In silico structure-based screening of versatile P-glycoprotein inhibitors using polynomial empirical scoring functions

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Abstract: P-glycoprotein (P-gp) is an ATP (adenosine triphosphate)-binding cassette transporter that causes multidrug resistance of various chemotherapeutic substances by active efflux from mammalian cells. P-gp plays a pivotal role in limiting drug absorption and distribution in different organs, including the intestines and brain. Thus, the prediction of P-gp–drug interactions is of vital importance in assessing drug pharmacokinetic and pharmacodynamic properties. To find the strongest P-gp blockers, we performed an in silico structure-based screening of P-gp inhibitor library (1,300 molecules) by the gradient optimization method, using polynomial empirical scoring (POLSCORE) functions. We report a strong correlation ($r^2=0.80$, $F=16.27$, $n=6$, $P<0.0157$) of inhibition constants ($K_{i_{exp}}$ or $pK_{i_{exp}}$; experimental $K_i$ or negative decimal logarithm of $K_{i_{exp}}$) converted from experimental $IC_{50}$ (half maximal inhibitory concentration) values with POLSCORE-predicted constants ($K_{i_{POLSCORE}}$ or $pK_{i_{POLSCORE}}$), using a linear regression fitting technique. The hydrophobic interactions between P-gp and selected drug substances were detected as the main forces responsible for the inhibition effect. The results showed that this scoring technique might be useful in the virtual screening and filtering of databases of drug-like compounds at the early stage of drug development processes.

Keywords: ATP-binding cassette transporter, P-gp inhibitors, multidrug resistance, molecular docking, POLSCORE

Introduction
P-glycoprotein (P-gp) is a member of the ATP (adenosine triphosphate)-binding cassette multidrug transporter superfamily. It mediates the removal of xenobiotic agents from living cells by a P-gp-mediated efflux mechanism, a major cause of multidrug resistance (MDR). P-gp plays an important role in limiting drug absorption and distribution in different organs, including the intestines and the brain (blood–brain barrier), where it is extensively distributed and expressed. P-gp is a 170 kDa transmembrane protein, which includes cytosolic nucleotide-binding domain together with N-terminal and C-terminal halves. Each half in turn is comprised of membrane spanning and transmembrane domains.

P-gp inhibitors are mainly weakly amphiphilic or hydrophobic substances such as chemotherapeutics, steroid hormones, different antibiotics, and anti-HIV (anti-human immunodeficiency virus) protease inhibitors. Since P-gp can affect the pharmacokinetics and pharmacodynamics of its substrates, increasing attempts were being made to search for potential P-gp inhibitors at the early stage of drug discovery and development processes.

A number of in vitro assays for P-gp-oriented drug screening, such as cell-based transwell transport, radioactivity-labeled ligand binding, and drug permeability,
have been largely utilized to identify the potential P-gp inhibitor candidates\textsuperscript{10} and assess P-gp–drug interactions.\textsuperscript{11} However, due to their expense and time, the in vitro methods are not entirely suitable for the screening of large databases of drug-like chemical compounds. Primarily, these methods are usually used at the later stages of drug development processes, after the thorough structure-based virtual screening of extensive databases of bioactive, drug-like, small molecules. Therefore, in silico screening, based on different algorithms implemented for molecular docking, to predict P-gp inhibitors has paved the road to a rational drug design and screening process.\textsuperscript{12–14} On the other hand, to harness the discovery of the strongest P-gp blockers, high-resolution, crystallographic molecular structures of P-gp would improve a molecular docking precision for in silico prediction models.

Although a variety of molecular docking models for P-gp inhibitors have been successfully used for prediction of receptor–ligand interactions,\textsuperscript{14–16} there is no general scoring function regarding the filtration and selection of the best hits. The empirical scoring functions, such as those used in AutoDock\textsuperscript{17} (Scripps Research Institute, San Diego, CA, USA), AutoDock Vina\textsuperscript{18} (Scripps Research Institute), and others are most widely applied to estimate the Gibbs free energy of binding (\textit{ΔG}).\textsuperscript{19–21} They are based on the counting of the number of hydrophobic and hydrophilic contacts and H-bonds between the P-gp receptor and its ligand.\textsuperscript{22} Therefore, to find the strongest P-gp blockers, we performed in silico structure-based screening of a P-gp inhibitor database via gradient optimization method, using the appropriate scoring techniques of AutoDock Vina and polynomial empirical scoring (POLSCORE) functions to calculate binding affinities and to correlate them to the experimentally determined half maximal inhibitory concentration (IC\textsubscript{50}) values.

