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APPENDICE

Insights into Saquinavir Resistance in the G48V HIV-1 Protease: Quantum Calculations and Molecular Dynamic Simulations

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ABSTRACT The spread of acquired immune deficiency syndrome has increasingly become a great concern owing largely to the failure of chemotherapies. The G48V is considered the key signature residue mutation of HIV-1 protease developing with saquinavir therapy. Molecular dynamics simulations of the wild-type and the G48V HIV-1 protease complexed with saquinavir were carried out to explore structure and interactions of the drug resistance. The molecular dynamics results combined with the quantum-based and molecular mechanics Poisson-Boltzmann surface area calculations indicated a monoprotonation took place on D25, one of the triad active site residues. The inhibitor binding of the triad residues and its interaction energy in the mutant were similar to those in the wild-type. The overall structure of both complexes is almost identical. However, the steric conflict of the substituted valine results in the conformational change of the P2 subsite and the disruption of hydrogen bonding between the –NH of the P2 subsite and the backbone –CO of the mutated residue. The magnitude of interaction energy changes was comparable to the experimental K_i data. The designing for a new drug should consider a reduction of steric repulsion on P2 to enhance the activity toward this mutant strain.

INTRODUCTION

The spread of acquired immune deficiency syndrome (AIDS) has constantly threatened the world because the disease leads to a significant loss of morbidity and mortality. Unfortunately, chemotherapy for the disease has, in many cases, failed to achieve complete viral suppression (Deeks, 2003). This relies on the fact that the human immunodeficiency virus (HIV) develops resistance to antiretroviral drugs by genetic mutation. The development of novel drug targets and HIV vaccine is promising but the results of those studies remain far from the clinical stage. Understanding the mutations that confer resistance to available drugs is thus an urgent issue in HIV chemotherapy.

The HIV type-1 protease (HIV-1 PR) is an important target for AIDS chemotherapy. This viral protein cleaves the *gag* and *pol* nonfunctional polypeptide into functional proteins essential for maturation of infectious HIV particles (Debouck et al., 1987). The protein is a homodimer. Each protein monomer consists of 99 amino acids (Meek et al., 1989). From x-ray data (Fig. 1 *B*), the substrate/inhibitor binding site is located at the dimer interface (Hong et al., 1996, 2000; Jaskolski et al., 1991; Krohn et al., 1991; Swain et al., 1990; Vondrasek and Wlodawer, 2002). As a member of the aspartyl protease family, HIV-1 PR is composed of the conserved sequences, so-called the binding triads: D25-T26-G27 and D25′-T26′-G27′, of which D25 and D25′ are known as the active site residues. These two ionizable residues play a major role in the catalytic reaction.

Because of the therapeutically important enzyme, structural and functional studies have been carried out to gain understanding of molecular mechanisms of the proteolytic cleavage process (Hyland et al., 1991; Northrop, 2001; Okimoto et al., 1999; Scott and Schiffer, 2000; Smith et al., 1996). The size and the availability of high-resolution x-ray structures of HIV-1 PR are amenable for molecular dynamics (MD) technique to investigate the relationship of structure, dynamics, and function of the enzyme (Collins et al., 1995; Harte et al., 1992, 1990; Levy and Caflisch, 2003; Piana et al., 2002; Scott and Schiffer, 2000) as well as to serve as a test system for developing computational methodology (Piana et al., 2004, 2001; Wang and Kollman, 2000; York et al., 1993a). The MD approach has provided insightful information on the enzyme-substrate interactions and binding conformations, the protonation states of the active site residues, the role of the flexible flap and the binding waters, and drug resistance. Characterizations of structural intermediates have been made useful for rational drug design (Randolph and DeGoey, 2004; Roberts et al., 1990; Rodriguez-Barrios and Gago, 2004).

Saquinavir (SQV, Fig. 1 *A*), a peptidomimetic protease inhibitor, is clinically used to treat infected HIV patients. The inhibitor containing a nonhydrolyzable hydroxyethylene isostere was designed based on the transition state structure in the enzyme-substrate complex. Combination of PR and reverse transcriptase inhibitors appears to be a highly effective treatment against HIV (Boucher, 1996). The PR inhibitor blocks the maturation step of the HIV life cycle, which is the

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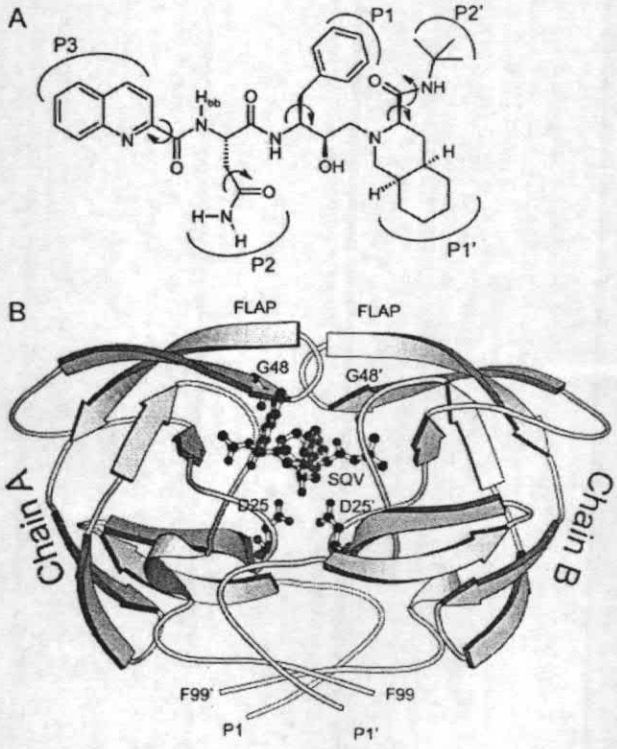

FIGURE 1 Schematic representation of saquinavir (*A*) and the wild-type HIV-1 protease-saquinavir complex (*B*). According to a conventional classification of the protease subsites, the binding pockets are designated by the inhibitor side chains P1, P2, P3, P1′, and P2′.

crucial stage in the formation of new viral particles. Nevertheless, the current cure with SQV has introduced several resistant variants of HIV-1 PR, some of which can dramatically reduce drug susceptibility (Vondrasek and Wlodawer, 2002). G48V and L90M are considered as the primary mutations commonly occurring in vivo or in vitro (Eberle et al., 1995; Vaillancourt et al., 1999). These "signature" residue mutations can be associated with a dramatic decrease in drug susceptibility. According to K_i values, the G48V, L90M, and G48V/L90M mutants decrease saquinavir sensitivity by 13.5-, 3-, and 419-fold with respect to that of the wild-type (wt) protease (Ermolieff et al., 1997).

