Supplemental Figures 1a-g. MALDI-O-TOF mass spectra of peptides resulted from in gel trypsin-digested protein spots excised from preparative pick gel. Mass spectra were acquired on a prOTOF 2000 ™ MALDI O-TOF mass spectrometer (PerkinElmer) in the positive ion mode using TOFworks ™, an integrated workflow-based software platform. The peptide ion mass (M + H) were accurate to within 30 ppm after external calibration. The labeled peptide ions (M+H) were used to generate statistically-significant matches to the proteins as indicated in Supplemental Table 2.

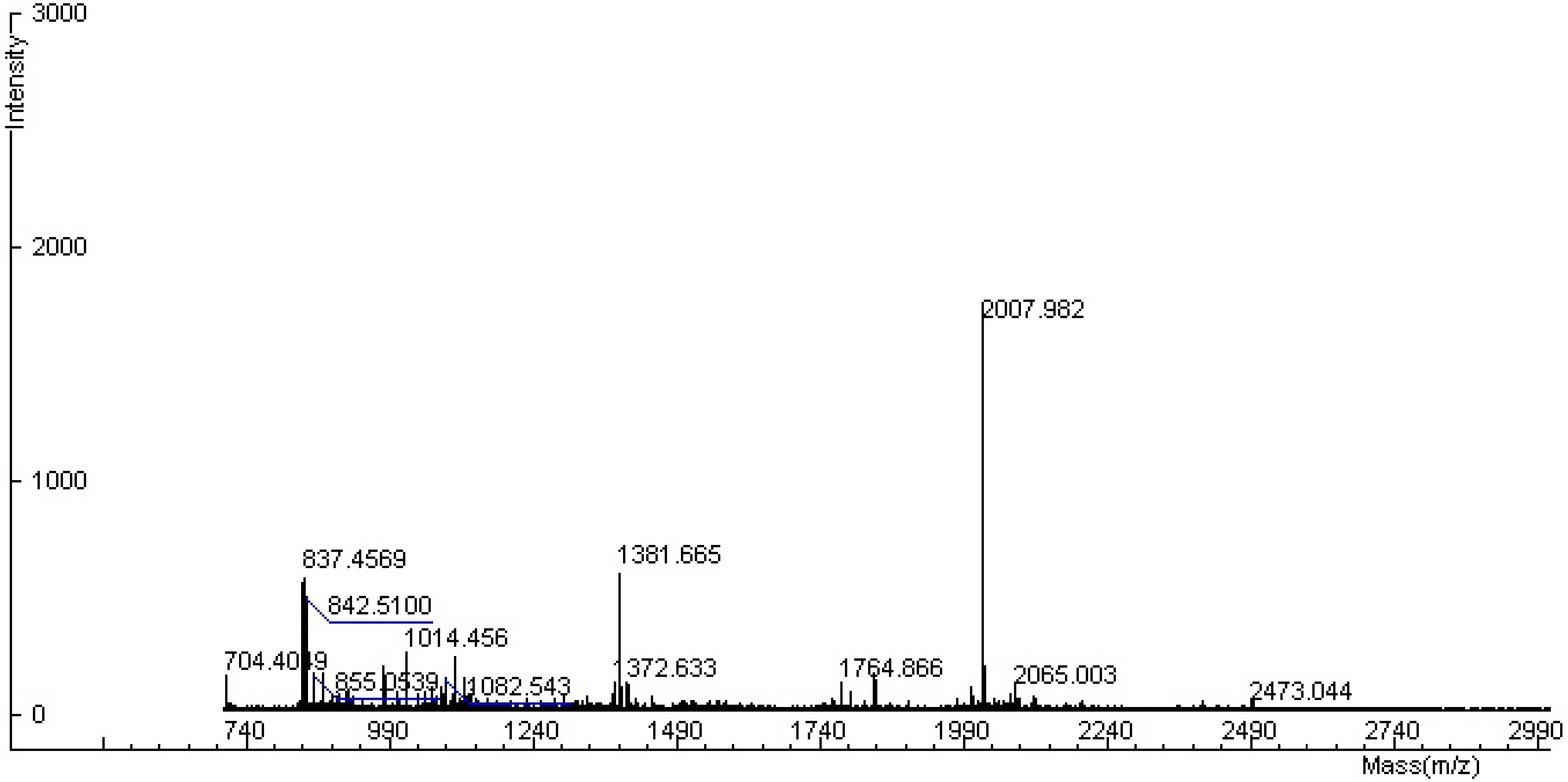

Figure 1a, spot no 24 (*Fetub*)

