IDENTIFICATION AND CHARACTERIZATION OF PUTATIVE DRUG TARGET IN DRUG RESISTANT TUBERCULOSIS USING SUBTRACTIVE GENOMICS APPROACH

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Recently, drug-resistant tuberculosis is of great concern owing to lack of new drugs. Rapid identification of unique drug targets against Mycobacterium tuberculosis DKC2 strain is crucial. In silico subtractive genomics methods identified 230 essential non-homologous proteins. Druggability analysis revealed 27 potential targets, including WP_003899075.1 (Catalase-peroxidase), with high virulence and antibiotic resistance and physico-chemical analysis supported its stability. Structure-based modelling and validation confirmed WP_003899075.1 as a promising drug target which could be useful for new antitubercular compounds.