Among common mutations associated with antiretroviral drug resistance, G48V is a unique mutation characteristically generated by SQV. In a view of substituted-type residue, glycine was replaced by a bulkier side-chain residue. The steric conflict of the mutant should involve in a destabilization of the complex. Although several x-ray structures of the HIV-1 PR provided valuable information on the inhibitor binding, this is not the case for the primary resistance to SQV. The crystal structure of the G48V complex is not yet available. With the aid of the available x-ray data, the molecular modeling techniques offer an opportunity to investigate the structural basis of the mutant enzyme (Prabu-Jeyabalan et al., 2003; Swain et al., 1990).

The missing hydrogens in the structural data have led to studies of the ionization state of the active site residues D25/D25′ (Smith et al., 1996; Wang et al., 1996; Wlodawer and Vondrasek, 1998; Yamazaki et al., 1994). This subject is important for drug design in a way to optimize the interactions of the inhibitor with the enzyme. Different protonation models were found depending upon the local environment of the enzyme-inhibitor complex. The single protonation at one of the two acidic residues has been most commonly observed with the binding of the hydroxylethylene-based inhibitors (Baldwin et al., 1995; Chen and Tropsha, 1995; Hyland et al., 1991; Smith et al., 1996; Wang et al., 1996; Wlodawer and Vondrasek, 1998). From NMR experiments, the neutral D25/D25′ side chain (diprotonation) was determined in the presence of inhibitor diol groups (Yamazaki et al., 1994), whereas the dianionic form (unprotonation) was observed in the free enzyme (Smith et al., 1996; Wang and Kollman, 2000).

In this study, we employed a computational approach to access information regarding molecular structure and dynamics of the G48V HIV-1 protease conferring to saquinavir resistance. The MD simulations were carried out for the wt and the G48V HIV-1 protease complexed with saquinavir in explicit aqueous solution. The study of the protonation state of the HIV-1 PR complexed with SQV has been carried out before exploring the structure and dynamic data of the signature resistance. The density functional theory (DFT), ONIOM, and molecular mechanics Poisson-Boltzmann surface area (MM/PBSA) methods have been performed to identify the protonation model of the active site residues. The MM/PBSA approach offers an efficient computation for calculating the binding free energy of biomolecules (Kollman et al., 2000; Srinivasan et al., 1998; Wang and Kollman, 2000). The method has been extensively used to study protein-ligand complexes. The quantum-based approach, DFT and ONIOM, has been useful in providing accurate energy information of the interested region. In particular, the hybrid quantum mechanical/molecular mechanical (QM/MM) method, ONIOM (our own *N*-layered integrated molecular orbital and molecular mechanics), developed by Morokuma, has been extended from small molecules to biological applications (Friesner and Beachy, 1998; Morokuma, 2002; Prabhakar et al., 2004; Torrent et al., 2002). Its efficiency has been improved over the years. Simply, the concept of the ONIOM approach is partitioning a large molecular system into onion skin-like layers, and applying the quantum mechanics and molecular mechanics methods to the defined different parts (Morokuma, 2002). In the partitioned system, the high-level quantum computations engage the essential part of the central activity, whereas the lower-level energy calculations take into account the contribution of the remaining region. The comparison of MD results of the two systems provides insightful details of how the G48V mutant is associated with saquinavir resistance. The study provided fundamental principles on the molecular mechanism of

inhibitor binding and resistance, which will be useful for designing an anti-HIV inhibitor to combat AIDS.

METHODS

Before starting the MD simulations, the problem of the protonated state of the active site residues was addressed, since such information cannot be directly obtained from the x-ray data. Our approach consists of molecular orbital energy calculations and solvent continuum free-energy calculations. However, structural data of the complexes, particularly the structure of the G48V-SQV, are not available, and the quantum-based computation for the whole enzyme-inhibitor complex is not feasible. A strategy is developed. First, MD simulations of the four protonation states for the wt and for the G48V complexes were performed to obtain the protonation models, which were subsequently subjected to calculate interaction and binding energies. Details of the methodology are described as follows.

Initial structure

The x-ray structure of the wt HIV-1 PR complexed with Ro 31-8959, saquinavir, (Protein Data Bank code 1HXB; 2.3 Å resolution) was used as a starting model. All missing hydrogens of the protein were added using the LEaP module in the AMBER 7 software package (Case et al., 2002). The protonation state of the ionizable residues, the C- and the N-termini, except for D25/25′, was assigned based on the predicted pKa values at pH 7. The pKas of ionizable residues were calculated based on the Poisson-Boltzmann free-energy calculations (see the pKa prediction). The results concluded that all Lys, Arg, Glu, Asp, and the terminal groups are charged, whereas His was in the neutral form. Protonation states of D25/25′ were explicitly assigned into four different ionizable states, including unprotonation, monoprotonation (each site of D25 and D25′), and diprotonation (protonated at both aspartyl residues). For the wt study, the simulated systems were labeled as wt-unpro, wt-mono25, wt-mono25′, and wt-dipro, respectively.

The starting structure and force-field parameters for the inhibitor were obtained as follows. Hydrogens were added to the x-ray coordinates of SQV (1HXB) by taking into account the hybridization of the covalent bonds. Geometric optimization was subsequently performed at the Hartree-Fock level with 6-31G** basis functions to adjust the bond-length involving hydrogens. Then, the RESP fitting procedure was employed to calculate partial atomic charges of the inhibitor (Cornell et al., 1993). Force-field parameters of the inhibitor were assigned based on the atom types of the Cornell et al. (1995) force-field model. Gaussian 98 (Frisch et al., 2002) was used to optimize the molecular structure, generate electrostatic potentials, and calculate ab initio energies. Partial charge generation and assignment of the force field were performed using the Antechamber suite (Wang et al., 2001).