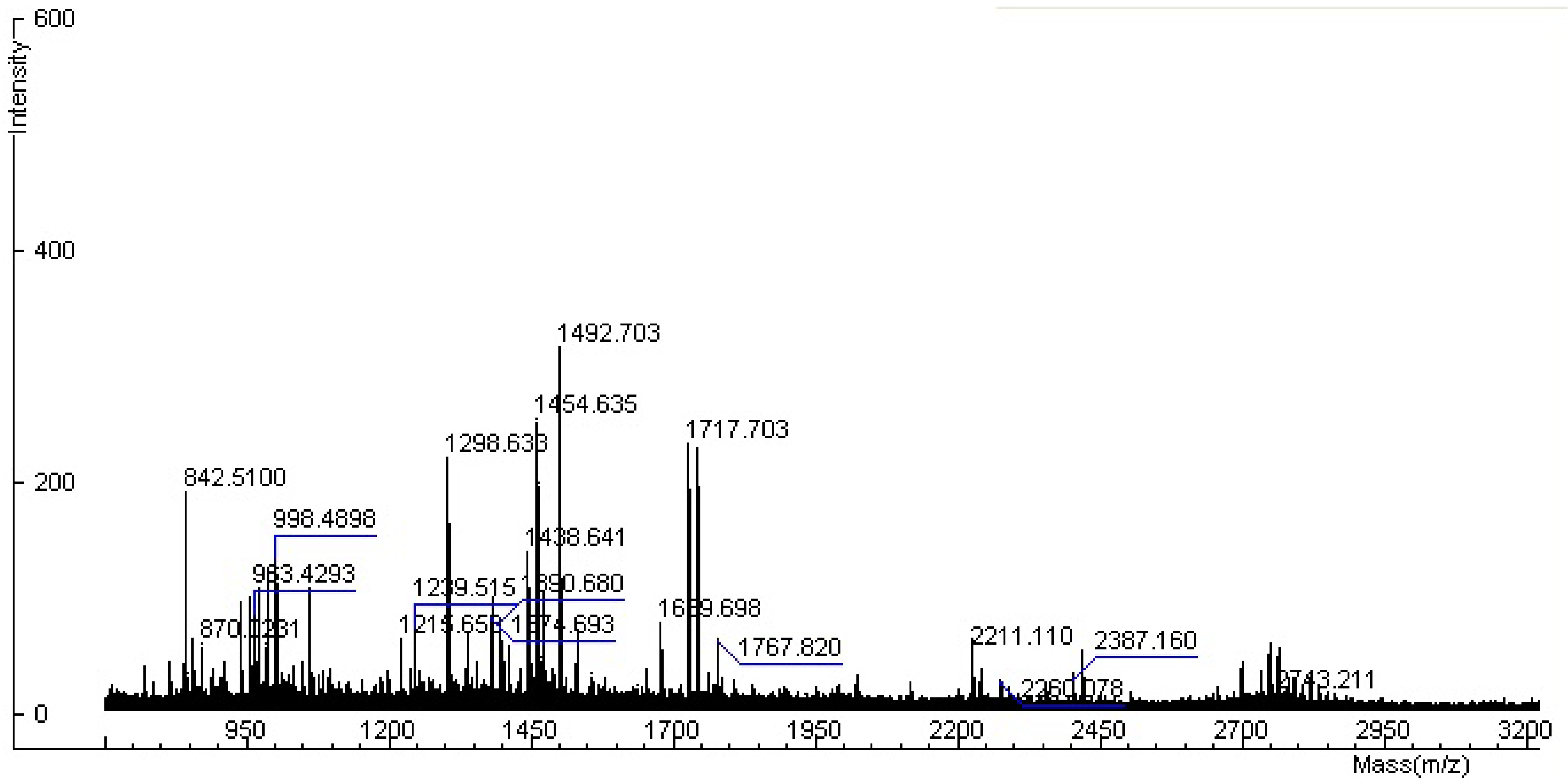

Figure 1b, spot no 25 (*Fga*)

