

## Supplementary materials

Figure S1

BTP20220610-10-02 :

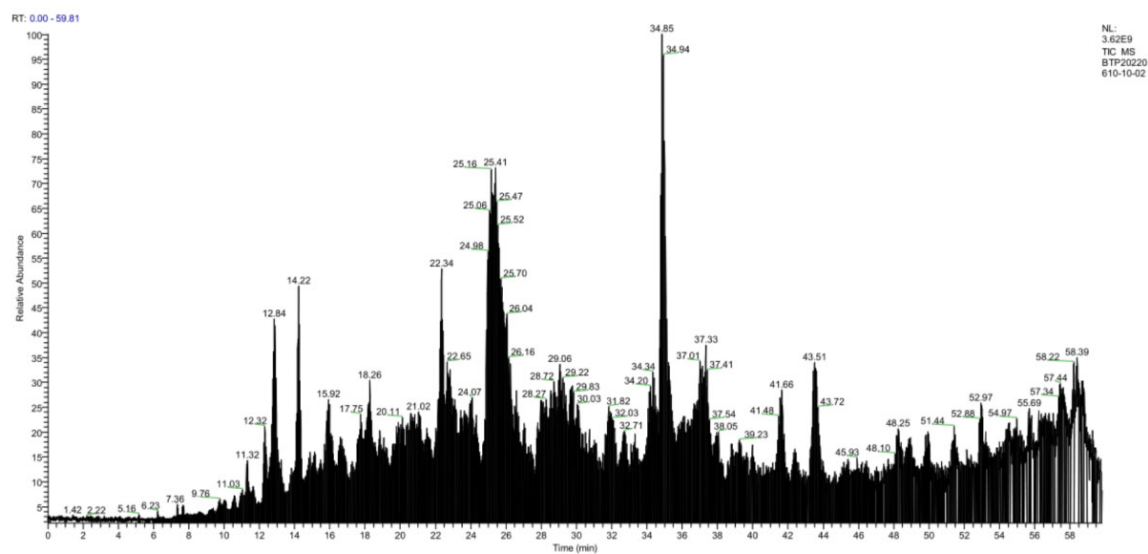


Figure S1 Chromatogram of protein with absorption peak 3.

