

**Zavod za molekularnu biologiju i Bakteriološka sekcija HMDa pozivaju  
Vas na predavanje**

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**Bioinformatics Approaches to Study Adaptive Strategies in UV-  
Resistant Microbial Extremophiles**

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Reactive oxygen species (ROS) produced in the mitochondria are a major cause of age-related, degenerative cell damage. The Keap<sub>1</sub>-Nrf<sub>2</sub> pathway controls the response to oxidative stress via Keap<sub>1</sub> ROS sensing, followed by binding of Nrf<sub>2</sub> to the antioxidant response element (ARE). While it is commonly associated with mammalian cells, Keap<sub>1</sub>-Nrf<sub>2</sub> pathway homology has been detected in *Caenorhabditis elegans* and has been postulated in bacteria. Based on these lines of evidence, we propose that microbial homologues of the Keap<sub>1</sub>-Nrf<sub>2</sub> pathway can be used as pharmacomimetic models to study the oxidative stress response in humans. In order to search for these microbial Keap<sub>1</sub>-Nrf<sub>2</sub> homologues, we have developed a novel bioinformatics tool for distant homology searching we call *DHSP*, and a taxonomic mapping tool to graphically display results from *DHAP* we have called *TaxMapper*. Results from data mining of microbial protein databases will be presented in this lecture.