

A unique Mycobacterium ESX-1 protein Inhibitors Identified by Virtual Screening and 4D Fingerprints

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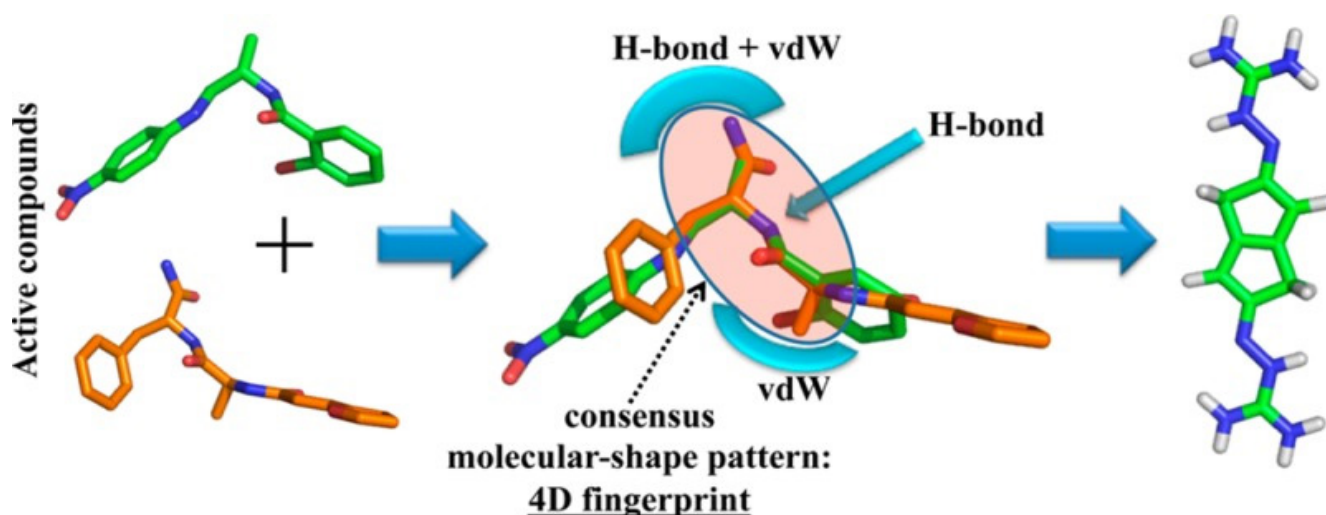
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Abstract

The rise of drug-resistant Mycobacterium tuberculosis lends urgency to the need for new drugs for the treatment of tuberculosis (TB). The identification of a serine protease, mycosin protease-1 (MycP1), as the crucial agent in hydrolyzing the virulence factor, ESX-secretion-associated protein B (EspB), potentially opens the door to new tuberculosis treatment options. Using the crystal structure of mycobacterial MycP1 in the apo form, we performed an iterative ligand- and structure-based virtual screening (VS) strategy to identify novel, nonpeptide, small-molecule inhibitors against MycP1 protease. Screening of ~485 000 ligands from databases at the Genomics Research Institute (GRI) at the University of Cincinnati and the National Cancer Institute (NCI) using our VS approach, which integrated a pharmacophore model and consensus molecular shape patterns of active ligands (4D fingerprints), identified 81 putative inhibitors, and in vitro testing subsequently confirmed two of them as active inhibitors. Thereafter, the lead structures of each VS round were used to generate a new 4D fingerprint that enabled virtual rescreening of the chemical libraries. Finally, the iterative process identified a number of diverse scaffolds as lead compounds that were tested and found to have micromolar IC₅₀ values against the MycP1 target. This study validated the efficiency of the SABRE 4D fingerprints as a means of identifying novel lead compounds in each screening round of the databases. Together, these results underscored the value of using a combination of in silico iterative ligand- and structure-based virtual screening of chemical libraries with experimental validation for the identification of promising structural scaffolds, such as the MycP1 inhibitors.



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Introduction

Mycobacterium tuberculosis, the agent causing tuberculosis (TB), is responsible for significant worldwide morbidity and mortality, estimated at more than 1.3 million deaths in 2012 according to the World Health Organization.¹ This ancient but persistent disease still lacks effective antimicrobial treatment regimens, particularly in cases of multi-drug-resistant tuberculosis.^{2,3} An attractive target for development of new antimicrobials is the recently identified mycobacterial protein-export machinery.^{4–6} M. tuberculosis relies on specialized ESX secretion systems, also called Type VII Secretion (T7S) Systems, to evade the human immune system and promote bacterial survival within host cells,^{7,8} and it possesses five gene clusters that encode sets of conserved proteins comprising the ESX systems.⁹ Each of these gene clusters, called ESX-1 through ESX-5, includes essential mycosin proteases, which are named MycP1 through MycP5, respectively.