Figure S2

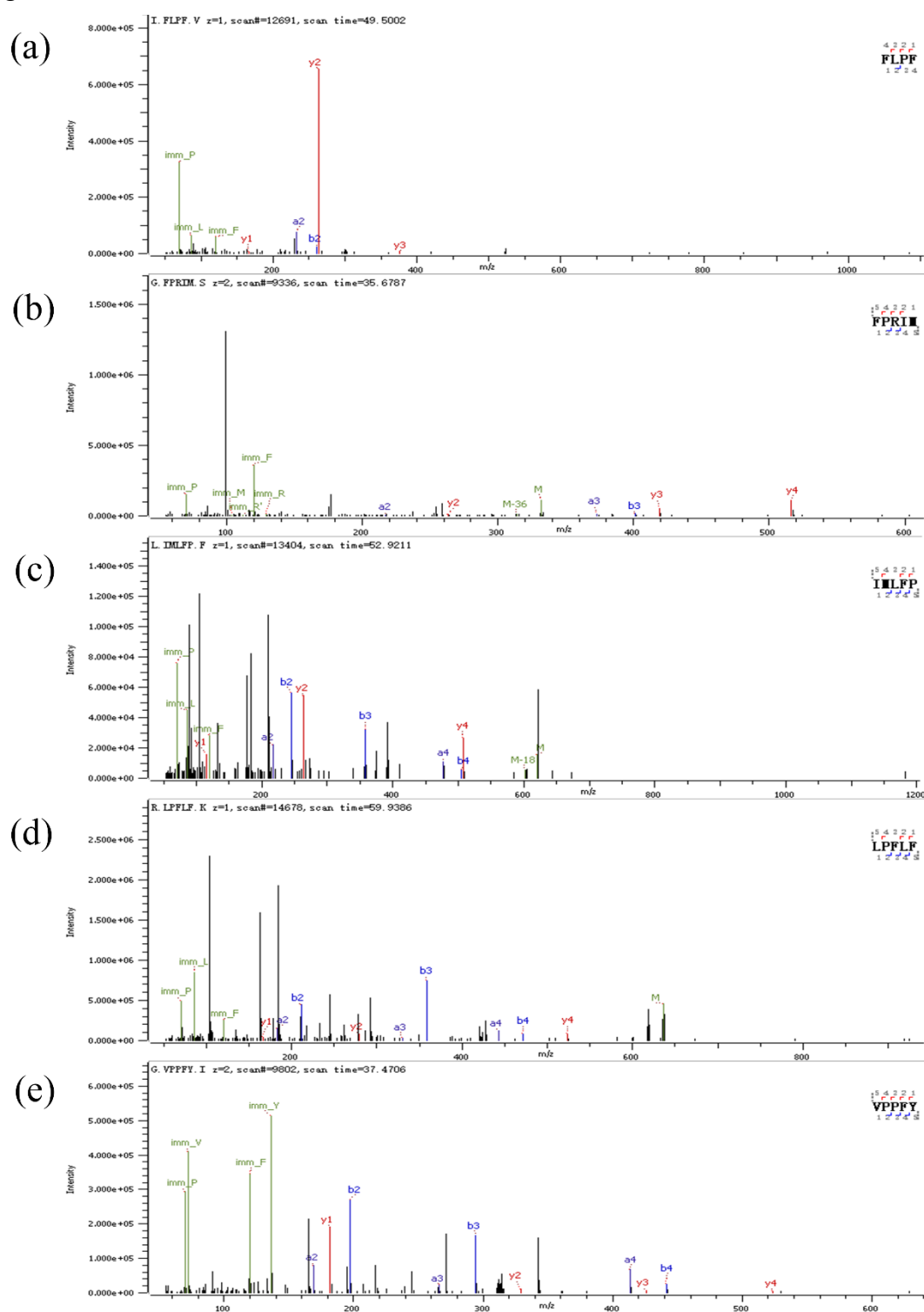


Figure S2. The secondary mass spectra of synthetic polypeptides FLPF(a), FPRIM(b), IMLFP(c), LPFLF(d), and VPPFY(e)

Table S1

Table S1 Partial peptide sequences identified by LC-MS/MS

| Name       | m/z value | Score | Retention time (s) | Amino acid abundance |
|------------|-----------|-------|--------------------|----------------------|
| TERGYSF    | 430.202   | 475.9 | 23.243             | 48537000             |
| RGPFH      | 307.164   | 365.3 | 9.5353             | 11691000             |
| DLRFQ      | 339.682   | 343.8 | 23.6806            | 9041300              |
| VPPFY      | 311.665   | 336.8 | 37.4706            | 17445000             |
| SPRPY      | 310.163   | 329.2 | 11.0649            | 2968900              |
| SYPYHS     | 377.169   | 296.0 | 10.1096            | 17334000             |
| HYNDPFY GK | 570.762   | 296.0 | 23.8012            | 30269000             |
| TWNDPR     | 394.689   | 295.2 | 15.5449            | 41088000             |
| YNDPFY GK  | 502.232   | 294.1 | 27.8544            | 16043000             |
| LAGY       | 423.225   | 285.5 | 20.8251            | 14202000             |
| TYRQL      | 340.690   | 285.0 | 14.6488            | 9056800              |
| TPRWK      | 344.195   | 276.7 | 19.3679            | 37496000             |
| PGFP       | 417.214   | 269.6 | 23.3069            | 11790000             |
| VGPF       | 419.230   | 268.6 | 29.4832            | 50535000             |
| GPFHF      | 302.647   | 268.1 | 35.0168            | 18109000             |

Elucidation: The m/z value as observed within the table pertains to the experimentally detected mass-to-charge ratio of the peptide. The computed mass (M+H) presented in the table corresponds to the theoretical molecular weight of the peptide moiety. In the tabular data, the mass error, quantified in parts per million (ppm), reflects the deviation in molecular weight. The score denoted in the table represents the quantitative assessment or rating of the peptide. The intensity value within the table is indicative of the relative abundance or prevalence of the peptide. The scan time specified in the table corresponds to the retention time of the peptide during the analytical process.