The preparation of the initial structure for the simulation of the G48V mutant-SQV complex was similar to that of the wt complex. The comparative model of the mutant was constructed based on 1HXB because the three-dimensional structure of the G48V-SQV complex is not available. It should be noted that the x-ray structure of the double mutant, G48V/L90M-SQV complex (1FB7) could be considered as an alternative template. However, the x-ray coordinates of the second monomer of the double mutant are not available. Thus, 1HXB is considered to be more appropriate as a template. The simulated systems of the mutant complex consist of four protonated states, which were defined similar to those of the wt complex, i.e., unprotonation (mt-unpro), monoprotonations (mt-mono25 and mt-mono25′), and diprotonation (mt-dipro).

The next step was to incorporate the solvent and counterions into the models previously prepared. The crystallographic waters were also included in the simulations. Each model was solvated with the TIP3P waters (Jorgensen et al., 1983) and neutralized by the counterions using the LEaP module. The total number of the TIP3P waters in the periodic box for all systems was in a range of 9100–9900 molecules.

Molecular dynamics simulations

Energy minimization and MD simulations were carried out using the SANDER module of AMBER 7 (Case et al., 2002) with the Cornell force field (Cornell et al., 1995). The whole systems were subjected to energy minimization within a range of 200–5000 steepest descent steps to avoid bad contacts. It should be noted that position-restrained minimizations of some particular regions were carried out for systems that clashed during minimization because of incidental overlay of atoms. This procedure was repeated until there was no sign of bad contacts. The resulting protein structure was compared with the before-minimized structure. Root mean-square displacement (RMSD) for nonhydrogen atoms of the compared protein structures showed that there were no RMSDs exceeding 0.1 Å in all systems.

The MD simulation was performed employing the periodic boundary condition with the NPT ensemble. A Berendsen coupling time of 0.2 ps was used to maintain the temperature and pressure of the systems (Berendsen et al., 1984). The SHAKE algorithm (Ryckaert et al., 1977) was employed to constrain all bonds involving hydrogens. The simulation time step of 2 fs was used. All MD simulations were run with a 12 Å residue-based cutoff for nonbonded interactions and the particle-mesh Ewald method was used for an adequate treatment of long-range electrostatic interactions (York et al., 1993a).

The simulation consists of thermalization, equilibration, and production phases. Initially, the temperature of the system was gradually heated from 0 to 298 K during the first 60 ps. Then, the systems were maintained at 298 K until MD reached 400 ps of the simulation. Finally, the production phase started from 400 ps to 1 ns of the simulation. The convergence of energies, temperature, pressure, and global RMSD was used to verify the stability of the systems. The MD trajectory was collected every 0.1 ps. The 600 ps trajectory of the production phase was used to calculate the average structure. All MD simulations were carried for 1 ns. Analysis of all MD trajectories i.e., RMSD, distances, torsion angles, etc. was carried out using the CARNAL and Ptraj modules of AMBER 7. The geometry and stereochemistry of the protein structure were validated using PROCHECK (Laskowski et al., 1996). In summary, a total of eight systems for the MD simulations were carried out.

Graphic visualization and presentation of protein structures were done using RasMol, Swiss-Pdb Viewer (Guex and Peitsch, 1997), WebLab Viewer (Accelrys, San Diego, CA), and MolScript (Kraulis, 1991).

The pKa prediction

An assumption used for assigning the protonation state of the ionizable residues in the simulations was inspected by the prediction of the pKa values. The method estimates the pKa shift by calculating the electrostatic free energy of ionizable residues in the neutral and the charge states in solution (Antosiewicz et al., 1994). The computations were done by solving finite different Poisson-Boltzmann equations implemented in the University of Houston Brownian Dynamics program (Davis et al., 1991). The protocols describe as follows. Polar hydrogens were added to the x-ray model using Insight II (Accelrys, San Diego, CA). For generating electrostatic potentials, the model was then placed in a $65 \times 65 \times 65$ dimension with a grid spacing of 2.5 Å. The focusing technique was additionally employed using finer grid spacing of 1.2, 0.75, and 0.25 Å for a cubic dimension of 15, 15, and 20, respectively (Antosiewicz et al., 1994; Yang et al., 1993). Atomic radii and charges available in the University of Houston Brownian Dynamics program were originally derived from optimized potentials for liquid simulations and CHARMm 22 parameter sets (Brooks et al., 1983; Jorgensen and Tirado-Rives, 1988). The 1.4 Å probe radius with a resolution of 500 dots/atomic-sphere was used. The calculations employed a solvent dielectric of 80 with 150 mM ionic strength, and a temperature of 298 K. A dielectric constant of HIV-1 PR was examined by varying to 1, 4, and 20. We found that a protein dielectric constant of 20 produced the best pKa prediction. A dielectric constant of 1 and 4 yielded unusual pKa values due to an overestimation of electrostatic potentials. This phenomenon is thoroughly discussed in an early work (Antosiewicz et al., 1994).

Protonation state of the HIV-1 PR

In an evaluation of the protonation state of D25/D25′, we employed three different approaches: density functional theory, ONIOM, and MM/PBSA methods. The DFT and ONIOM methods provide the interaction energy of the complex, whereas the MM/PBSA calculates the binding free energy ($\Delta G_{binding}$). It should be noted that properties of the system should be analyzed using the structure ensemble from the MD trajectory. However, quantum chemical methods are too expensive to calculate such enormous structural data. Alternatively, the statistically averaged structure obtained from the 600 ps production phase of the MD trajectory was chosen as the studied model.

The DFT method

In each protonation model, the cluster consists of the two triad residues, D25-T26-G27 and D25′-T26′-G27′, and SQV (see Fig. 3 *A*). Atoms that are not within the selected part were removed. To reduce possible terminal-charge effect, both ends of the triad fragments were capped by CH_3NH- and $-COCH_3$ groups. Geometric optimization was performed for the added atoms. The energy for the model was computed using a single-point calculation method with mixed basis sets. B3LYP/6-31 + G** was defined explicitly on the carboxylate oxygens of D25 and D25′, and B3LYP/6-31G** was assigned on all the remaining atoms. The quantum calculations were carried out using the program Gaussian 98 (Frisch et al., 2002).