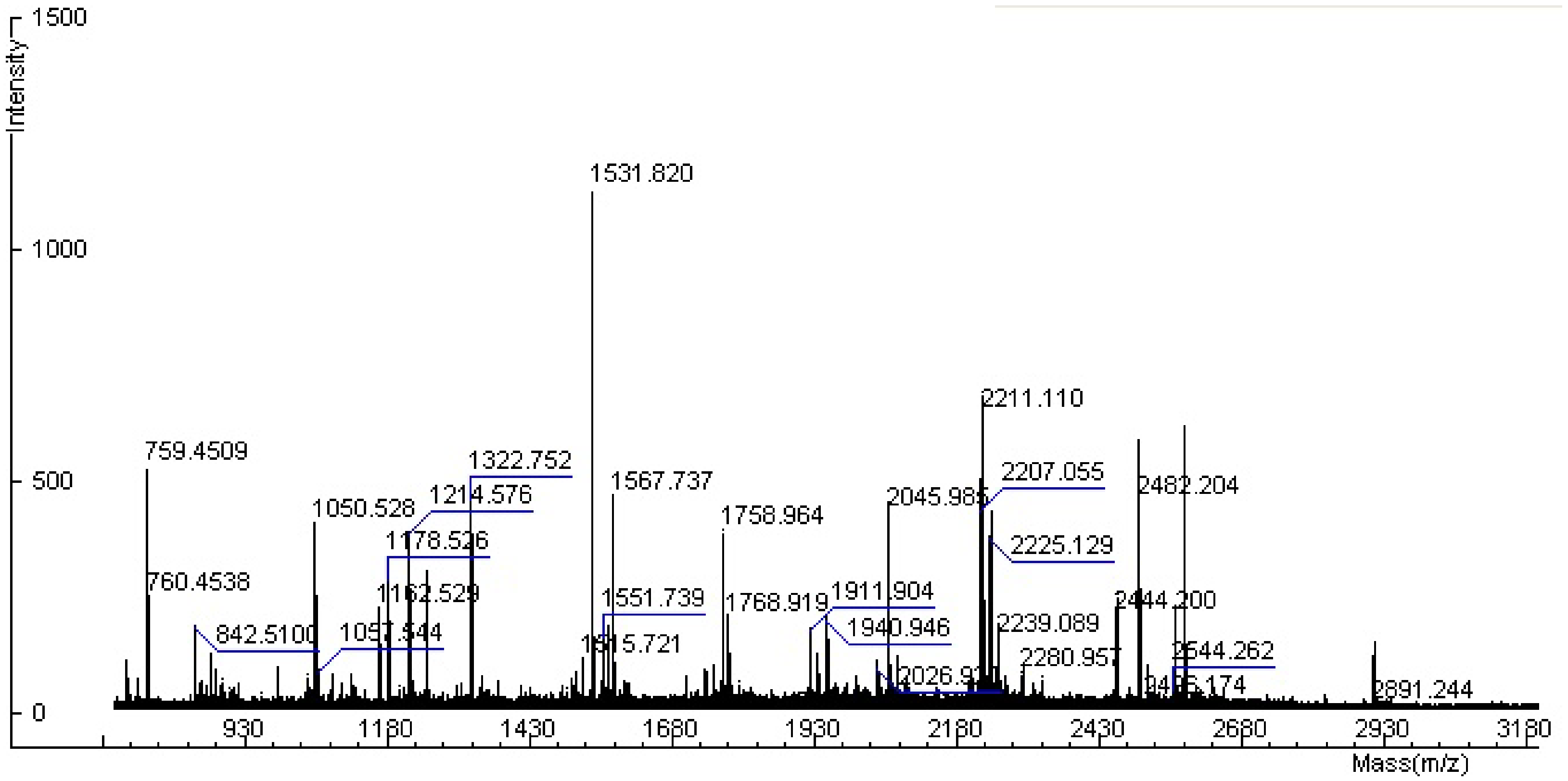

Figure 1c, spot no 27 (*Fgg*)

