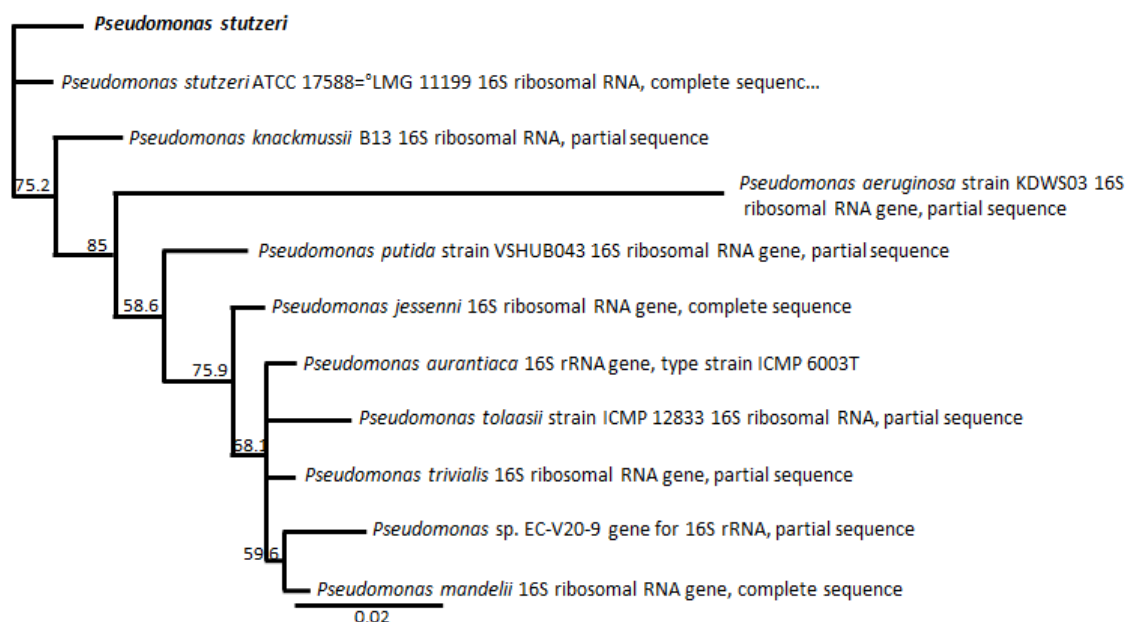
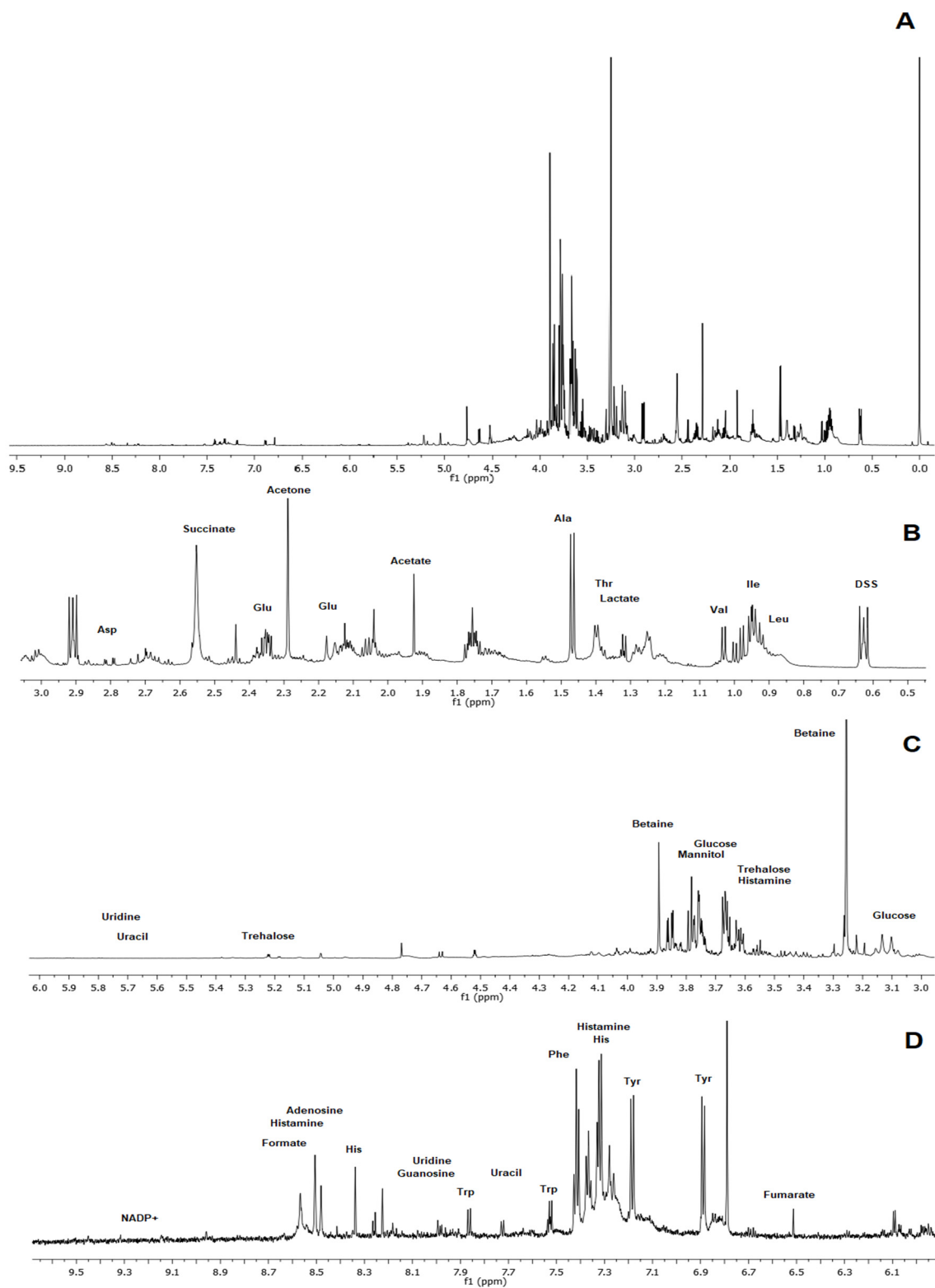


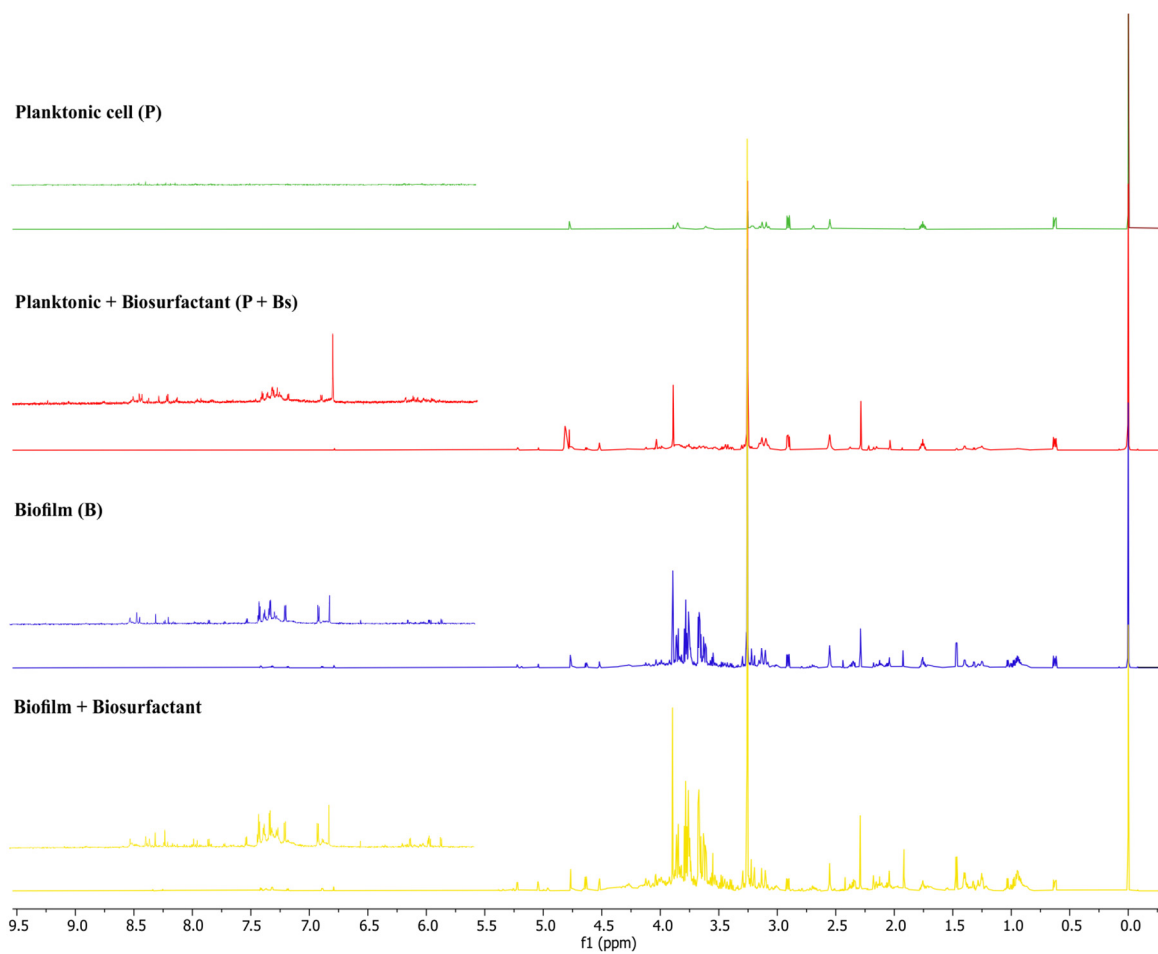