A general form of the interaction energy calculation of the enzyme-inhibitor complex (ΔE_{EI}) is the subtraction of the energy of the complex (E_{EI}) from that of the free enzyme (E_E) and that of the free inhibitor (E_I).

$$\Delta E_{EI} = E_{EI} - E_E - E_I. \tag{1}$$

In this case, the model system contains a cluster of the two triads and SQV. Thus, interaction energy of the complex ($\Delta E_{cluster}$) was estimated by

$$\Delta E_{cluster} = E_{cluster} - E_{triadA} - E_{triadB} - E_{SQV}, \tag{2}$$

where $E_{cluster}$ is the total energy of the cluster, and E_{triadA}, E_{triadB}, and E_{SQV} are the total energy of the isolated triads of chain A and B and the unbound SQV, respectively.

The ONIOM method

To account for an effect of the protein environment, the QM/MM ONIOM method was used. Here, the three-layers approach (ONIOM3) was performed to reduce the boundary effect at the QM/MM junction but maintain considerably accurate energy information. The method is described as follows. The model of the HIV-1 PR-SQV complex was divided into three regions: *A*, *B*, and *C* (see the Appendix). The ONIOM layers were represented by inner (*A*), intermediate (*A* + *B*), and real (*A* + *B* + *C*). The inner layer, the "hot spot" region, consisting of D25, D25′, and SQV, was treated at the high-level of quantum chemical calculations using density functional theory (B3LYP/6-31G**). The intermediate layer contains a total of 36 residues including D25-D30, I47-F53, P80-I84, and L90. These residues are located within a 5 Å distance from SQV. This intermediate layer was treated with the semiempirical method using PM3. Lastly, the real layer includes the entire enzyme. The molecular mechanic method using universal force field (UFF) was applied to this layer. All calculations based on the ONIOM approach were carried out using the program Gaussian 98 (Frisch et al., 2002).

Hence, the total energy obtained from the ONIOM3 calculations (E^{ONIOM3}) herein can be defined by (see the Appendix):

$$E^{oniom3}[ABC] = E_{[UFF,ABC]} + E_{[PM3,AB]} + E_{[B3LYP,A]} - E_{[UFF,AB]} - E_{[PM3,A]}. \tag{3}$$

For the overlap regions, the subtraction energy terms are introduced to substitute the low-level energy calculations with the high-level one. Therefore, the total interaction energy ($\Delta E^{oniom3}_{total}[ABC]$) between SQV and the enzyme using the ONIOM3 method can be expressed as independent energy components from each layer as follows:

$$\Delta E^{oniom3}_{total}[ABC] = \Delta E_{[UFF,ABC]} + \Delta E_{[PM3,AB]} + \Delta E_{[B3LYP,A]} - \Delta E_{[UFF,AB]} - \Delta E_{[PM3,A]} \tag{4}$$

$$\Delta E^{oniom3}_{total}[ABC] = \Delta E_{[B3LYP,A]} + \Delta\Delta E_{[PM3,AB-A]} + \Delta\Delta E_{[UFF,ABC-AB]} \tag{5}$$

$$\Delta\Delta E_{[PM3,AB-A]} = \Delta E_{[PM3,AB]} - \Delta E_{[PM3,A]} \tag{6}$$

$$\Delta\Delta E_{[UFF,ABC-AB]} = \Delta E_{[UFF,ABC]} - \Delta E_{[UFF,AB]}, \tag{7}$$

where $\Delta E_{[B3LYP,A]}$ is the interaction energy in the region *A* evaluated at the B3LYP/6-31G(d,p) level. $\Delta\Delta E_{[PM3,AB-A]}$ is the interaction energy contributed from the region *B* evaluated at the PM3 level, and $\Delta\Delta E_{[UFF,ABC-AB]}$ is the interaction energy contributed from the region *C* evaluated at the UFF molecular mechanics.

The MM/PBSA method

In general, the free energy of the inhibitor binding, $\Delta G_{binding}$, is obtained from the difference between the free energy of the receptor-ligand complex (G_{cpx}), and the unbound receptor (G_{rec}) and ligand (G_{lig}) as follows:

$$\Delta G_{binding} = \Delta G_{cpx} = G_{cpx} - (G_{rec} + G_{lig}). \tag{8}$$

The MM/PBSA approach calculates $\Delta G_{binding}$ on the basis of a thermodynamic cycle. Therefore, Eq. 8 can be approximated as

$$\Delta G_{binding} = \Delta E^{MM} - T\Delta S + \Delta G_{sol}, \tag{9}$$

where ΔE^{MM} is related to the enthalpic changes in the gas phase upon binding and obtained from molecular mechanics van der Waals and electrostatic energies, $T\Delta S$ involves the entropy effect, and ΔG_{sol} is the free energy of solvation. The ΔG_{sol} is composed of the electrostatic and nonpolar contributions (Srinivasan et al., 1998), and therefore can be expressed as

$$\Delta G_{sol} = \Delta G^{PB} + \Delta G^{SA}, \tag{10}$$

where ΔG^{PB} is calculated using a continuum solvent model with Poisson-Boltzmann solution (Gilson et al., 1987), and ΔG^{SA} is estimated from the solvent-accessible surface area (SASA) (Sitkoff et al., 1994).

The $\Delta G_{binding}$ was obtained using the MM/PBSA module in the program AMBER 7, which interfaces the program DelPhi 4 (Rocchia et al., 2001). To calculate electrostatic free energy of solvation, the grid resolution of 0.5 Å with the boundary conditions of Debye-Huckel potentials was employed. Atomic charges were taken from the Cornell force field (Cornell et al., 1995). The water and protein dielectric was set to 80 and 4, respectively. The SASA was calculated using a 1.4 Å probe radius. Atomic radii were taken from the PARSE parameter set (Sitkoff et al., 1994). The nonpolar free energy of solvation was obtained by 0.00542 × SASA + 0.92 kcal mol^{-1} (Sitkoff et al., 1994).

In the study, the contribution of the entropy ($T\Delta S$) was not included. An estimation of the entropy effect from normal mode analysis requires the high computation demands. The effect should be very small because all system models are very similar. In addition, we considered the relative values of the binding free energy.

RESULTS

Hydrogen bonding in the binding site

One of the most important HIV-1 PR-SQV interactions is the formation of the hydrogen bond at the active site. This

observation is estimated from the x-ray data by the close proximity between the terminal side chain of the two aspartyl residues and the hydroxylethylene isostere moiety (−OH) of the inhibitors. Due to the lack of hydrogen position in the structure, the pattern of this typical hydrogen bond is investigated here. Therefore, it is necessary to monitor the active site structure of the MD results and determine the most preferential interactions.