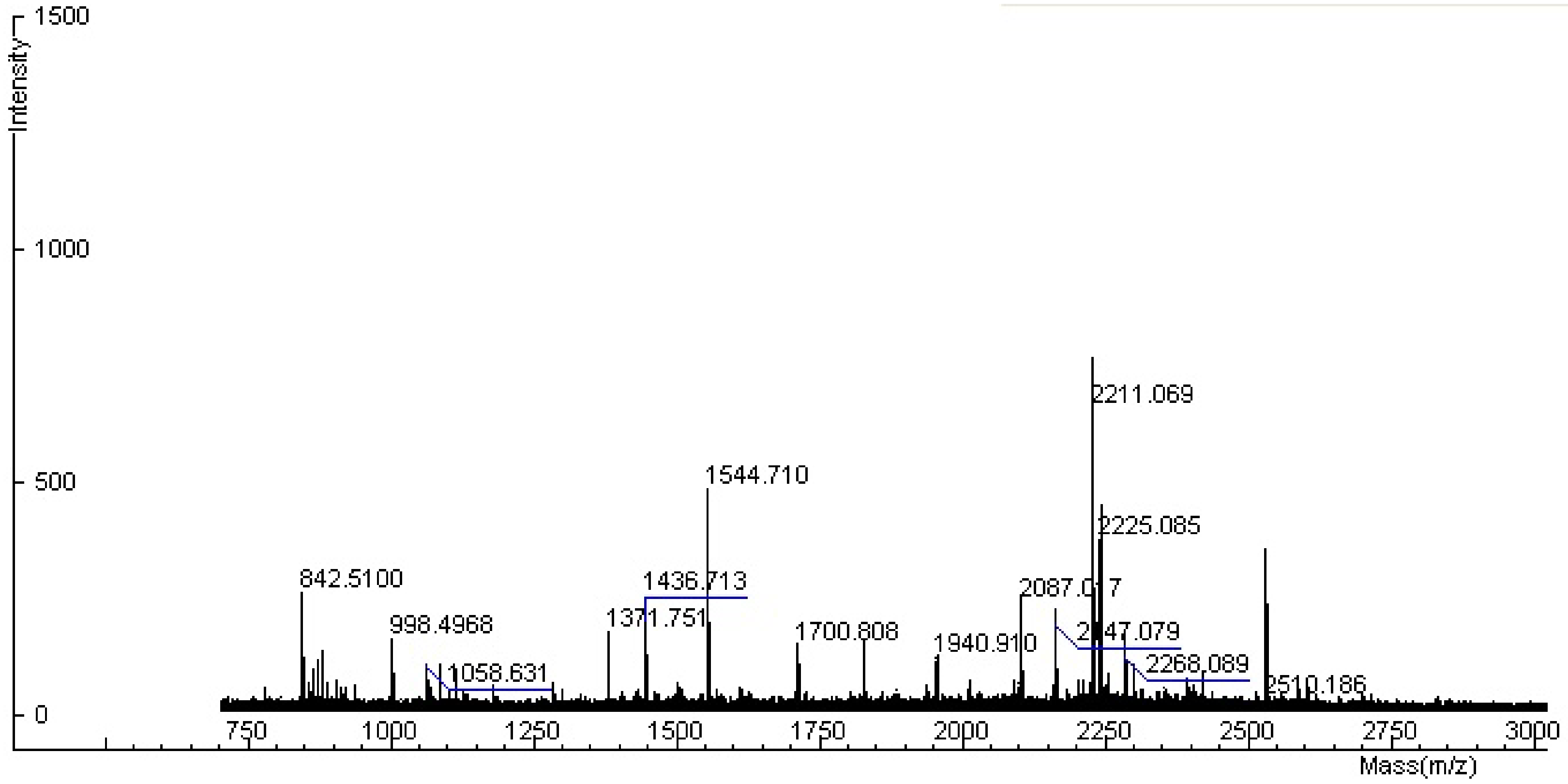

Figure 1d, spot no 30 (*Gda*)

