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Identification of the Natural Substrate Pool of Mycobacterium Tuberculosis Chaperonins

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Mycobacterium tuberculosis (Mtb) is the most common fatal infectious agent. As anti-TB drugs have a traditional mode of action, Mtb becomes resistant to them. Therefore, it is necessary to create anti-TB medicines with a different mode of action. Chaperonins can be a potential target for the development of anti-TB medicines as they promote protein folding in the cell under both normal and stressful situations. Understanding Mtb chaperonins and their interactions with substrate proteins is essential for the development of this novel anti-TB antibiotics. The substrates of Mtb chaperonins (Chaperonin60.1 and Chaperonin60.2) were identified in this study. Mtb chaperonins were first cloned and expressed in Mtb H37Rv followed by co-immunoprecipitation (Co-IP) of the expressed cell lysates. Co-IP proteins were further analysed to identify the natural substrate proteins of those chaperonins using mass spectrometry (MS). The folding of natural substrate proteins needs to be observed to comprehend the chaperonin function of Mtb chaperonins. Purification of the substrate protein and chaperonins will be the next step in order to do in vitro chaperone-assisted protein folding investigations. The development of novel anti-TB medications will be facilitated by this molecular understanding of protein folding in Mtb.