Electronic Supplementary Material (ESI) for Food & Function.

Table S1 Docking score of collagen peptides and CaMKII.

Collagen peptides	Sequence	−CDOCKER energy (kcal/mol)	−CDOCKER interaction energy (kcal/mol)	Molecular weight
E-Lig (positive control)	–	44.6786	74.8737	–
Ser-Gly-Glu	SGE	74.2159	66.2844	292.11
Thr-Gly-Glu	TGE	79.4866	61.8682	306.13
Ala-Gly-Glu	AGE	79.5302	67.5198	276.12
Ala-Ser-Gly-Glu	ASGE	85.8736	78.0877	363.15
Gly-Glu-Ala-Gly-Ala-Gln	GEAGAQ	123.286	91.3123	532.24
Gly-Pro-Ala-Gly-Glu	GPAGE	80.7422	67.5909	430.19
Gly-Pro-Ala-Gly-Glu-Arg	GPAGER	86.3603	82.0704	293.65
Gly-Asp-Thr-Gly-Ala-Lys	GDTGAK	121.996	93.5175	548.27

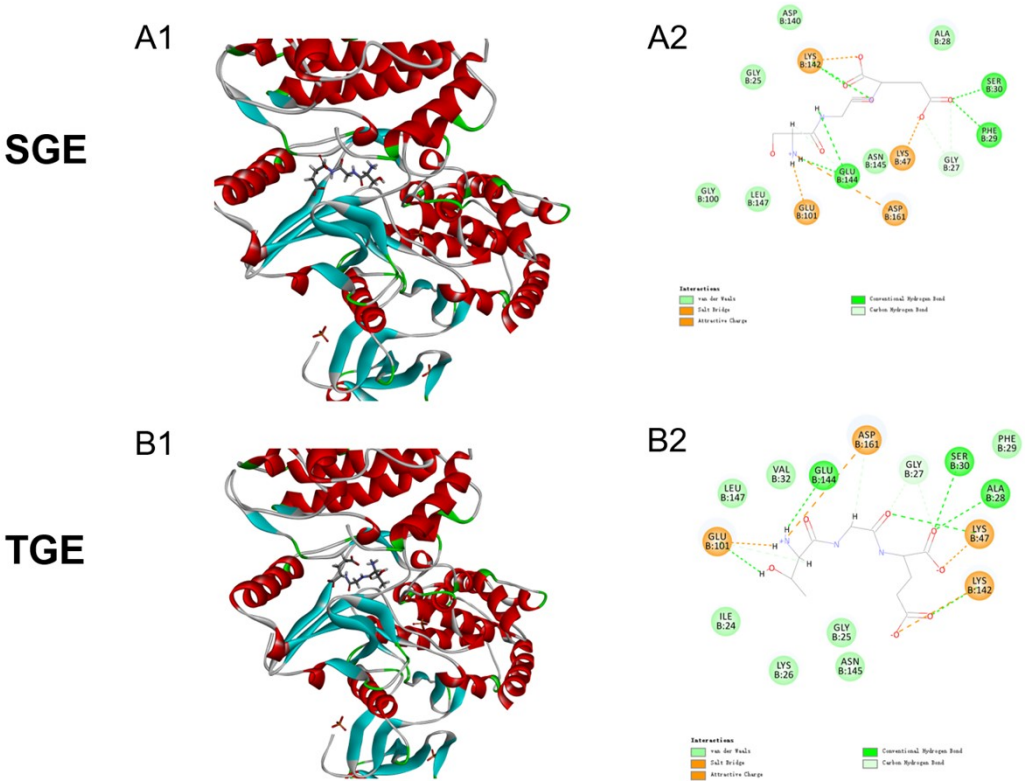

Fig. S1 Molecular docking analysis. (A1) The predicted binding sites of Ser-Gly-Glu in the active pocket of CaMKII; (A2) The detail binding mode between Ser-Gly-Glu and active pocket; (B1) The predicted binding sites of Thr-Gly-Glu in the active pocket of CaMKII; (B2) The detail binding mode between Thr-Gly-Glu and active pocket.

