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Exploration of Mycobacterium tuberculosis Structural Proteome: An In-silico Approach

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Highlights

- Exploration of pharmacophoric space via multiple-complex based pharmacophore modeling of *Mycobacterium tuberculosis* structural proteome.
- Highlight the liaisons between the pharmacophore models and the affinity of inhibitors for the off-targets within the proteome.
- Offer solutions to make a stringent hypothesis for a specific protein class to reduce its affinity for the off-targets.
- Upliftment of pharmacophore models and their subsequent utilization as an efficient pharmaceutical filter to design a coherent inhibitor strategy.

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