**Computational methods**

The electron diffraction of murine P-gp as a holo-structure (3G60) at 3.8 Å resolution with a cyclic-tris-(R)-valineselenazole (QZ59-RRR) ligand\textsuperscript{3} was retrieved from the Protein Data Bank as a PDB file. The P-gp molecule was processed for the ligand extraction and subjected to the initial molecular dynamics refinement by using the FG-MD (Fragment-Guided Molecular Dynamics) server.\textsuperscript{23} The VADAR (Volume, Area, and Dihedral Angle Reporter) server\textsuperscript{24} was implemented for stereochemical validation of the P-gp molecule to investigate the \(\phi\)–\(\psi\) dihedral angles in a Ramachandran plot. Altogether, observed statistics showed that 70\% and 23\% of all residues were in core and allowed regions before, 82\% and 12\% after the molecular dynamics refinement. The expected values for the comparison were 90\% and 7\%, respectively, for the same regions obtained elsewhere, from the literature.\textsuperscript{25,26} The P-gp inhibitor database included 1,300 molecules, which were assembled by the ADME (absorption, distribution, metabolism, and excretion) research team from the Functional Nano and Soft Materials Laboratory (FUNSOM, Suzhou, People’s Republic of China) and distributed through the scientific community for virtual screening and analysis.\textsuperscript{27}

Prior to the virtual screening procedure, PyRx software (Scripps Research Institute)\textsuperscript{28} was used to optimize the dataset. Gasteiger charges were added, and polar hydrogen atoms were assigned. The rotatable bonds were set up, and SDFs (structure-data files) were converted into PDBQT (Protein Data Bank, Partial Charge [Q], and Atom Type [T]) format.

The QZ59-RRR-associated binding site was reconstructed as a visual representation of the solvent-excluded molecular surface, known as the Connolly surface,\textsuperscript{29,30} by MOE 2009.10 (Chemical Computing Group, Montreal, Canada) modeling software. The solid molecular surface was generated with 1.4 Å of probe sphere radius and within 4.5 Å from the ligand atoms (Figure 1).

Rigid-flexible molecular docking was applied to the center of the QZ59-RRR-associated binding cavity with the AutoDock Vina docking engine,\textsuperscript{18} adopted for a structure-based virtual screening via the iDOCK (Department of Computer Science and Engineering, Chinese University of Hong Kong, Hong Kong) modification,\textsuperscript{31} using the following Cartesian coordinates: \(x = 19.11\ \text{Å}\), \(y = 52.37\ \text{Å}\), and \(z = -0.30\ \text{Å}\). The docking grid with a dimension size of 30 Å \(\times\) 30 Å \(\times\) 30 Å was used in the study. The AutoDock Vina output results

![Figure 1](https://www.dovepress.com/)

**Abbreviation:** QZ59-RRR, cyclic-tris-(R)-valineselenazole.
represented the docking scores as ΔG values. They were further converted to the predicted inhibition constants (Ki_{pred}). The Ki_{pred} values for analyzed docking poses were calculated from the ΔG parameters as follows:

\[
\Delta G = RT \ln(K_{i_{pred}}),
\]

\[
K_{i_{pred}} = e^{\frac{\Delta G}{R T}},
\]

where R (gas constant) is 1.98 cal*(mol*K)^{-1}, and T (room temperature) is 298.15 Kelvin.

The ΔG_1−ΔG_3 binding affinity predictions were made for a human homology model, a mouse 3G60 model, and a mouse 3G61 model of P-gp using the same docking method and support vector machine algorithm integrated into the Althotas virtual laboratory webserver (Virtua Drug Ltd, Budapest, Hungary). The affinities were further converted in a similar fashion to their corresponding inhibition constants (Ki[pKi_i]−Ki_i[pKi_i]).

