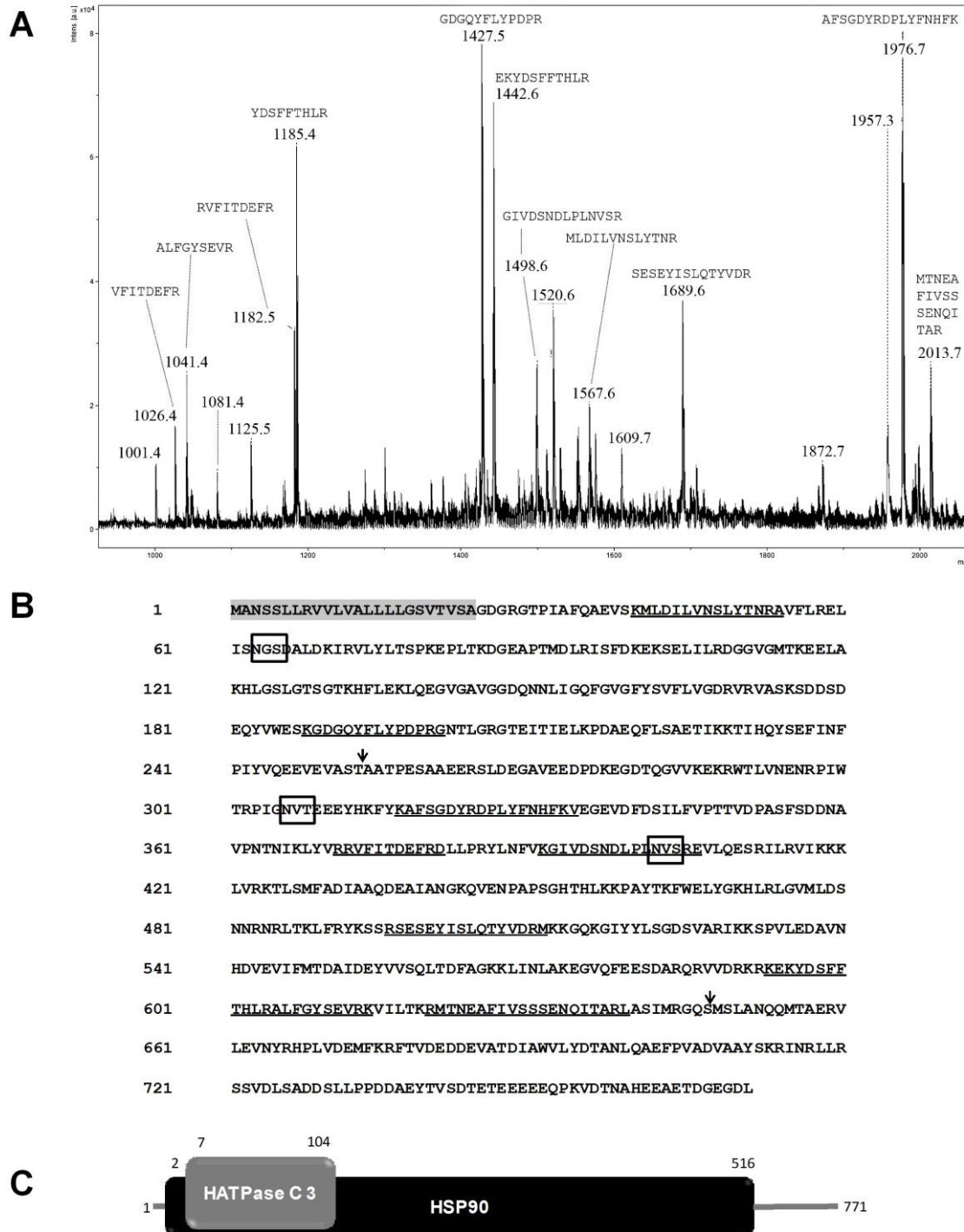


Supplementary Fig. 1 File:



Supplementary Figure 1. Mass spectrometric and bioinformatics analysis of HBPLc. **A**, MALDI mass spectrum of reduced and alkylated HBPLc following incubation with trypsin. Monoisotopic masses of 18 proteolytic peptides are shown; **B**, Amino acid sequence of HBPLc determined from tryptic peptides by mass spectrometry (complete underline) and alignment in MASCOT database submitted to analysis in pBLAST implemented in UNIPROT KB: tr|A4I4C9|A4I4C9_LEIIN - Putative lipophosphoglycan biosynthetic protein; Gene: *LPG3*; Organism: *Leishmania infantum*.

Identification in pBLAST inside TritypDB: LinJ. 29.0790. The signal sequence (gray highlight) was removed to optimize the construction of the plasmid; Squares indicate predicted *N*-linked glycosylation sites and arrows indicated predicted *O*-linked glycosylation site; C, Scheme of domains present in the protein with initiators and terminators amino acids.