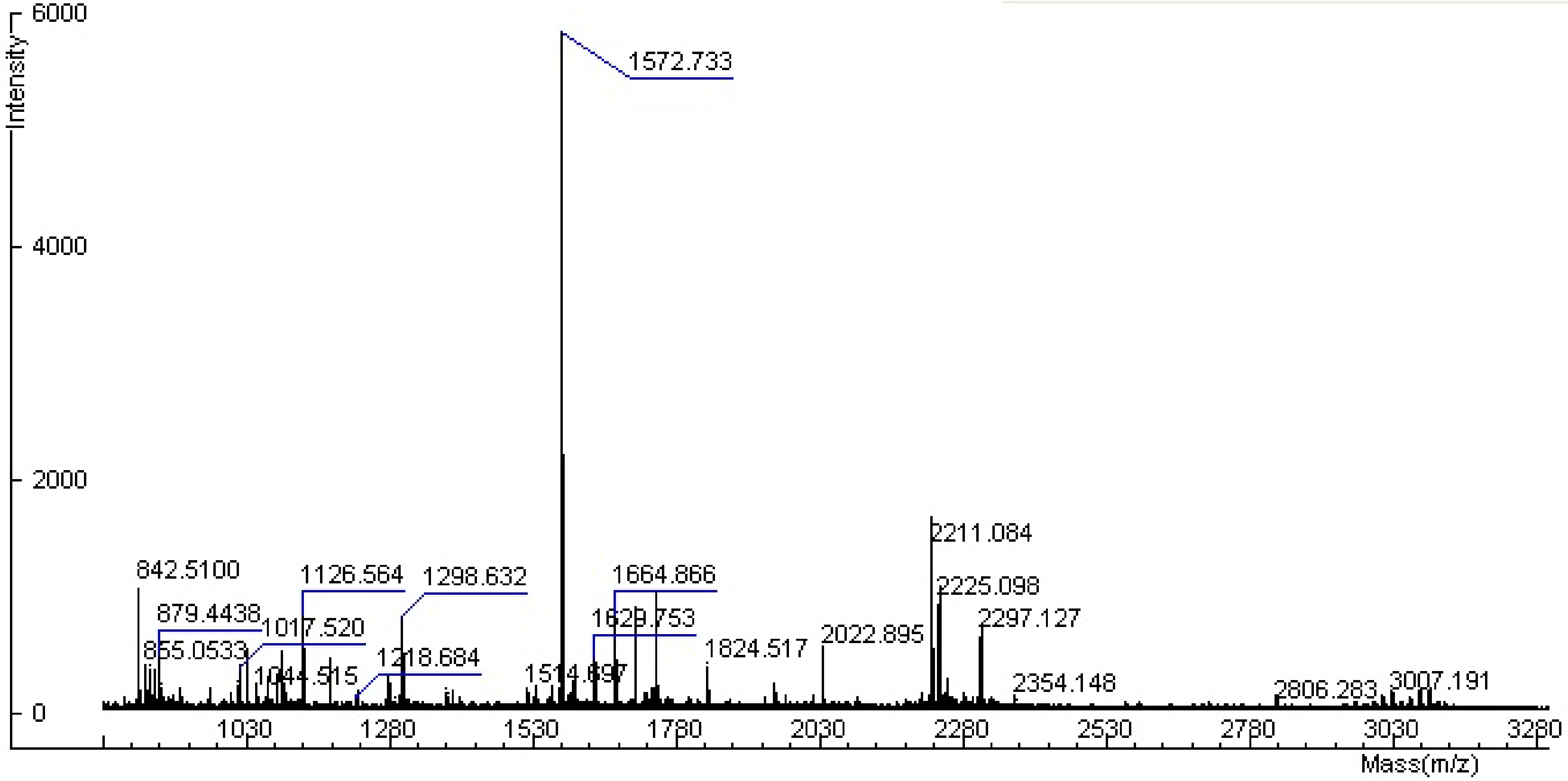

Figure 1e, spot no 34 (*Hbb*)

