Figure S3.

Theoretical two-dimensional map of the predicted molecular mass (kDa) and pI of iTRAQ labelled proteins identified within the proteome of *Clostridium difficile* strain 630.

The most acidic protein identified was a putative phage protein (pI = 4.29), which was also the lowest molecular mass protein (Mr = 8.55 kDa) detected. The most basic protein was the 50S ribosomal protein L2 (pI = 10.64) whereas the heaviest protein identified was a formylglycinamidine ribonucleotide synthetase (Mr = 140.71 kDa).