## Supplementary material



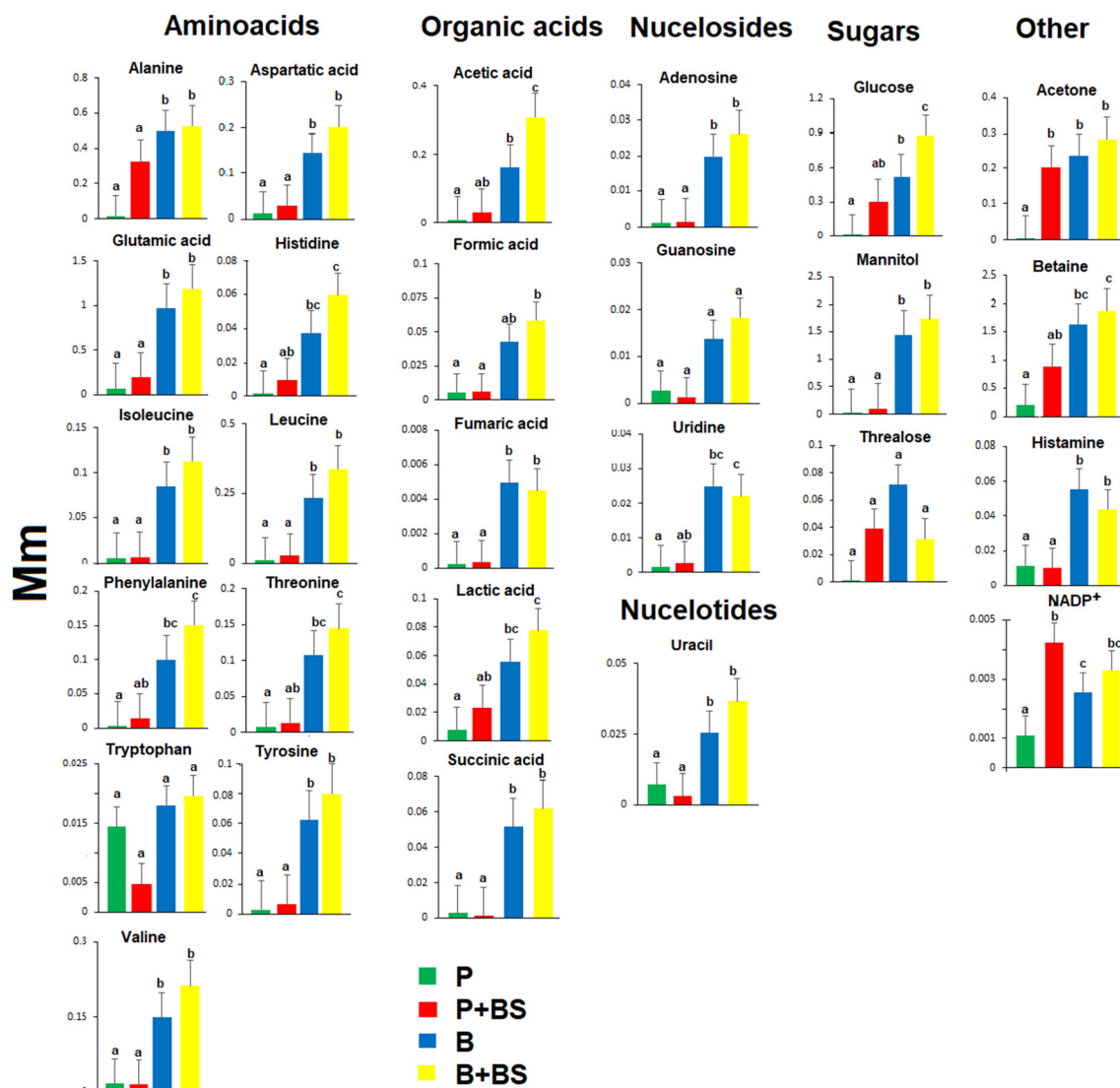
**Figure S1.** Phylogenetic tree analysis of *Pseudomonas stutzeri*. Based on the 16S rRNA gene using Neighbor-Joining (NJ) and Tamura-Nei distance model. The number above branches indicate bootstrap support values.



