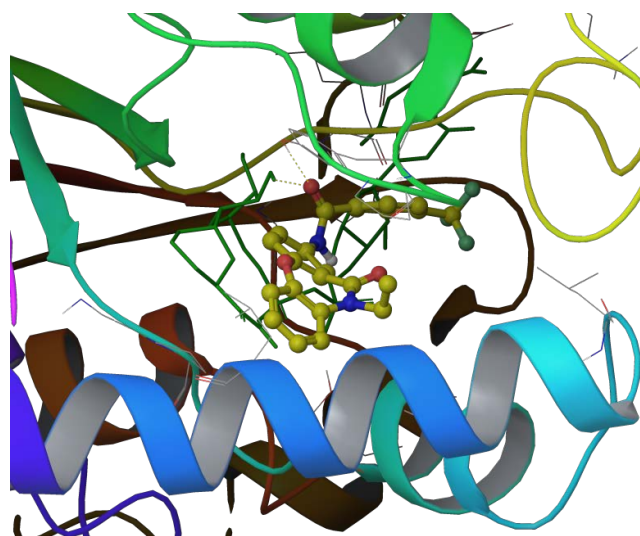


## Antituberculosis library

Designed with receptor-based approach, this library comprises potential drug candidates possessing activity towards InhA enzyme - specific protein of *M.tuberculosis* that is responsible for cell wall synthesis of the bacteria, but is not present in mammals. The structure of InhA protein and binding mode of known inhibitors were studied based on the analysis of crystal structure records in PDB. This has given us a detailed understanding of the protein-ligand interaction mechanism.

At the next step, Life Chemicals' in-stock compound collection was processed according to ADME requirements; also, all undesirable groups were filtered out. Resulted drug-like set of compounds was screened by molecular docking using Glide program (Schrödinger software). 3FNH and 2H7I PDB entries were selected for the docking studies due to the most favorable ligand binding and high resolution of the crystal structures. The referent set of active ligands [1,2]

was used for evaluation of the docking procedure. The presence of the  $\text{NAD}^+$  coenzyme was taken into account in virtual screening as it is involved into a ligand binding. After the docking, the compounds have been selected by ligand efficacy and comparison with binding mode of the referent inhibitors. A set of 3,625 potential antituberculosis agents capable of binding with InhA protein was obtained (Fig.1).



**Fig. 1.** Ligand F2269-0132 forms strong hydrogen bond with Tyr158 and protein coenzyme  $\text{NAD}^+$ . High hydrophobic interaction observed between fused aromatic rings and large hydrophobic pocket of InhA.

### References

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To download a file with compound structures for this library, please follow this link:

[http://www.lifechemicals.com/downloads/Screening\\_Libs/13056/antituberculosis](http://www.lifechemicals.com/downloads/Screening_Libs/13056/antituberculosis)