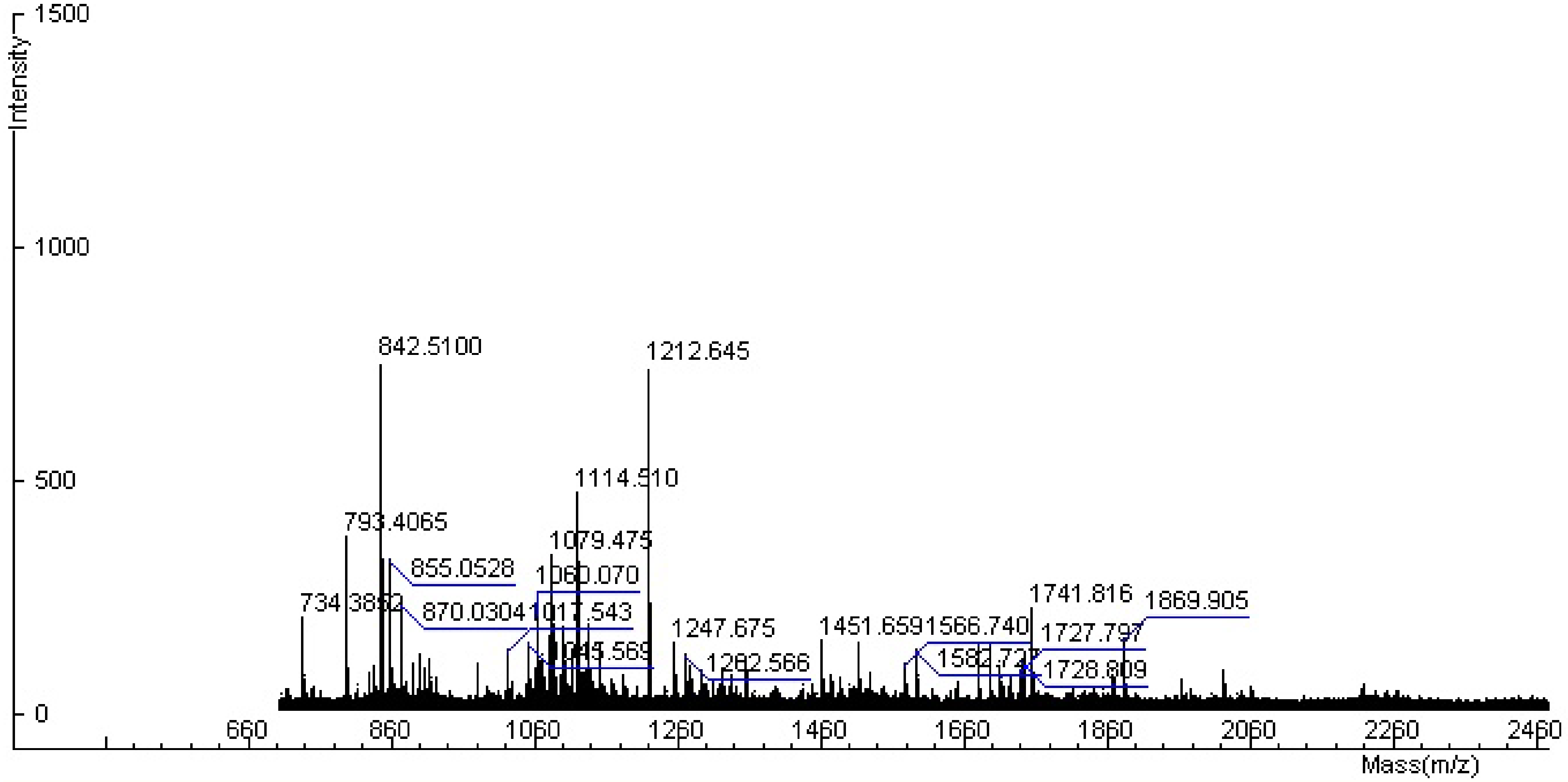

Figure 1f, spot no 37 (*Hpx*)

