

## DIVING INTO THE MOUSE MACROPHAGE CYTOSKELETAL PROTEOME UPON THE INTERACTION WITH *CANDIDA ALBICANS*

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Host-pathogen studies open interesting opportunities for the search of new virulence determinants and new targets for antimicrobial therapies. To study the host response, we have chosen the murine macrophage cell line RAW 264.7, in the light of the importance of macrophages for optimal host protection against *C. albicans* systemic infections. We have performed a sub-proteomic study about the induced expression/repression of proteins from macrophages when they are in contact with *C. albicans*, based on DIGE.

RAW 264.7 cells were allowed to interact with *C. albicans* SC 5314 cells for 3h, and an important differential protein expression was observed in these macrophages compared to control ones in the 4 fractions analysed: organelle, cytoplasm, nucleus and cytoskeleton. Of 120 spots with differential protein expression, 21 proteins have been identified. Of these 120 spots, 70 were in cytoskeletal fraction, but only 3 spots were identified. The same sample was analyzed on LTQ mass spectrometer and the identifications showed that most of the proteins in this fraction were neither cytoskeletal nor related proteins. Thus, other cytoskeletal extraction protocols have been assayed, highly increasing the number of cytoskeletal proteins identified. This will allow us the study of the cytoskeletal proteins changes in macrophages during the interaction with *Candida albicans* using iTRAQ technology.