The success of *Mycobacterium tuberculosis* (*M. tuberculosis*) as a highly adaptable human pathogen relies upon its ability to switch to dormancy or non-replicating persistence (NRP) and establish an infection despite the assaults of host’s immune system and hostile living microenvironment. The survival strategies employed by the pathogen depend on transcriptional reprogramming, metabolic alteration and development of phenotypic resistance to antimicrobial agents. Dormant mycobacteria are of particular interest; since they are believed to be associated with latent tuberculosis infection (LTBI) and persisting infections. One of the research priorities includes identifying the panoply of genes or pathways involved in dormancy that will progress our understanding on LTBI and also potentiate as candidate vaccines and biomarkers for diagnosis of *M. tuberculosis* infection.