The mycosins are membrane-bound serine proteases belonging to the subtilisin family of proteases.^{10,11} The crystal structures of MycP1 and MycP3 revealed that these mycosins are characterized by a relatively deep, broad, substrate-binding groove and by the absence of an autoinhibitory propeptide, making them the first subtilisins that do not undergo post-translational processing.^{12–14} MycP1 is known to hydrolyze the important virulence factor ESX secretion-associated protein B (EspB).^{15–17} MycP1 cleaves the unstructured C-terminal part of EspB, possibly activating EspB for phospholipid binding.¹⁸ Most importantly, inactivation of MycP1 leads to decreased virulence of M. tuberculosis and increased survival in the mouse model of TB.¹⁷ These data, combined with the availability of MycP1 crystallographic structures, make MycP1 an attractive target for development of antimicrobial compounds for the treatment of TB.^{19,20} The structural characteristics of the MycP1 substrate-binding pocket differ substantially from known subtilisins whose structures were solved with bound inhibitors,²¹ and the commercially available subtilisin inhibitors and protease inhibitor cocktails displayed little or no inhibition of MycP1 (Supporting Information Table 1).

In vitro High Throughput Screening (HTS) in conjunction with in silico virtual screening represent complementary methods for the identification of MycP1 inhibitors. Although HTS alone has been used successfully to identify new leads in drug discovery, it remains a costly and time-consuming process. Various computational approaches are available at present to complement HTS technologies, including the popular, virtual screening (VS) techniques.^{22–25} VS consists of approaches that either

take the structure of the target protein into account (structure-based screening) or rely solely on structures of known bioactive molecules (ligand-based screening). The ligand- and structure-based VS strategies are not mutually exclusive and are often used in parallel. We and others have reported the successful application of these VS methods for lead structure identification,^{26–29} and many VS software packages are available,^{30–32} as summarized by Reddy.³³ Although the algorithms for these VS methods exploit different types of structural “fingerprints” and scoring functions, their performance varies significantly depending on the specific targets.^{34–36}

As part of an integrated, reiterative program of virtual in silico lead identification, in vitro screening, and laboratory synthesis, we developed two approaches that enhance the effectiveness of the combined ligand- and structure-based VS and hold promise for the development of new classes of MycP1 inhibitors. Previously, we reported an efficient 3D shape-based similarity algorithm including an effective 3D shape-fitting procedure and a robust scoring function (HWZ score).³⁷ We also improved the VS algorithm using an enhanced molecular shape-density model called Shape Approach Based Routines Enhanced (SABRE),³⁷ and we applied this algorithm to a number of medically relevant proteins.^{38–42} SABRE is unique in that it takes advantage of the structural features of known ligands to generate a consensus molecular-shape pattern (i.e., a “4D fingerprint”) that filters out unacceptable candidates and identifies desired candidates that fit in the binding pocket. The successful performance of SABRE^{37,43,44} in ranking screened compounds for the 40 databases of the Directory of Useful Decoys (DUD) prompted us to apply this method to the challenging MycP1 target for which no inhibitors have been thus far reported.

We now report the successful application of this ligand- and structure-based virtual screening approach in the discovery of inhibitors that target the active site of the MycP1 protease. Four compounds were identified by SABRE that showed inhibitory activity against MycP1 with IC₅₀ values in the micromolar range and that provide diverse scaffolds as starting points for the development of small-molecule antagonists of MycP1. This study further validated the SABRE 4D fingerprint algorithm as a means of identifying potential inhibitors and providing departure points for laboratory synthesis.

Methods

To identify potential inhibitors of MycP1 protease, we employed VS, according to the flowchart in Figure 1, using a merged compound library from GRI and the NCI downloaded from the ZINC

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database.⁴⁵ The structure-based VS (docking) study utilized the recently reported X-ray structure of *M. thermoresistibile* MycP1 protease (PDB ID: 4HVL).¹² We generated multiple conformations of each ligand in the database using OMEGA (OpenEye Scientific Software).^{46–48} Atom typing, energy calculations, and geometry optimization in OMEGA were performed using the Merck Molecular Force Field (MMFF). The maximum allowed number of conformations per compound was 200, and the energy window, which was the value used to discard high-energy conformations, was set at 10 kcal/mol.