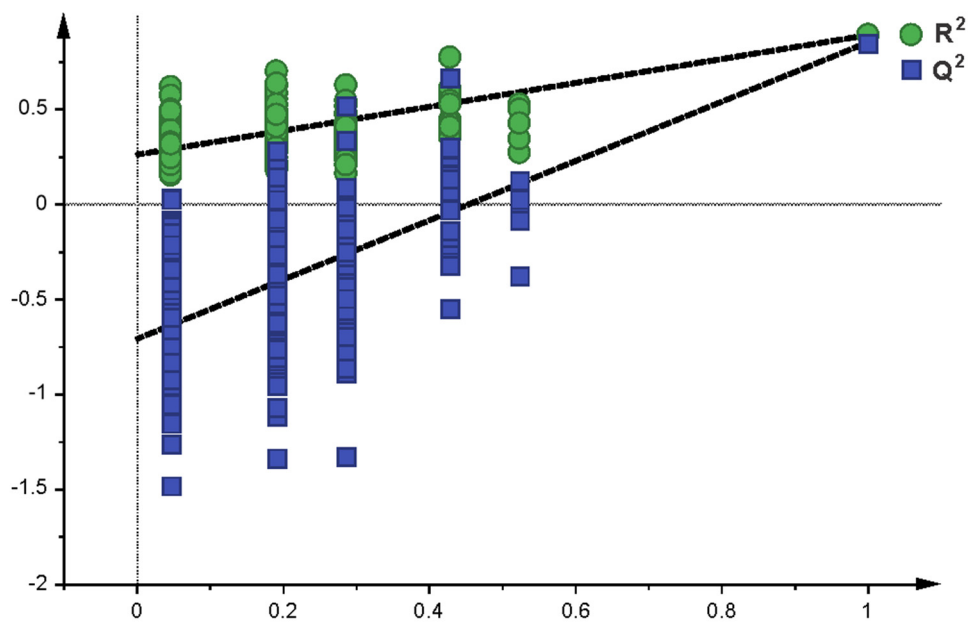
**Figure S2.**  $^1\text{H}$ -NMR spectrum obtained at 750 MHz from aqueous extracts of *Pseudomonas stutzeri*.



**Figure S3.**  $^1\text{H}$ -NMR spectrum of planktonic cells (P), biofilm (B) of *Pseudomonas stutzeri* and with the addition of crude biosurfactant of *B. niabensis* in both conditions (P+BS, B+BS).



**Figure S4.** Relative concentration of metabolites presents in planktonic cells (P), biofilm (B) of *Pseudomonas stutzeri* and with the addition of crude biosurfactant of *B. niabensis* in both conditions (P+BS, B+BS).



**Figure S5.** Cross-validation plot of the OPLS-DA model in the different conditions of culture of *Pseudomonas stutzeri*. Plaktonic cells (P), biofilm (B) and with the addition of crude biosurfactant of *B. niabensis* in both conditions (P+BS, B+BS). (Values intercepts,  $R^2 = 0.0, 0.25$ ;  $Q^2 = 0.0, -0.70$ ).