The MD snapshot of the dipro, mono25, mono25′, and unpro systems for the wt and the G48V complexes is illustrated in Fig. 2, *A–H*. The D25/D25′ side chains and the $^{-}$OH of SQV of all protonated states, except for the unprotonation, occupies the positions suitable for the formation of the hydrogen bond. The distal separation between the active site residues and the hydroxylethylene isostere of SQV maintains similarity to the x-ray structure. The structure of the wt-unpro and the mt-unpro provide the worst scenario of the complex (Fig. 2, *D* and *H*). A majority of MD data shows that the active site residues adopted to a conformation completely different from the x-ray data. Hence, the wt-unpro and mt-unpro systems are not an appropriate state for the formation of the HIV-1 PR-SQV complex.

In comparing the four protonated states, the binding pattern of the −OH of SQV to the D25/D25′ was remarkably different. Nevertheless, when comparing the wt with the mutant structure of the same protonated state, the binding pattern at the active site was similar. The results allow drawing a simple scheme of the hydrogen bond pattern at the active site, which is illustrated in Fig. 2, *I–L*.

Protonation state of the wild-type complex

From the pKa prediction, the D25/D25′ in the free wt HIV-1 PR exhibited different protonation states depending on the examined pHs of 4, 5, 6, and 7 because the assay of the HIV-1 PR is measured between pH 5 and 6, and in the basic solution the enzyme precipitates (Wang et al., 1996). However, the dianionic form was the most apparent state between pH 6 and 7. The protonation state at pH 4 and 5 remains inconclusive. In this study, these results were not fully understood. It is possibly associated with the used parameters (atomic charges and radii, dielectric constant, etc.) and the studied model. This awaits further investigation.

Table 1 shows the resulting energy calculated from DFT, ONIOM, and MM/PBSA approaches. Here, the term "the stabilization energy" is used for a simpler and more straightforward definition. The negative sign of the stabilization energy suggests that the protonation model of wt-dipro, wt-mono25, and wt-mono25′ systems are energetically favorable. From the full quantum DFT treatment, the $\Delta E_{\text{cluster}}$ wt-mono25 compared to that of wt-dipro and wt-mono25′ was lower by 7.62 and 17.22 kcal mol^{-1}, respectively. The lowest ΔE_{cpx} from the ONIOM3 method also took place on the protonation model of the wt-mono25. The energy difference was 14.13 and 16.63 kcal mol^{-1} more stable than that of the wt-dipro and of the wt-mono25′, respectively. From the MM/PBSA method, the stabilization energy of the wt-mono25 system was slightly lower in energy than the other two states. Apparently, all the three approaches showed that the monoprotonation at D25 was the most energetically favorable state.

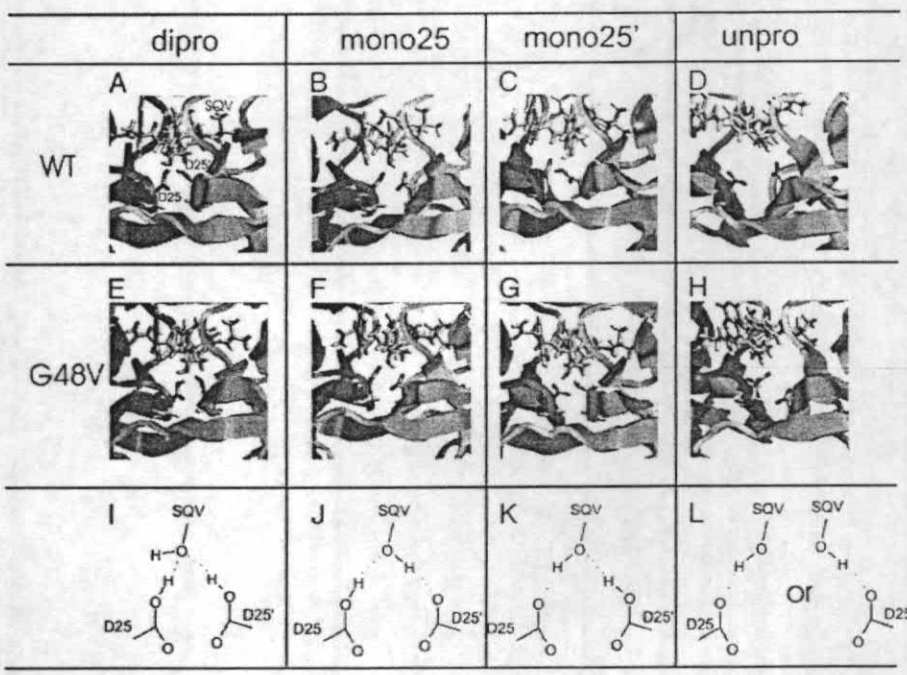

FIGURE 2 MD snapshots showing interactions in the binding pocket of the wt and G48V for various protonation states: diprotonation (dipro), monoprotonation of D25 (mono25), monoprotonation of D25′ (mono25′), and unprotonation (unpro). Saquinavir (SQV) and the active site residues D25 and D25′ of the enzyme are shown in stick mode. Chain *A* and *B* of the enzyme are colored as blue and green.

TABLE 1 The stabilization energy (kcal mol^{-1})

	DFT	ONIOM3	MM/PBSA
System	$\Delta E_{cluster}$	ΔE_{cpx}	ΔG_{cpx}
wt-dipro	−59.32	−64.22	−91.62
wt-mono25	−66.94	−78.35	−94.44
wt-mono25′	−49.72	−61.72	−92.91

The stabilization energy shown in Table 1 was decomposed into individual energy components (Table 2) for analyzing quantitatively essential interactions of the different protonation models. From the DFT method, an order of the $\Delta E_{triadA+SQV}$ ranging from the lowest value was wt-dipro < wt-mono25 < wt-mono25′. The sum of $\Delta E_{triadA+SQV}$ and $\Delta E_{triadB+SQV}$ was used to account for interactions of SQV to the triad residues. Still the wt-dipro was the first preferential protonation model with the lowest energy of −34.19 kcal mol^{-1}. Considering the sum of $\Delta E_{triadA+SQV}$ and $\Delta E_{triadB+SQV}$ of wt-mono25, the energy difference was 7.51 kcal mol^{-1} greater than that of wt-dipro. On the other hand, its $\Delta E_{triadA,B}$ value accounting for the triad-triad interactions has significantly gained by 13.16 kcal mol^{-1} over the wt-dipro system. These data suggested the interactions between the triads were essential to the complex stability.

