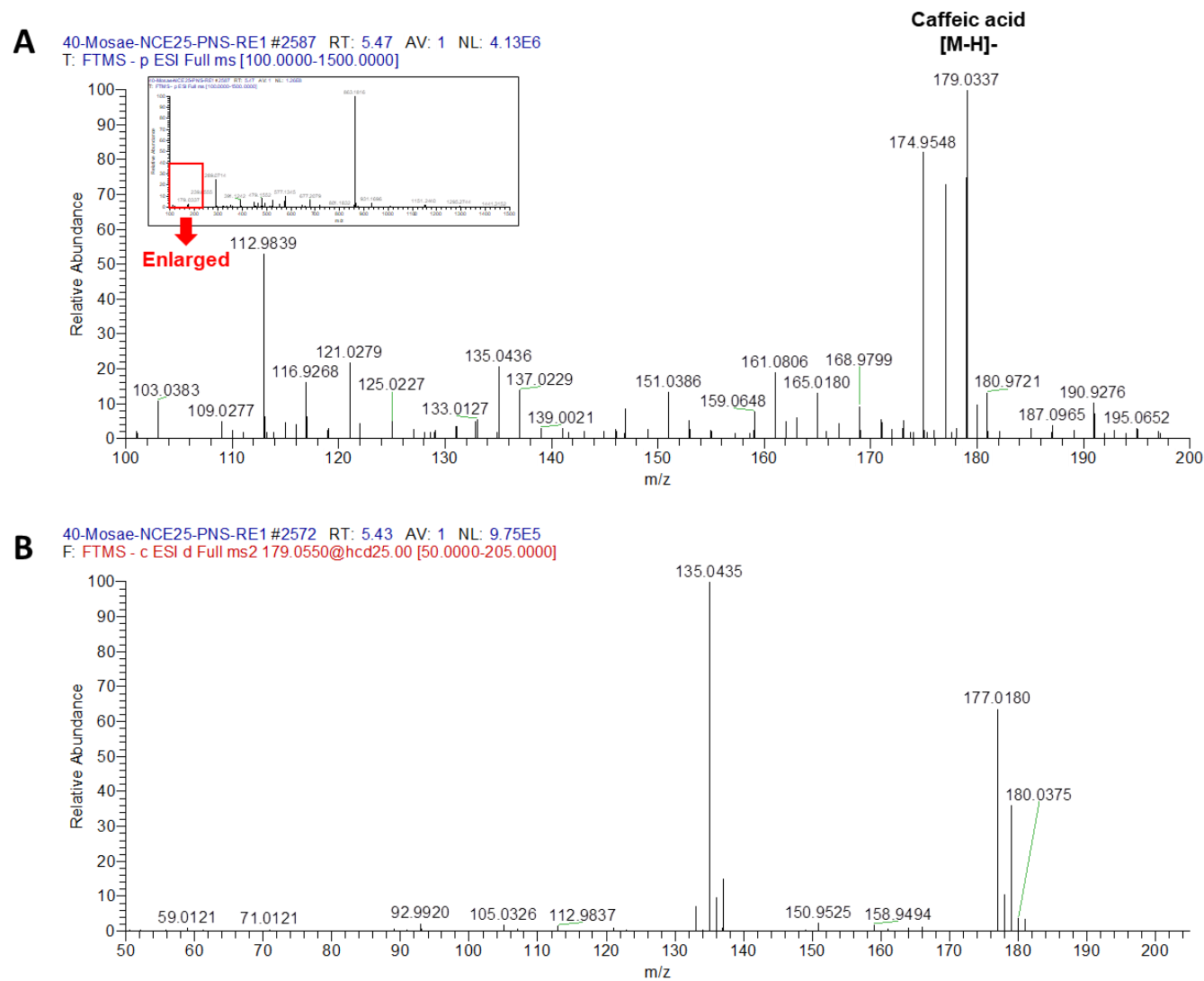


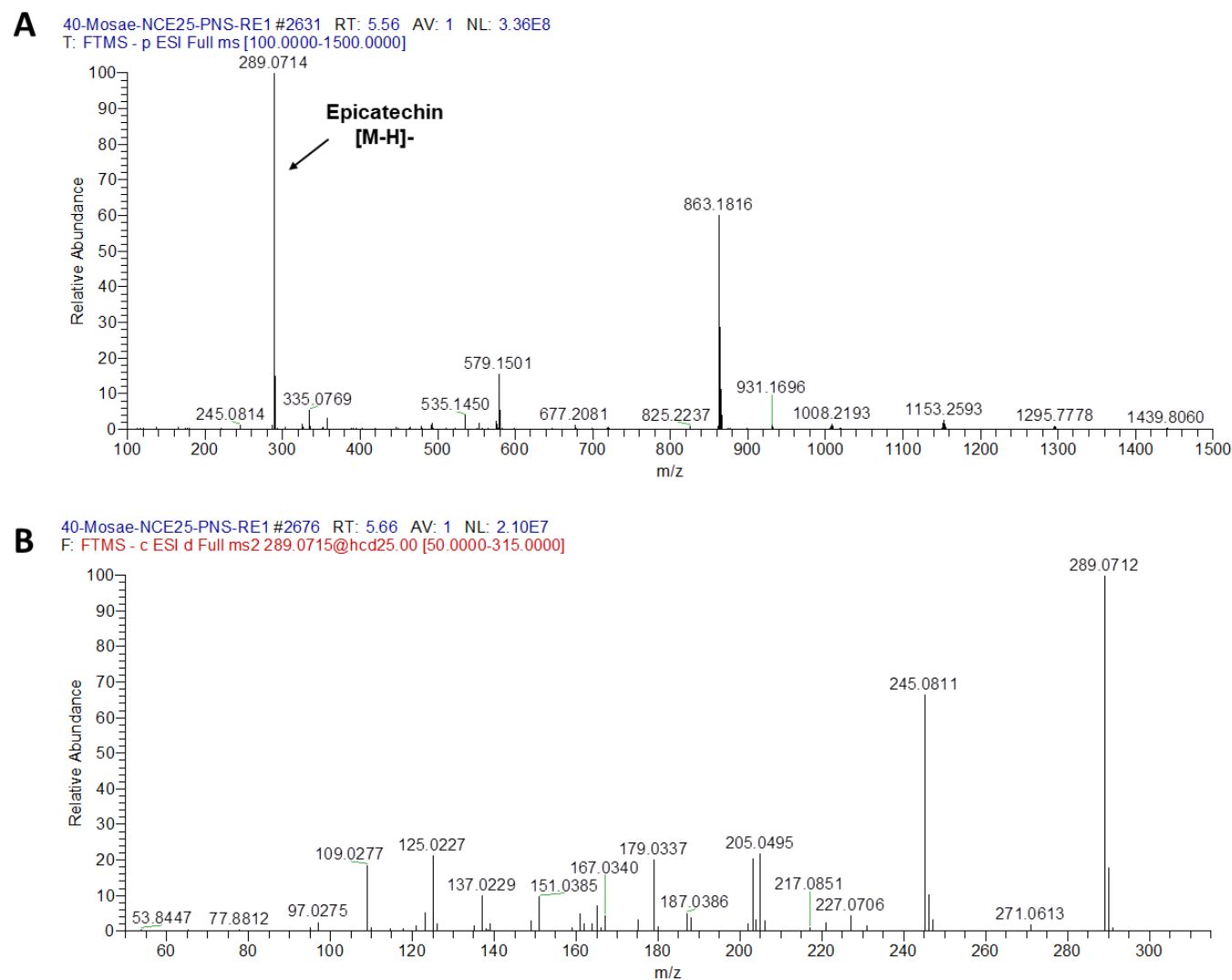
## Supplementary materials

### *Q-Exactive quadrupole-orbitrap mass spectrometer condition*

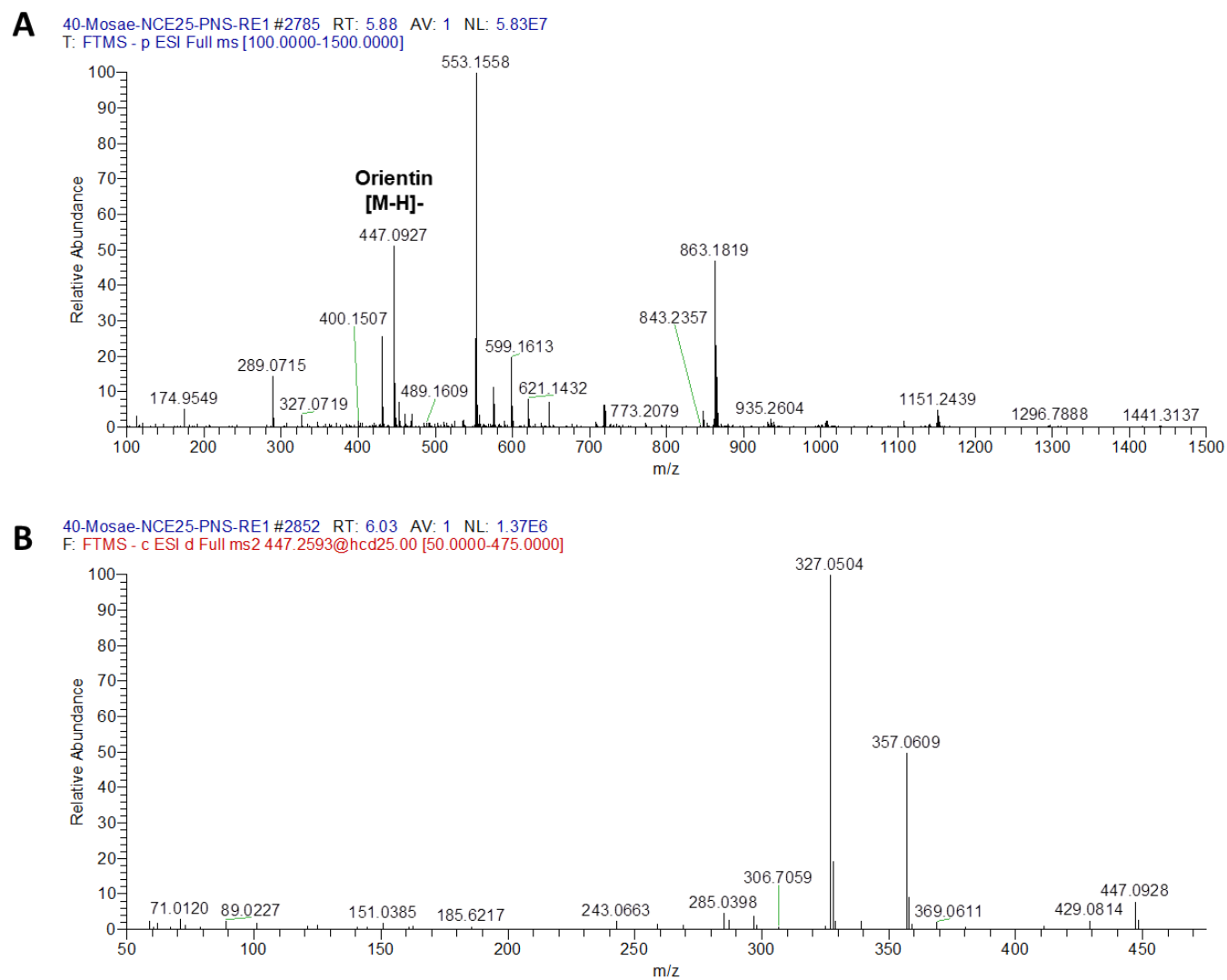
MS/MS analysis was conducted using a Q-Exactive quadrupole-orbitrap mass spectrometer that equipped with a heated electrospray ionization (HESI) interface. The ionization source was optimized using the following parameters: positive and negative ion-switching mode; spray voltage, 3.5 kV; capillary temperature, 350°C; sheath gas pressure, 40 arbitrary units (au); auxiliary gas pressure, 10 au; and S-lens RF level 50. MS spectra were acquired in full MS and dd-MS<sup>2</sup> (top N) scan mode. This mode acquired full MS scans followed by a set of data-dependent (dd) scans with fragmentation energy applied. The full MS acquisition parameters were set as follows: ion scan range 100-1500 m/z; resolution of MS scan, 70000; automatic gain control (AGC) target, 1.0E6; maximum injection time (IT), 100 ms; and profile spectrum data type. The MS2 optimized acquisition parameters were as follows: resolution of MS/MS scan, 17500; AGC target, 1.0E5; maximum IT, 50 ms; count of loop, 10; count of MSX, 1; and normalized collision energy, 25 eV. All data acquisition and analysis were performed using Xcalibur v.4.2 and Tracefinder v.4.0 software (Thermo Fisher Scientific).



