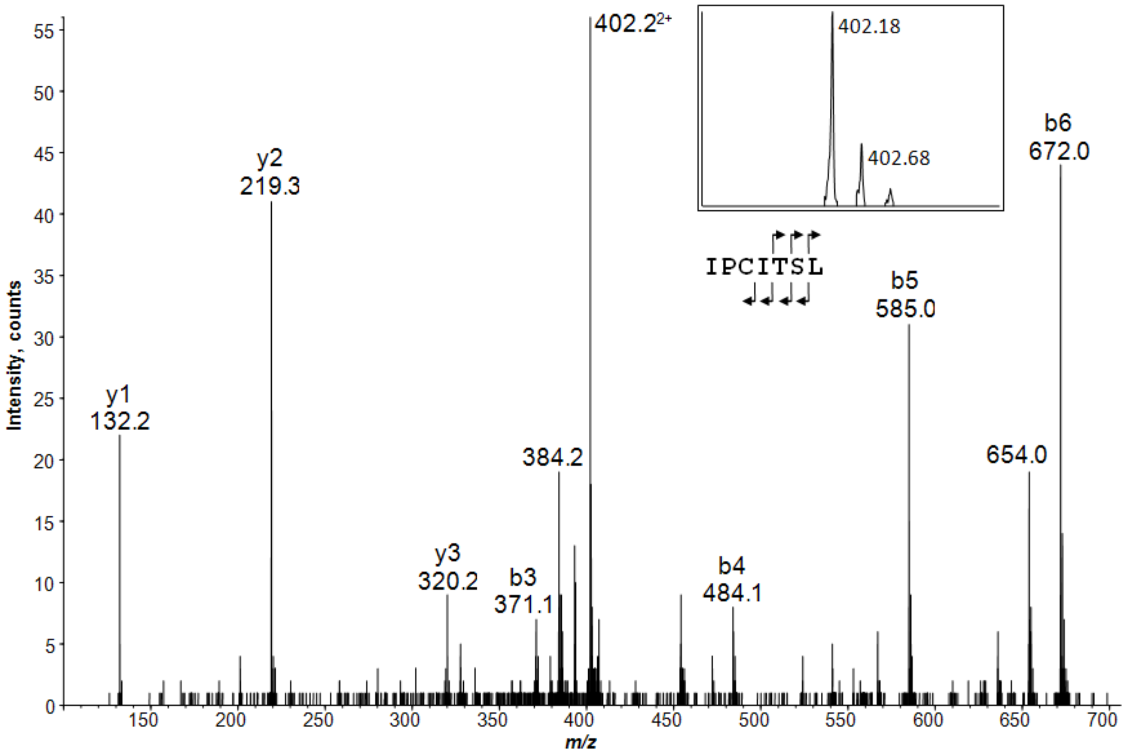
Supplementary Figure 2



Supplementary Fig. 2. LC-ESI-MS/MS sequencing of paragidin-br1. A chymotrypsin digest was performed in order to elucidate the position of the isobaric amino acids Ile and Leu within the peptide sequence. MS/MS of precursor at *m/z* 402.2 (802.4 Da). The inset shows the precursor ion *m/z* value and the schematic shows the sequence ions that were detected (indicated by arrows). The major sequence ions are labeled in the spectrum.