The ONIOM3 results showed the lowest $\Delta E_{[B3LYP,A]}$ took place on wt-mono25. It should be noted that $\Delta E_{[B3LYP,A]}$ has considered the interactions of SQV to D25 and to D25′, and between D25/D25′. This is still the case when accounting for interactions of the 5 Å neighboring residues to SQV ($\Delta E_{[PM3,AB-A]}$). The $\Delta E_{[UFF,ABC-AB]}$ of the three states are almost equivalent. There was no significant change of the stabilization energy with an addition of $\Delta E_{[UFF,ABC-AB]}$. Thus, the effect of the protein environment at the long distance-range interactions is negligible.

In the MM/PBSA method, there was no substantial difference of ΔE^{MM} for all three systems, whereas the ΔG_{sol} of the wt-mono25 revealed the lowest values. This observation suggests the solvation free-energy values dominate the contribution of the stabilization energy. The molecular mechanics energy term cannot discriminate the protonation model.

Interaction energy at the catalytic site: the wild-type versus G48V

We have illustrated previously that the quantum-based approach gave promising results to the characterization of the complex model. Here, the approach has been further exploited by calculating the enzyme-inhibitor interaction energy of the G48V complex. The interaction energy of the triads/SQV in the wt complex. $\Delta E_{cluster}$, previously obtained using the DFT method (Table 1) was used for a comparison.

The results illustrated in Fig. 3 suggested that in the G48V-SQV complex, the lowest $\Delta E_{cluster}$ also took place at the monoprotonated D25 model. The interaction energy for both the wt and the G48V in the mono25 was ~8 and 17 kcal·mol^{-1} lower than those from the dipro and the mono25′, respectively. At the same protonation state, the $\Delta E_{cluster}$ of the G48V was no essentially different from that of the wt. This conclusion followed from the fact that the thermal fluctuation at room temperature of ~0.6 kcal·mol^{-1}, equivalent to 1 kT, where T is 300 K and k is the Boltzmann constant. Thus the interactions of the two triad residues and SQV remain unchanged by the G48V mutation.

Those results discussed previously lead us to conclude that the monoprotonation at D25 is the most energetically favorable state. Therefore, further comparison and discussion for both the wt and the mutant complex were focused only on the results of monoprotonation D25.

The energies and RMSD plots (Fig. 4) demonstrated a well-behaved MD simulation for both the wt and G48V-SQV systems. After 400 ps, the RMSD fluctuates 1.27–1.78 Å for the wt and 1.29–1.80 Å for the mutant. The fluctuation is <0.5 Å over the entire production phase. This structural fluctuation is not uncommon in the typical MD simulation of protein, indicating the reliable equilibration of the system in this study. In Table 3, the low RMSD values calculated from 100 snapshot structures taken from the production phase suggested the structures in each set were similar to each other. This allows useful information to be extracted from the MD trajectories. Analysis of some statistic quantities such as structure and dynamics was performed from the trajectories of wt-mono25 and mt-mono25 systems.

TABLE 2 Decomposition of the stabilization energy (kcal mol^{-1})

	DFT			ONIOM3			MM/PBSA	
System	$\Delta E_{triadA+SQV}$	$\Delta E_{triadB+SQV}$	$\Delta E_{triadA,B}$	$\Delta E_{[B3LYP,A]}$	$\Delta E_{[PM3,AB-A]}$	$\Delta E_{[UFF,ABC-AB]}$	ΔE^{MM}	ΔG_{sol}
wt-dipro	−23.81	−10.38	−27.64	−11.45	−36.66	−16.11	−109.42	17.81
wt-mono25	−12.27	−14.41	−40.80	−33.63	−28.34	−16.38	−109.83	15.39
wt-mono25′	−6.33	−6.88	−41.53	−18.33	−27.48	−15.91	−109.88	16.98

$\Delta E_{triadA+SQV}$ or $\Delta E_{triadB+SQV}$ account for interactions of the triad residues of chain *A* or *B* to SQV, and $\Delta E_{triadA,B}$ accounts for interactions between the triad residues of chain *A* and those of chain *B*.

$\Delta E_{[B3LYP,A]}$ accounts for interactions of D25, D25′, and SQV.

$\Delta E_{[PM3,\ AB-A]}$ represents interactions of SQV and the 5 Å surrounding residues, excluding D25 and D25′, and $\Delta E_{[UFF,ABC-AB]}$ represents interactions of SQV and the remaining residues.

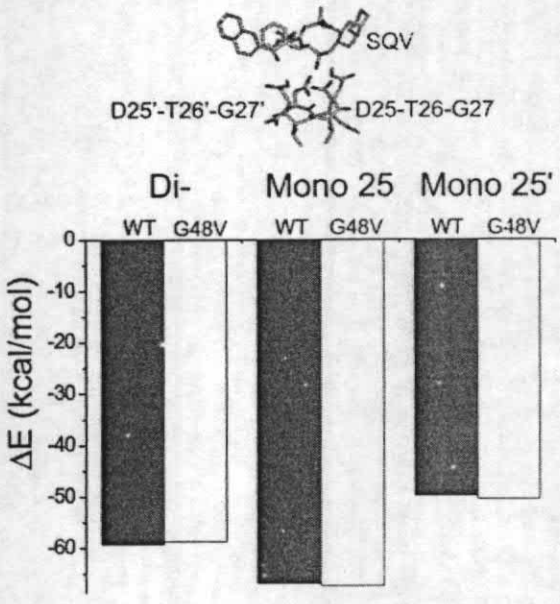

FIGURE 3 ΔE_{cpx} between the triad residues and saquinavir of the wt and the G48V complexes for the dipro, mono25, and mono25′ systems.

Structural similarity between the wild-type and the mutant

The global backbone RMSD of the x-ray versus the average MD structure of the wt of 1.04 Å indicates that overall main-chain structures of the complex in the crystal state and in solution are similar. In addition, comparison of the two average MD structures between the wt and the G48V mutant resulted in a backbone RMSD of 0.70 Å. This suggests that the tertiary structure of the G48V mutant was insignificantly different from the native enzyme.

