Deorphaning anti-tuberculosis compounds using chemogenomic approaches and data from the ChEMBL database

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Background:

The emergence of drug resistant strains of *Mycobacterium tuberculosis* (*Mtb*), the causative agent of tuberculosis (TB), calls for an urgent need for new drugs that have distinct mechanisms of action. To date, several thousands of active compounds against tuberculosis have been identified through high throughput screening (HTS). The challenge then rests identifying the molecular targets and characterising the mechanism of action of these actives.