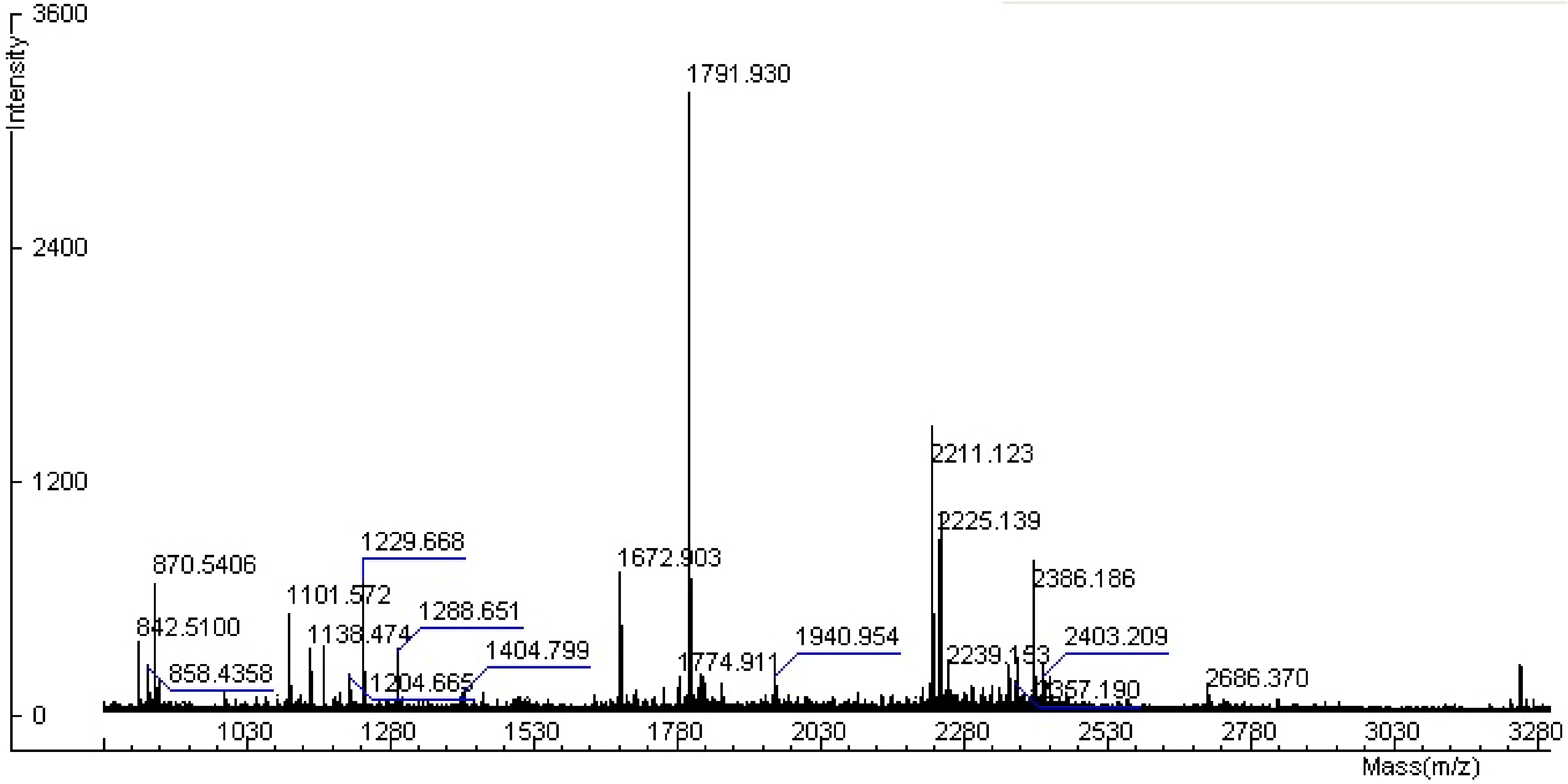

Figure 1g, spot no 49 (*Pzp*)