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

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PII: S0022-5193(17)30528-3
DOI: 10.1016/j.jtbi.2017.11.021
Reference: YJTBI 9277

To appear in: *Journal of Theoretical Biology*

Received date: 20 September 2016
Revised date: 19 July 2017
Accepted date: 28 November 2017

Please cite this article as: Mohsin Yousuf Lone , Sivakumar Prasanth Kumar , Mohd Athar , Prakash Chandra Jha , Exploration of Mycobacterium tuberculosis Structural Proteome: An In-silico Approach, *Journal of Theoretical Biology* (2017), doi: 10.1016/j.jtbi.2017.11.021

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.