Detailed analysis of RMSD per residue is illustrated in Fig. 5. One can see that most regions of the enzyme, except for the flexible loop of the first subunit, exhibited a small difference in backbone conformation of the wt enzyme with respect to the mutant. Particularly, RMSDs of E21–D30 residues, covering the triad sequence of the enzyme, were in a range from 0.11 to 0.36 Å. This indicates no essential structure alteration of the main-chain hydroxyethylene isostere of SQV and the surrounding residues. Thus, the contacts between the hydroxyl of SQV and the active site residues were independent of the amino acid substitution at residue 48. This result supported the evidence discussed previously that interaction energies of the two triad residues and saquinavir were not significantly changed by mutation of G48V.

Structural difference between the wild-type and the mutant

In Fig. 5, the apparent difference between the wt and the mutant HIV-1 PR-SQV complexes was observed around the

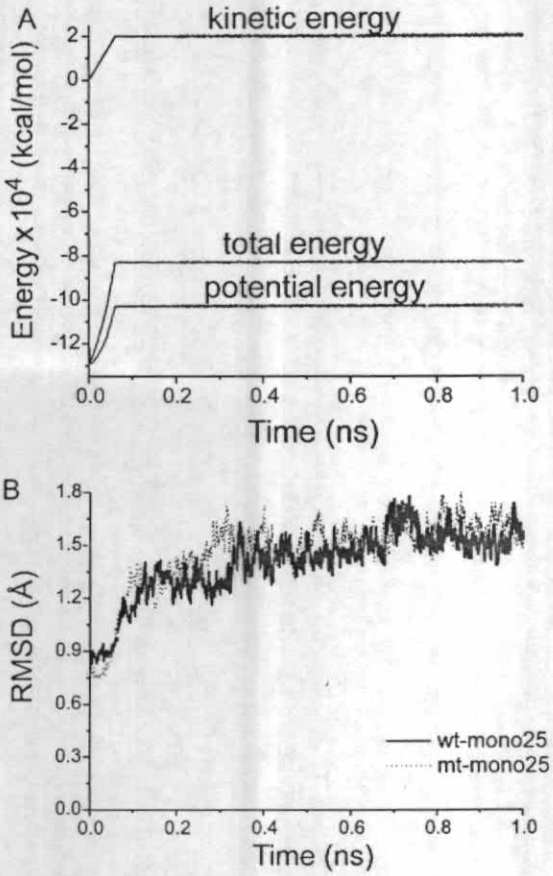

FIGURE 4 Plots of the energies (*A*) and RMSDs (*B*) versus the simulation time for the wt and G48V-SQV complex. The obtained RMSD was computed using the structure at $t = 0$ as a reference.

protein flap (residues 46–55). In this region, overall RMSD values of chain *A* were relatively greater than those of chain *B* (Fig. 6). The structure of the flap *B* of the G48V is similar to that of the wt enzyme, whereas the β-hairpin structure of the flap *A* of the mutant does not superimpose well. Surprisingly, the tip of flap *A* of the G48V-SQV complex shifted slightly toward the twofold axis of symmetry of HIV-1 PR. However, distance separations between the tips, residues 49–51 in the mutant, were not significantly different from that in the wt complex.

Flexibility and conformational changes of SQV subsites

Flexibility and conformational changes of the inhibitor side chains P1, P1′, P2, P2′, and P3 were investigated in terms of torsion angle fluctuations of χ_{P1}, $\chi_{P1'}$, χ_{P2}, $\chi_{P2'}$, and χ_{P3}, respectively. From Fig. 7 *A*, an oscillation of all dihedral angles throughout the simulations, which was no greater than $\pm 10°$, suggested that in the wt complex, all SQV side chains undergo a narrow range of dynamic fluctuation. In other

TABLE 3 Mean global RMSD values calculated from a set of 100 snapshot structures of the 600 ps production phase

		<RMSD>(Å)			
		Dipro	Mono25	Mono25′	Unpro
wt	Backbone	0.90 ± 0.13	0.86 ± 0.12	0.87 ± 0.11	0.83 ± 0.11
	Heavy atoms	1.56 ± 0.22	1.45 ± 0.17	1.48 ± 0.18	1.39 ± 0.15
G48V	Backbone	0.83 ± 0.11	0.86 ± 0.13	0.85 ± 0.12	0.86 ± 0.12
	Heavy atoms	1.39 ± 0.18	1.52 ± 0.22	1.51 ± 0.21	1.47 ± 0.19

words, the inhibitor side chains were inflexible and retained their starting conformation during the course of the MD trajectory. In the case of the G48V mutant, all torsion angles except for χ_{P2} adopted the values similar to that of the wt (Fig. 7 *B*). This indicated that the conformations of these subsites are unchanged. However, a remarkable shift in χ_{P2} implied a rotation of the P2 subsite starting from ~−70° to its equilibrium value ~90°. This suggested a substantial rotation of the P2 of SQV in the G48V (Fig. 8). In addition, the ±40° fluctuation of χ_{P2} in the mutant larger than that of the wt indicated that the P2 side chain looses its rigidity. The rearrangement of the P2 was related to the event of the flap motion as describe previously. Moreover, it involves a decrease of the strength of the hydrogen bond between the mutated residue and the P2 subsite (described in the next topic). The overall change in terms of torsion angles is supposed to explain a decrease of saquinavir sensitivity.

Decrease of hydrogen bond strength

The MD results show that the conformational difference in SQV subsites between the wt and the G48V complexes was located at the P2 side chain. Among residues surrounding the P2 subsite, position 48 is critical to conformational change of the inhibitor subsite. Direct contacts from the backbone oxygen of the mutated residue (O(48)) to the side-chain amide group (HN_{P2}) of P2, and to the backbone amide proton (HN_{bb}) of the inhibitor are illustrated by Fig. 8.

The O(48)-HN_{bb}(SQV) distance was, on average, 1.95 Å for the wt and extends to 2.25 Å in the G48V complex (Fig. 9 *A*). An increase of the distance is an evidence of decreasing the hydrogen bond strength.