The docked conformations were ranked using the POLSCORE algorithm based on 25 POLSCORE functions to evaluate binding affinity from the P-gp−ligand complexes by calculated pKi values (pKi_{POLSCORE}). The thorough scoring calibration has been previously performed to use geometric parameters, calculated from the atomic coordinates, to evaluate the experimental pKd (pKi) values as closely as possible to a training set composed of hundreds of co-crystallized protein–ligand complexes. The weights obtained from this training set were used to build appropriate POLSCORE functions.

The IC_{50}−to-Ki converter was used to compute Ki values from experimentally determined IC_{50} values for inhibitors of proteins and enzymes that obey classic Michaelis-Menten kinetics of protein–ligand interactions. The IC_{50} values were obtained from the study of Keogh and Kunta as determined when investigating the inhibition of human P-gp transport of 30 nM [3H]-digoxin. The values were converted into the experimental inhibition constant values (Ki_{exp} or pKi_{exp}) according to the protein−ligand interaction equation for competitive species:

\[
K_{i_{exp}} = \frac{IC_{50}}{L_{50} + P_0 + K_d + 1}.
\]

where P_0 is free protein at 0% inhibition (positive control), L_{50} is free ligand at 50% inhibition, IC_{50} is free inhibitor at 50% inhibition, and K_d is the dissociation constant. The default parameters for protein concentration (P =0.03 μM) and dissociation constant (K_d =0.0179 μM) were used. The ligand concentration (L =2.0 μM) was specified according to the GF120918 compound's ability to achieve the entire P-gp inhibition.

Molecular graphics and visualization were performed with the LigPlot+ program (EMBL-EBI, Wellcome Trust Genome Campus, Hinxton, UK) in order to build two-dimensional interaction diagrams from three-dimensional coordinates. Statistical analyses were performed using a linear regression analysis, followed by graphic representation using GraphPad Prism v.4 (GraphPad Software, San Diego, CA, USA).

Results and discussion

Our search for a strong inhibitor focused on an inhibitor that allows for better intestinal drug absorption and blood–brain barrier transfer after inhibition. We wanted to improve inhibitor selection by extensive in silico prescreening. For this, we considered the P-gp inhibitor dataset, including 1,300 molecules, among which 796 molecules (61.2%) were P-gp inhibitors, and 504 molecules (38.8%) were P-gp non-inhibitors (Supplementary material 1). The experimental data were retrieved and compiled from 104 pieces of published literature to increase the molecular diversity of the database. Data from Ramu and Ramu(34,35) (347 molecules) and Bakken and Jun(36) (609 molecules) were important sources of the P-gp inhibitor dataset. The experimental ratio for MDR reversal agents was used as a determining parameter of whether a compound is an inhibitor. Since the holo-P-gp structure does not bind ligands, an inward-facing apo-P-gp conformation was chosen as a reliable drug-binding model. This conformation represents an initial stage of the transport cycle that is competent for inhibitor binding. Therefore, we screened the P-gp inhibitor database against the binding site associated with the removed QZ59-RRR ligand of murine P-gp protein by calculating the Gibbs free energy of binding. A standard rigid-flexible AutoDock Vina technique produced two main results: a particular conformational sampling as a docking pose of the ligand molecule within the binding site, and an affinity (ΔG) describing the receptor–ligand interaction strength. All docking poses were ranked according to their ΔG values, which ranged from −13.904 to −1.682 kcal*mol^{-1} (Supplementary material 2). To detect the false-positive docking results, we selected the top-ranked 120 compounds with minimal ΔG values, ranging from −13.904 to −10.002 kcal*mol^{-1}. Of these, 106 (88.3%) were P-gp inhibitors, with a mean value of −10.62 kcal*mol^{-1} and a standard deviation of 0.57 kcal*mol^{-1}, and 14 molecules (11.7%) were P-gp non-inhibitors, with a mean value of −10.74 kcal*mol^{-1} and a standard deviation of 0.96 kcal*mol^{-1} (Figure 2A). To detect the false-negative docking results, we selected the bottom-ranked
150 compounds with maximal ΔG values from −6.998 to −1.682 kcal*mol$^{-1}$. Of these, 40 (26.7%) were P-gp inhibitors, with a mean value of −6.58 kcal*mol$^{-1}$ and a standard deviation of 0.37 kcal*mol$^{-1}$, and 110 molecules (73.3%) were P-gp non-inhibitors, with a mean value of −6.28 kcal*mol$^{-1}$ and a standard deviation of 0.77 kcal*mol$^{-1}$ (Figure 2B). These results indicated that in almost 90% of top-ranked compounds, virtual screening worked better at predicting the P-gp inhibitory potencies than separating non-inhibitors for bottom-ranked molecules (substances with high ΔG values), which might be P-gp substrates with a propensity to attach to the P-gp binding cavity. In addition, the area under the receiver operating characteristic curve (AUC) was also examined since the true positive and the true negative are known in this study.

