

## EXTENDED PROTEOME AND MEMBRANE SUBPROTEOME OF MYCOPLASMA GENITALIUM

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Mycoplasmas represent one of the simplest biological systems and are good examples of a true autoreplicative minimum cell. The proteome of *Mycoplasma genitalium* has been analyzed in deep using gel-based and gel-free technologies. The proteome has been analyzed in the exponential growth phase and we have achieved the identification of 343 proteins (70.4%) of the 487 predicted ORF, being 274 of these proteins not identified in previous proteomic analysis.

The whole proteome has been analyzed using the biotin protein labeling with the capture of labeled proteins in a sepharose column with immobilized streptavidin. Analyzing the proteome of this microorganism we have identified 340 proteins (69.8%) of the 487 predicted ORF, being 271 of these proteins not identified in previous proteomic analysis. In previous studies the proteome of *M. genitalium* (Wasinger *et al.*) was analyzed identifying the 28.3% of the total proteome, but the membrane proteins were under represented due to their hydrophobicity. For this reason, the membrane proteins have been studied using three different approaches to find the proteins present in the membrane and to find the best technique to study them. These techniques are phase separation using Triton X-114, biotinylation of cell surface proteins and CyDye labeling of cell surface proteins. Analyzing the membrane subproteome of this microorganism we have identified 140 proteins (28.7%) of the 487 predicted ORF.

This is the most extensive analysis performed in this microorganism not only of the total proteome but also the membrane subproteome.