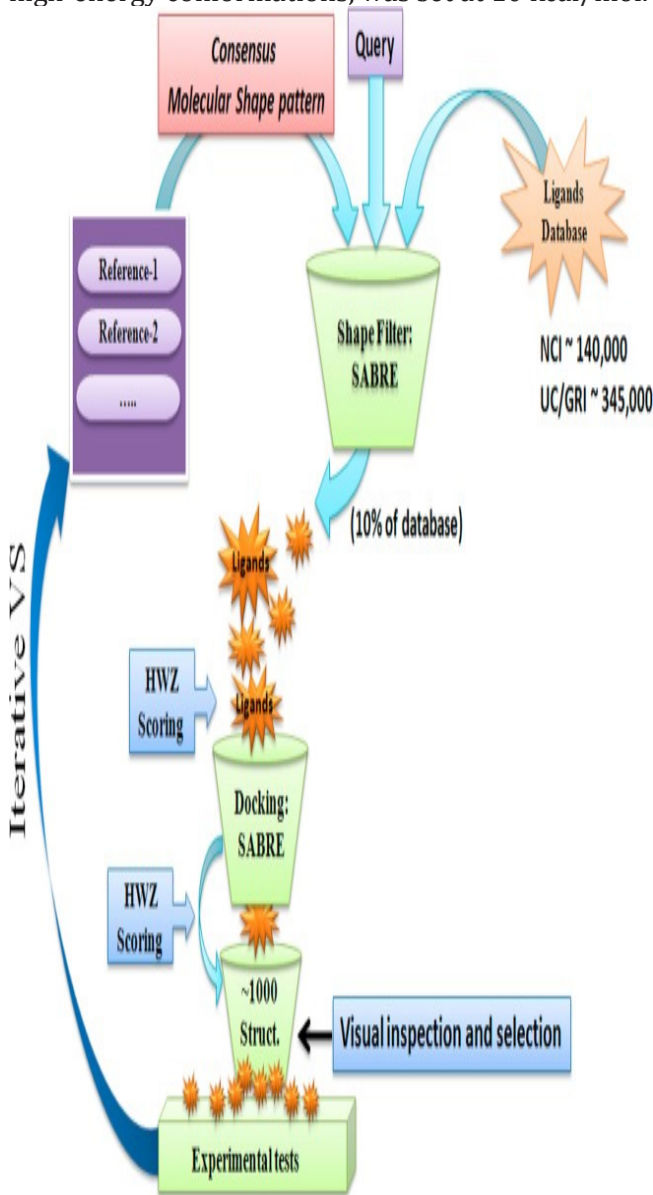


Figure 1: Flowchart of the VS process.

Ligand Shape-Based Virtual Screening

The ligand 3D-shape-based similarity method of SABRE was used as the first filter in the VS strategy.^{37,43,44} Briefly, the shape-based VS method takes into account both the structural diversity of each ligand and the HWZ scoring function. Thus, the superimposition of molecules A and B is scored according to the shape-density overlap VAB between

the query (molecule A) with shape-density VA and testing structure (B) with shape-density VB. Subsequently, the ligands are ranked according to a uniform scoring function, denoted by Hamza-Wei-Zhan (HWZ) score for convenience.³⁷

The coefficients a_k , b_k , and c_k have been recalibrated from the previous version.

The VS approach includes two stages: the calculation of the optimal coefficients of the shape-density function using a set of known lead compounds and the utilization of these optimal coefficients during the automated ligand/structure shape-based screening of candidate structures. The active structures are ranked according to how well they complement the shape of the binding site and by the degree of differences in molecular shape between the active ligand and inactive (decoy) molecules. SABRE builds a consensus molecular-shape pattern (i.e., a 4D fingerprint) defined by the coefficients $[c_1, c_2, \dots, c_n]$ using a set of active ligands, in which the maximum diversity of pharmacophores is taken into account during the screening of the compound library.^{43,44}

Unlike other ligand based shape-overlapping methods,^{36,49,50} our approach efficiently detects the key pharmacophore groups of the active ligands responsible for binding to the target. The main improvement in our method lies with consideration of “virtual” similar inactive structures (decoys) during the consensus molecular shape pattern detection process. After similarity scoring, the selected structures are further ranked according to the shape complementarity of the receptor-binding site.

In the SABRE algorithm, the shape-density model is enhanced and defined as a linear combination of weighted atomic Gaussian functions.³⁷ Thus, the molecular shape-density is the sum of all individual weighted pharmacophore densities, and the molecular volume can be rewritten as where V_{kpharm} is the volume of the pharmacophore k .

The optimal coefficients C_k are determined by iteratively adjusting the coefficients using the set of known active ligands $\{A_i\}$ and “virtual” decoy structures $\{B_i\}$ (virtual decoys are chemically possible compounds that are not necessarily synthetically feasible) until they satisfy these two criteria: for $A \in \{A_i\}$ The algorithm builds an efficient consensus molecular-shape pattern in which the optimal coefficients $\{C_k\}$ define the 4D fingerprint of the entire set of active ligands and take into account the structural similarity and chemical features of inactive structures (decoys).^{37,44} Therefore, the “4D fingerprint” encodes the (3D) shapes of the known active ligand structures in their multi conformational states (1D).

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