The P-gp inhibitor D559 and polypeptide antibiotic actinomycin D were associated with the best binding modes, which represent the minimal ΔG values: −13.904 and −13.126 kcal*mol$^{-1}$. Of these, 40 (26.7%) were P-gp inhibitors, with a mean value of −6.58 kcal*mol$^{-1}$ and a standard deviation of 0.37 kcal*mol$^{-1}$, and 110 molecules (73.3%) were P-gp non-inhibitors, with a mean value of −6.28 kcal*mol$^{-1}$ and a standard deviation of 0.77 kcal*mol$^{-1}$ (Figure 2B). These results indicated that in almost 90% of top-ranked compounds, virtual screening worked better at predicting the P-gp inhibitory potencies than separating non-inhibitors for bottom-ranked molecules (substances with high ΔG values), which might be P-gp substrates with a propensity to attach to the P-gp binding cavity. In addition, the area under the receiver operating characteristic curve (AUC) was also examined since the true positive and the true negative are known in this study. The result showed a good performance for the AutoDock Vina docking run, with an AUC value of 0.62 and a standard error of 0.048 (P<0.032); while a random selection performance presented with a 0.5 AUC value (Figure 3). The P-gp inhibitor D559 and polypeptide antibiotic actinomycin D were associated with the best binding modes, which represent the minimal ΔG values: −13.904 and −13.126 kcal*mol$^{-1}$. These results indicated that in almost 90% of top-ranked compounds, virtual screening worked better at predicting the P-gp inhibitory potencies than separating non-inhibitors for bottom-ranked molecules (substances with high ΔG values), which might be P-gp substrates with a propensity to attach to the P-gp binding cavity. In addition, the area under the receiver operating characteristic curve (AUC) was also examined since the true positive and the true negative are known in this study. The result showed a good performance for the AutoDock Vina docking run, with an AUC value of 0.62 and a standard error of 0.048 (P<0.032); while a random selection performance presented with a 0.5 AUC value (Figure 3).

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Table 1  Predicted (pKi\textsubscript{POLSCORE}) parameters for P-gp selected inhibitors calculated from POLSCORE functions

<table>
<thead>
<tr>
<th>Compound</th>
<th>Rank</th>
<th>pKi\textsubscript{POLSCORE}</th>
<th>HC</th>
<th>VdW</th>
<th>DE</th>
</tr>
</thead>
<tbody>
<tr>
<td>GF120918</td>
<td>8</td>
<td>9.09</td>
<td>1261.77</td>
<td>-976.08</td>
<td>12.5</td>
</tr>
<tr>
<td>Itraconazole</td>
<td>224</td>
<td>7.92</td>
<td>1179.65</td>
<td>-1046.45</td>
<td>17.5</td>
</tr>
<tr>
<td>Ketaconazole</td>
<td>150</td>
<td>8.59</td>
<td>1193.98</td>
<td>-872.73</td>
<td>10.0</td>
</tr>
<tr>
<td>Astemizole</td>
<td>96</td>
<td>8.09</td>
<td>1050.91</td>
<td>-789.02</td>
<td>8.0</td>
</tr>
<tr>
<td>Quinidine</td>
<td>516</td>
<td>7.49</td>
<td>965.38</td>
<td>-640.29</td>
<td>9.5</td>
</tr>
<tr>
<td>Verapamil</td>
<td>1104</td>
<td>7.42</td>
<td>940.09</td>
<td>-747.46</td>
<td>11.5</td>
</tr>
</tbody>
</table>

Abbreviations: DE, deformation effect; HC, hydrophobic contact; P-gp, P-glycoprotein; pKi, negative decimal logarithm of inhibition constant; POLSCORE, polynomial empirical scoring; VdW, Van der Waals forces (energy).