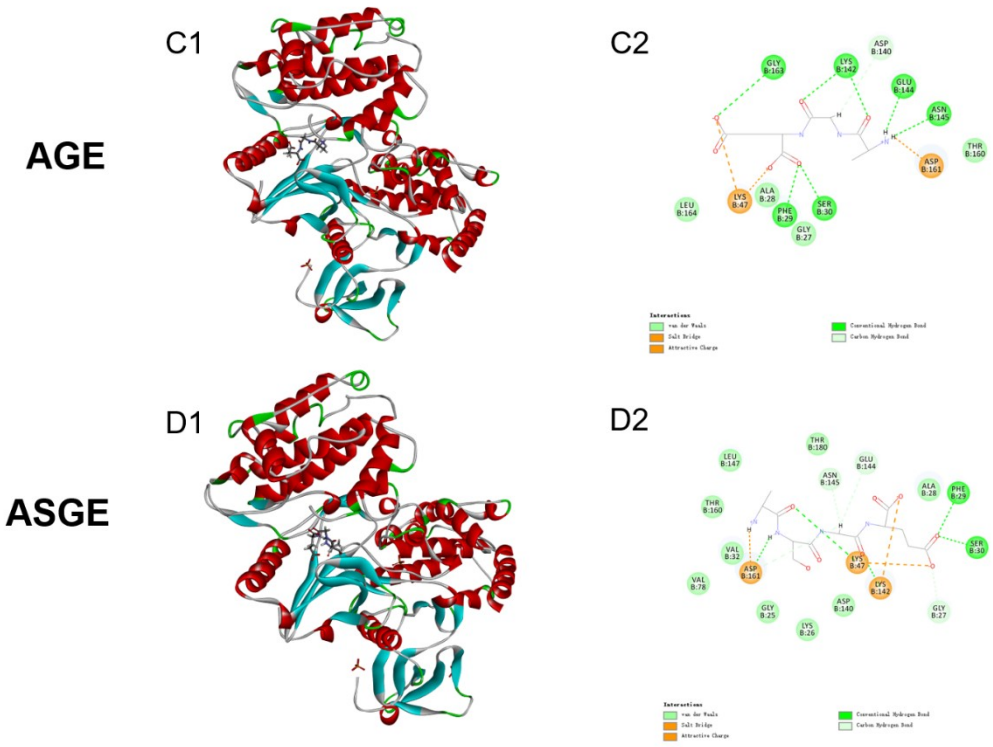

Fig. S2 Molecular docking analysis. (C1) The predicted binding sites of Ala-Gly-Glu in the active pocket of CaMKII; (C2) The detail binding mode between Ala-Gly-Glu and active pocket; (D1) The predicted binding sites of Ala-Ser-Gly-Glu in the active pocket of CaMKII; (D2) The detail binding mode between Ala-Ser-Gly-Glu and active pocket.