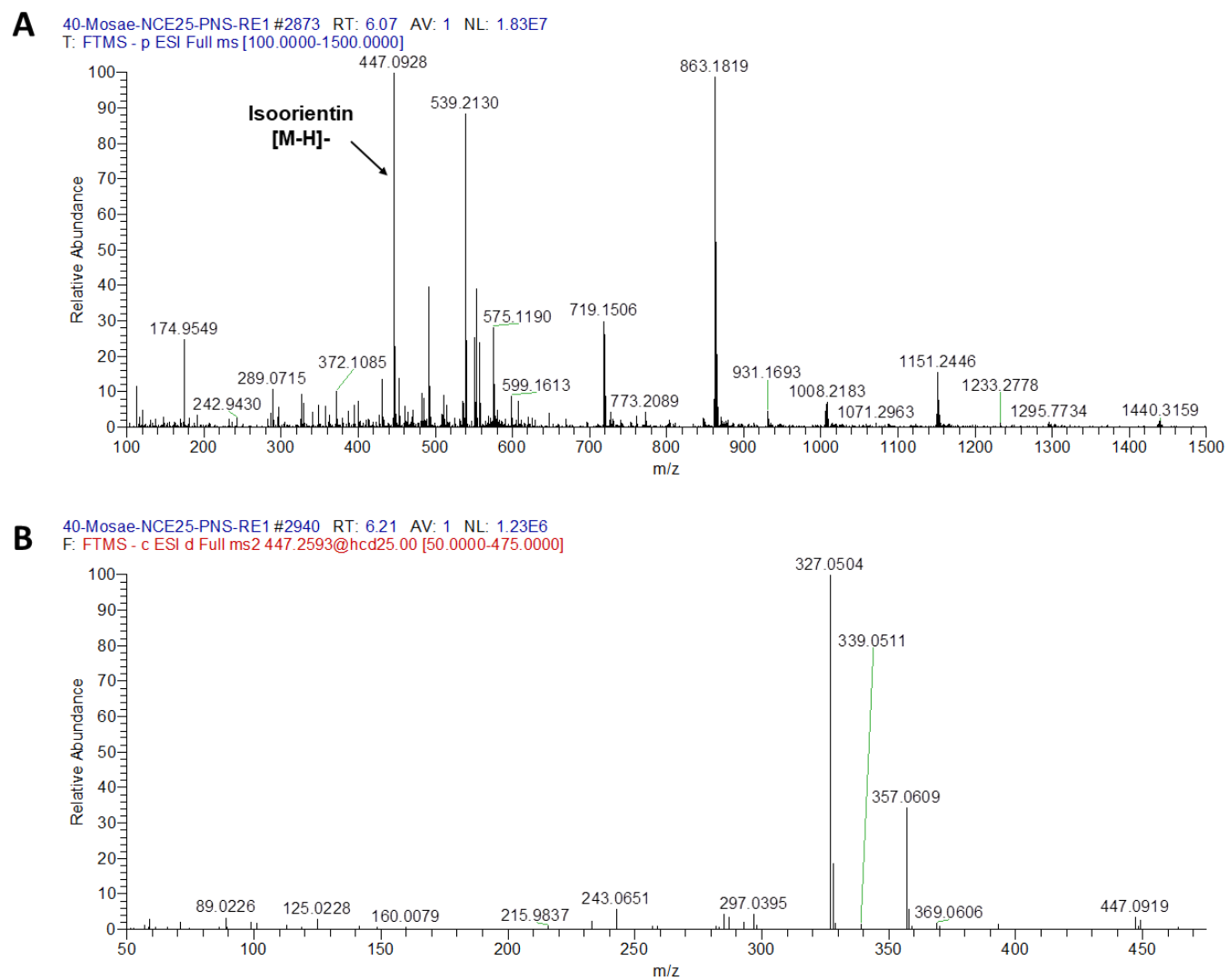
**Figure S1.** Full scan mass spectrum (A) and MS2 spectrum (B) of caffeic acid



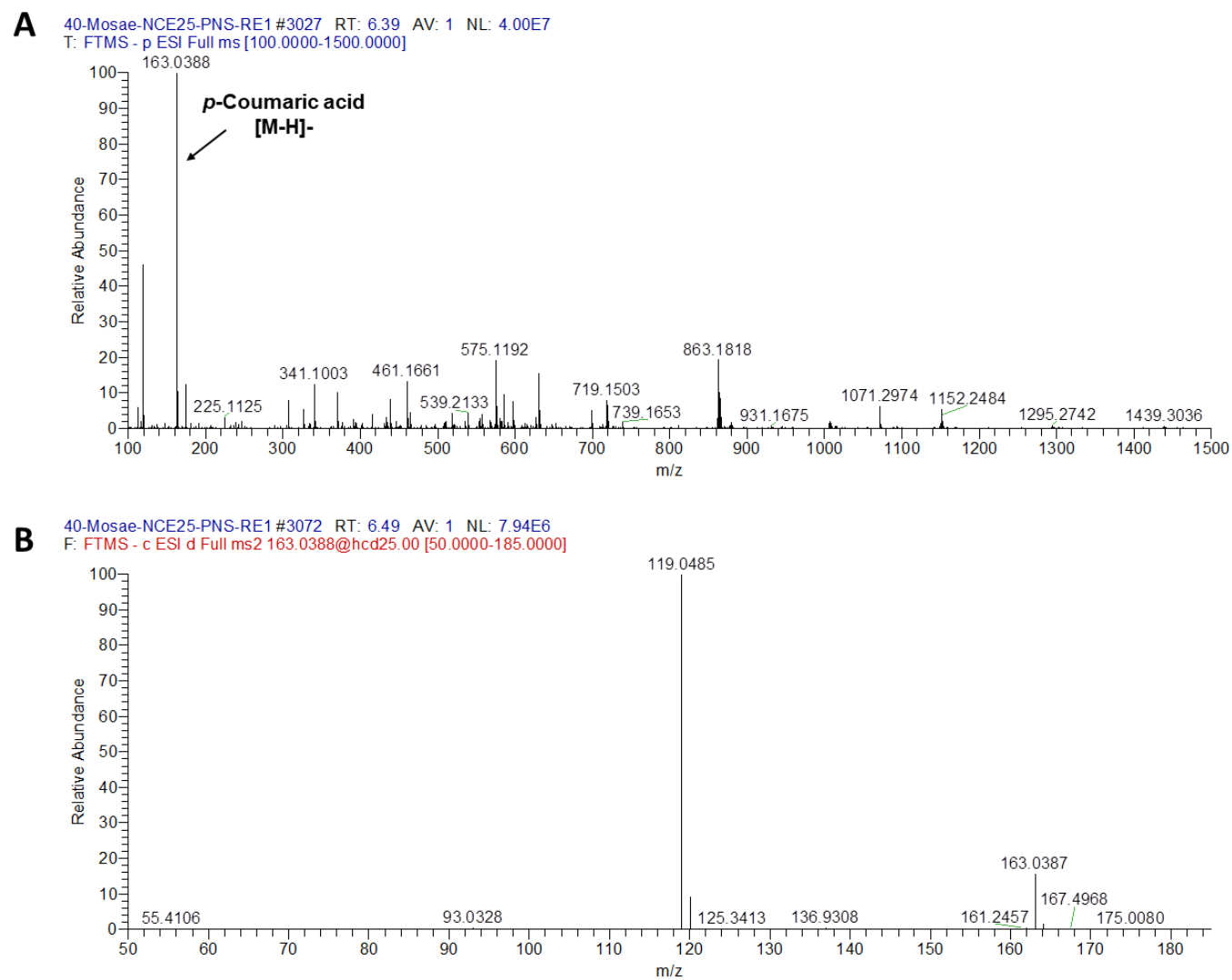
**Figure S2.** Full scan mass spectrum (A) and MS2 spectrum (B) of epicatechin



**Figure S3.** Full scan mass spectrum (A) and MS2 spectrum (B) of orientin



**Figure S4.** Full scan mass spectrum (A) and MS2 spectrum (B) of isoorientin



**Figure S5.** Full scan mass spectrum (A) and MS2 spectrum (B) of *p*-coumaric acid