Table 2  Experimental (pKi\textsubscript{exp}) and predicted (pKi\textsubscript{pred}) parameters for selected P-gp inhibitors calculated from IC\textsubscript{50} and ΔG values

<table>
<thead>
<tr>
<th>Compound</th>
<th>IC\textsubscript{50} (μM)</th>
<th>pH\textsubscript{IC\textsubscript{50}}</th>
<th>Ki\textsubscript{exp} (μM)</th>
<th>pKi\textsubscript{exp}</th>
<th>ΔG (kcal/mol)</th>
<th>pKi\textsubscript{pred}</th>
</tr>
</thead>
<tbody>
<tr>
<td>GF120918</td>
<td>0.18±0.06</td>
<td>6.74</td>
<td>0.001</td>
<td>9.0</td>
<td>-11.8</td>
<td>8.68</td>
</tr>
<tr>
<td>Itraconazole</td>
<td>0.95±0.28</td>
<td>6.02</td>
<td>0.008</td>
<td>8.09</td>
<td>-9.6</td>
<td>7.06</td>
</tr>
<tr>
<td>Ketaconazole</td>
<td>1.34±0.28</td>
<td>5.87</td>
<td>0.012</td>
<td>7.92</td>
<td>-9.8</td>
<td>7.21</td>
</tr>
<tr>
<td>Astemizole</td>
<td>2.27±0.54</td>
<td>5.64</td>
<td>0.02</td>
<td>7.69</td>
<td>-10.1</td>
<td>7.34</td>
</tr>
<tr>
<td>Quinidine</td>
<td>9.40±2.98</td>
<td>5.03</td>
<td>0.083</td>
<td>7.08</td>
<td>-8.7</td>
<td>6.40</td>
</tr>
<tr>
<td>Verapamil</td>
<td>8.07±3.53</td>
<td>5.09</td>
<td>0.071</td>
<td>7.15</td>
<td>-8.03</td>
<td>5.91</td>
</tr>
</tbody>
</table>

Note: IC\textsubscript{50} values presented as mean ± standard deviation.

Abbreviations: ΔG, Gibbs free energy of binding; Ki\textsubscript{exp}, experimental inhibition constant; IC\textsubscript{50}, half maximal inhibitory concentration; pH\textsubscript{IC\textsubscript{50}}, negative decimal logarithm of half maximal inhibitory concentration; P-gp, P-glycoprotein; pKi, negative decimal logarithm of inhibition constant; pred, predicted.
Table 3 Predicted (pKi₁–pKi₃) parameters for selected P-gp inhibitors calculated from ΔGᵢ–ΔGᵢ values

<table>
<thead>
<tr>
<th>Compound</th>
<th>ΔGᵢ (kcal/mol⁻¹)</th>
<th>pKiᵢ</th>
<th>ΔGᵢ (kcal/mol⁻¹)</th>
<th>pKiᵢ</th>
<th>ΔGᵢ (kcal/mol⁻¹)</th>
<th>pKiᵢ</th>
</tr>
</thead>
<tbody>
<tr>
<td>GF120918</td>
<td>−11.1</td>
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<td>−10.9</td>
<td>8.02</td>
<td>−10.6</td>
<td>7.79</td>
</tr>
<tr>
<td>Itraconazole</td>
<td>−11.5</td>
<td>8.46</td>
<td>−9.2</td>
<td>6.77</td>
<td>−10.0</td>
<td>7.36</td>
</tr>
<tr>
<td>Ketoconazole</td>
<td>−10.5</td>
<td>7.72</td>
<td>−8.9</td>
<td>6.55</td>
<td>−8.7</td>
<td>6.4</td>
</tr>
<tr>
<td>Astemizole</td>
<td>−11.5</td>
<td>8.46</td>
<td>−9.7</td>
<td>7.14</td>
<td>−9.3</td>
<td>6.84</td>
</tr>
<tr>
<td>Quinidine</td>
<td>−9.1</td>
<td>6.69</td>
<td>−8.1</td>
<td>5.96</td>
<td>−8.2</td>
<td>6.03</td>
</tr>
<tr>
<td>Verapamil</td>
<td>−9.2</td>
<td>6.77</td>
<td>−7.0</td>
<td>5.15</td>
<td>−6.8</td>
<td>5.0</td>
</tr>
</tbody>
</table>

Abbreviations: ΔG, Gibbs free energy of binding; Ki, inhibition constant; P-gp, P-glycoprotein; pKi, negative decimal logarithm of inhibition constant.