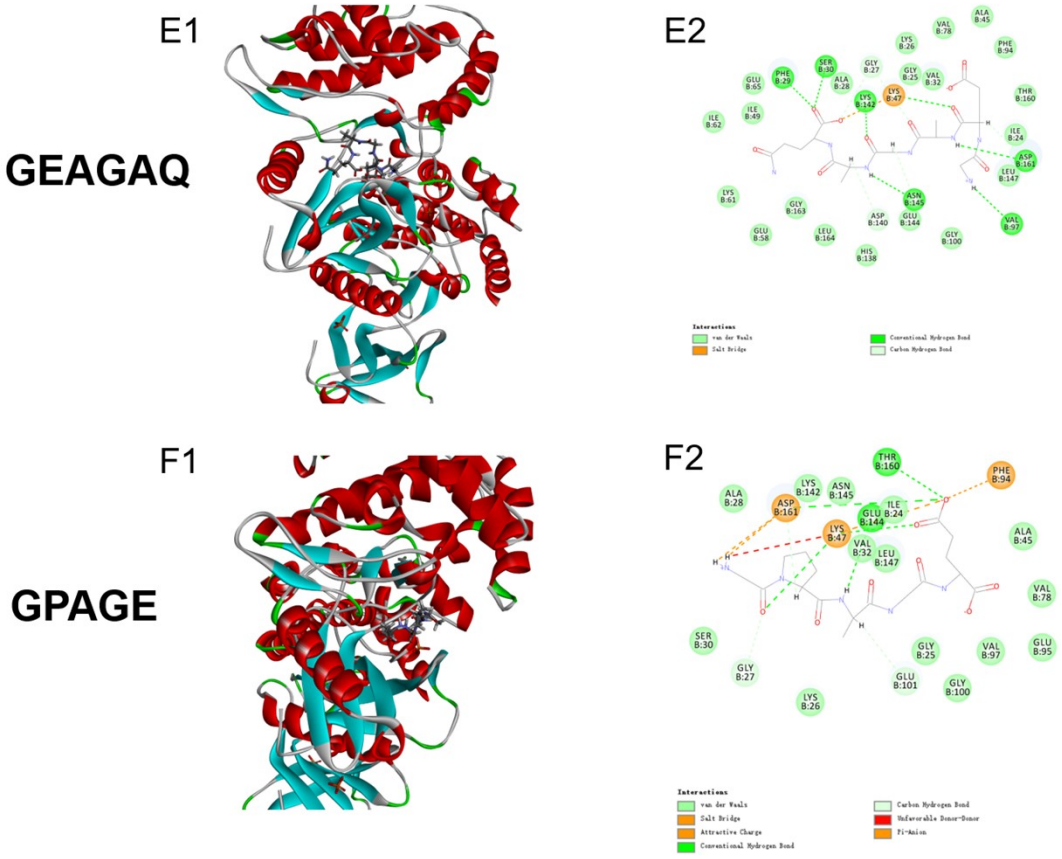

Fig. S3 Molecular docking analysis. (E1) The predicted binding sites of Gly-Glu-Ala-Gly-Ala-Gln in the active pocket of CaMKII; (E2) The detail binding mode between Gly-Glu-Ala-Gly-Ala-Gln and active pocket; (F1) The predicted binding sites of Gly-Pro-Ala-Gly-Glu in the active pocket of CaMKII; (F2) The detail binding mode between Gly-Pro-Ala-Gly-Glu and active pocket.

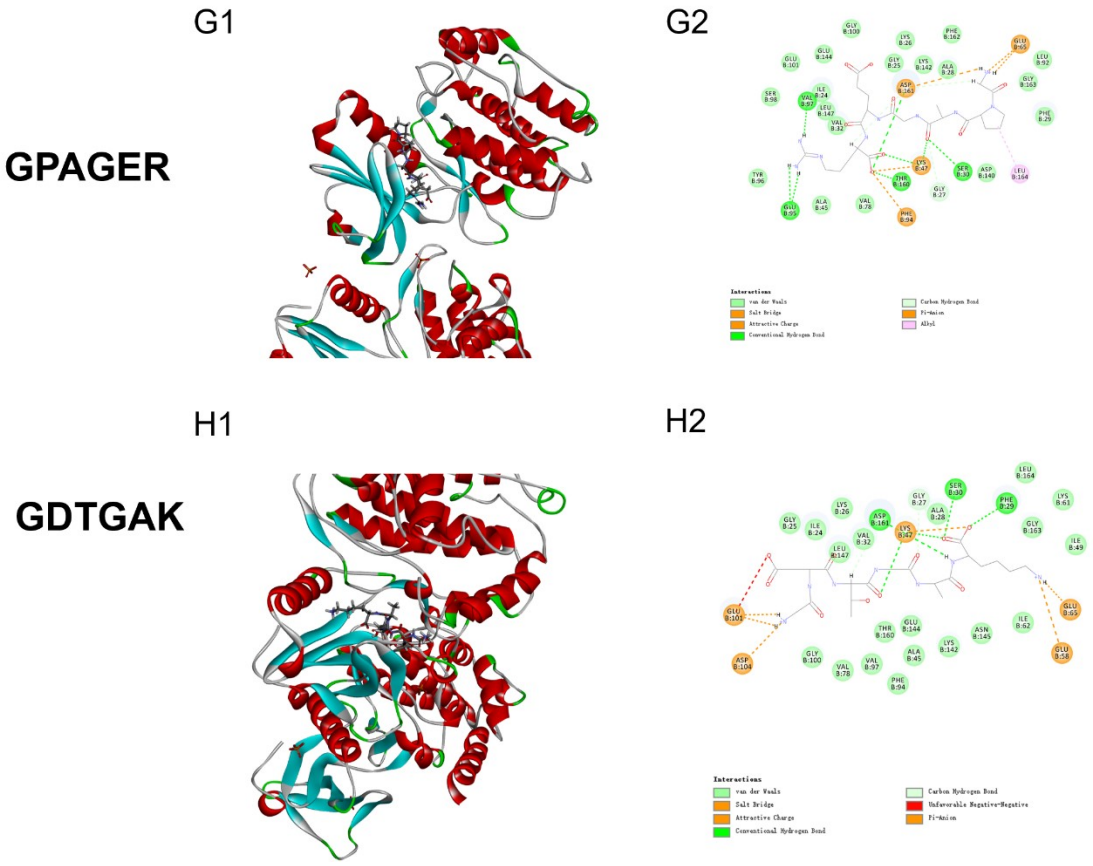

Fig. S4 Molecular docking analysis. (G1) The predicted binding sites of Gly-Pro-Ala-Gly-Glu-Arg in the active pocket of CaMKII; (G2) The detail binding mode between Gly-Pro-Ala-Gly-Glu-Arg and active pocket; (H1) The predicted binding sites of Gly-Asp-Thr-Gly-Ala-Lys in the active pocket of CaMKII; (H2) The detail binding mode between Gly-Asp-Thr-Gly-Ala-Lys and active pocket.