Mycobacterium tuberculosis (Mtb), the etiologic agent of tuberculosis (TB), kills 1.5 million people a year. An estimated one-third of the human population harbors a latent TB infection (LTBI), an asymptomatic form of the disease. The dormant bacteria associated with LTBI are phenotypically resistant to most antibiotics, making LTBIs difficult to treat or cure. Most metabolic processes are reduced or absent in dormant Mtb, which limits LTBI enzyme targets. Yet Mtb viability in dormancy and during reactivation relies on enzymes that process fatty acids as an energy and carbon source. Moreover, lipid metabolism is central to all stages of Mtb pathogenesis. The Mtb esterases are critical lipid hydrolyzing enzymes, playing roles in cell wall remodeling, growth, division, nutrient acquisition, dissemination, and pathogenesis. There are approximately 40 esterases and treatment with a lipase inhibitor (e.g., Orlistat) inhibits the growth of non-replicating and replicating Mtb. All of these features make the Mtb esterases attractive targets for new drugs against both latent and active TB. We recently analyzed esterase activities in replicating, dormant, and reactivating cultures of Mtb using both activity-based probes (ABPs) and fluorogenic (“turn-on”) esterase substrates. Using mass-spectrometry based proteomics, we found 22 esterases. Among those, we identified five esterases that remained active in dormant Mtb using ABPs, and three of these were catalytically active in all three culture conditions. Fluorogenic probes additionally revealed additional esterases that were not identified by ABPs. Esterases with persistent activity are potential diagnostic biomarkers or therapeutic targets for Mtb-infected individuals with latent or active tuberculosis.