**Figure 4** Relationship between experimental (pKiᵢ) and predicted pKi values using linear regression analysis to measure correlation strength for examined chemical compounds. The predicted values were calculated from the iDOCK runs (Department of Computer Science and Engineering, Chinese University of Hong Kong, Hong Kong) (pKiᵢ₁) and POLSCORE (pKiᵢPOLSCORE) (A and B). The Althotas virtual laboratory webserver (Virtua Drug Ltd, Budapest, Hungary) was used to estimate the inhibition constants (pKiᵢ₁–pKiᵢ₃) applying the human homology and mouse P-gp models, respectively (C–E).

Abbreviations: pKi, negative decimal logarithm of inhibition constant; pred, predicted; POLSCORE, polynomial empirical scoring; P-gp, P-glycoprotein.
Interestingly, both important Phe724 and Val978 residues are present in the interaction. It has been previously shown that these residues in mice and Phe728/Val982 in humans are playing pivotal roles in P-gp protection from MTS (methanethiosulfonate) labeling by verapamil, indicating their importance for drug binding.44,45

Additionally, due to the hydrophobic effect, the number of aromatic rings in selected molecules might also play a role in establishing the \( \pi-\pi \) stacking interactions between them and aromatic residues of P-gp. In this regard, the GF120918 compound is composed of a maximal number of aromatic rings (four) to be driven by a significant contribution from stacking interactions between its rings and the aromatic bases of Phe299, 310, 766, and 833, and Tyr303 and 306 residues. The other molecules include three aromatic rings for itraconazole and astemizole, two rings for ketoconazole and verapamil, and one ring for quinidine. Hence, it can be concluded that the presence of aromatic rings involved in the \( \pi-\pi \) stacking interactions is also important for the binding activity of the inhibitors.

Figure 5 Receptor–ligand interaction diagrams for six binding sites of the same protein (murine 3G60 P-glycoprotein) each with a different ligand molecule bond. The ligands are: (A) GF120918, (B) itraconazole, (C) ketoconazole, (D) astemizole, (E) quinidine, and (F) verapamil. The spoked arcs represent protein residues making nonbonded (hydrophobic) contacts with the ligand. The contacted ligand atoms are shown with spokes radiating back. The red ellipses in each plot indicate protein residues that are in common to those associated with the QZ59-RRR ligand.

Abbreviation: QZ59-RRR, cyclic-tris-(R)-valineselenazole.
Conclusion
In this current study, we report an extensive in silico structure-based screening of 1,300 different P-gp inhibitors by the gradient optimization method, using POLSCORE functions. On the basis of the large amount of data on versatile P-gp inhibitors, the filtering and ranking of chemical compounds was performed and examined systematically. The use of AutoDock Vina, together with POLSCORE, to estimate the pKi values for P-gp–inhibitor complexes was concomitant with experimentally determined affinities (IC50 or pIC50) for GF120918, itraconazole, ketoconazole, astemizole, quinidine, and verapamil compounds. A strong correlation (r2=0.80, F=16.27, n=6, P<0.0157) was observed for inhibition constants (Ki(exp) or pKi(exp)) calculated from experimental IC50 values and POLSCORE-predicted constants (Ki_POLSCORE or pKi_POLSCORE) using a linear regression fitting technique. The hydrophobic forces involved in the interaction between the P-gp protein and analyzed molecules largely contributed to the inhibition effect.

To our knowledge, this is the first attempt to filter and examine a large P-gp inhibitor database by gradient optimization docking algorithm combined with POLSCORE functions.

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Disclosure
The authors report no conflicts of interest in this work.

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