pocket	Gln281	√	-
	His353	√	-
	Lys511	-	-
	His513	√	-
	Tyr520	√	-