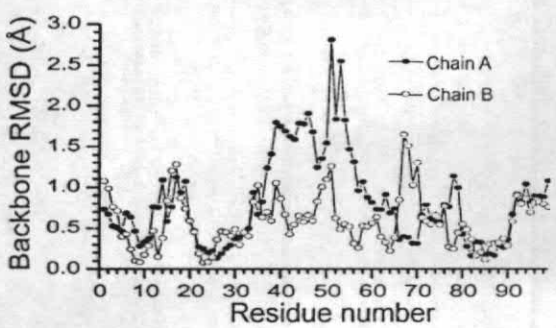

FIGURE 5 Backbone RMSD between the wild-type and the G48V structure.

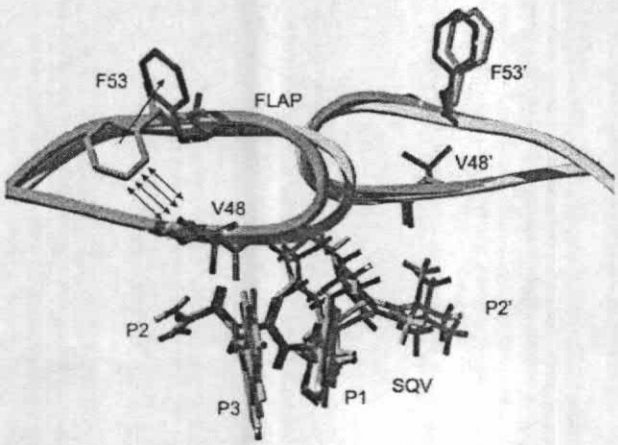

FIGURE 6 HIV-1 PR flap structures of the wt (*green*) and the G48V (*yellow* and *blue*). Some selected residues and saquinavir are presented in stick mode. Hydrogen atoms of the enzyme are not shown for simplification.

A loss of the hydrogen bond interactions of residue 48 to SQV in the mutant complex was confirmed by a very large distance between O(48) and HN_{P2}(SQV) (Fig. 9 *B*). The wt complex shows the close proximity between O(48) and HN_{P2}(SQV). On the other hand, it is clear that the O(48)-HN_{P2} (SQV) distance in the mutant was not in a range of hydrogen bonding. The rotation of the P2 side chain as described previously is the cause of the disruption of the hydrogen bond of O(48)-HN_{P2} (SQV).

Analysis of these MD results indicates that the mutation at position 48 decreases the capability of inhibitor binding. A reduction of the interactions was estimated by calculating the ab initio energy. The $\Delta E_{G48\text{-}SQV}$ decreased ~3.5 kcal·mol^{-1} with respect to the $\Delta E_{V48\text{-}SQV}$. The magnitude of changes in the interaction energy of V48-SQV supports the experimental K_i data that explain a small decrease (13.5-fold) of saquinavir sensitivity.

DISCUSSION

The MD simulations were carried out to compare structure and dynamics of the wt and the G48V HIV-1 PR-saquinavir complex. In addition, the MD simulations for the four protonation systems were carried out to obtain structural models before an evaluation of the ionization form of the active site residues. The study of protonation state of the HIV-PR-SQV complex was achieved with extensive energy calculations using the DFT, ONIOM, and MM/PBSA methods. Based on our data, both quantum chemical and molecular dynamics free-energy calculations confirm that the protonation model of wt-mono25 is the most energetically favorable case.

The results were in agreement with NMR studies of the hydroxyethylene isostere inhibitors, pepstatin and KNI-272,

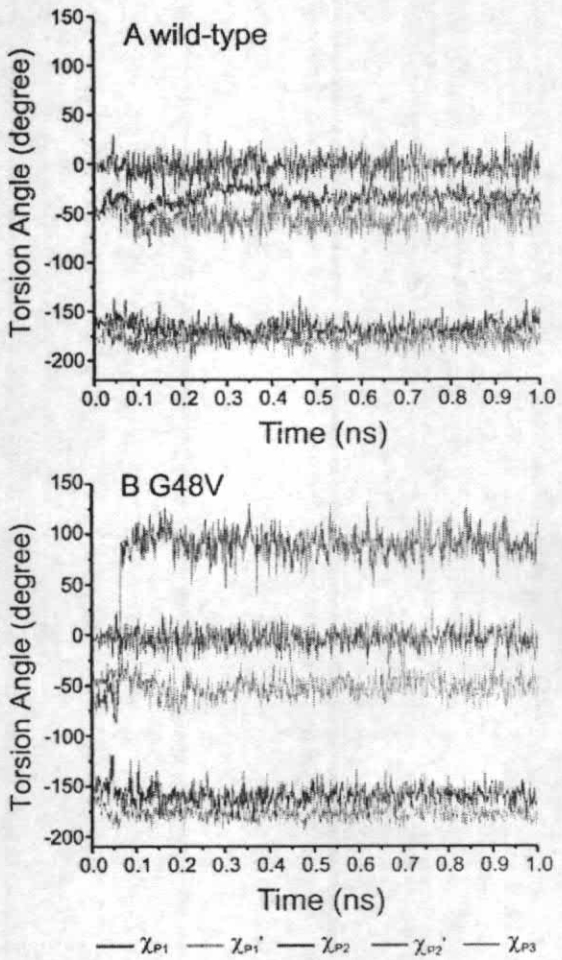

FIGURE 7 Fluctuation of χ_{P1}, $\chi_{P1'}$, χ_{P2}, $\chi_{P2'}$, and χ_{P3} corresponding to the dihedral angles of the inhibitor side chains P1, P1′, P2, P2′, and P3, respectively.

complexed with the enzyme (Smith et al., 1996; Wang et al., 1996). In this study, the protonation takes place only on the D25 side chain. Although the experimental data are not available for the HIV-1 PR-SQV complex, the structure of KNI-272 is almost identical to that of saquinavir. They share the most common features of drug specificity, including the capability of binding between the central hydroxylethylene isostere of the protease inhibitor and the catalytic residues of the enzyme.

Recently, the protonation state of the HIV-1 PR-SQV complex was studied using quantum and free-energy perturbation methods (Lepsik et al., 2004; Nam et al., 2003). The interaction energy of SQV and the active-site residues were obtained based on the model taken from the x-ray structure. The protonation model proposed from those studies was also monoprotonated D25.

It is worth nothing that the quantum-based method is a promising tool for the study of receptor-ligand complexes. The determination of the protonation state of the HIV-PR active site residues is achievable on the basis of the QM results. In particular, the ONIOM method has extended the limitation of system size by the pure QM method. As demonstrated by the ONIOM results, the enzyme-inhibitor interactions of the catalytic region and the 5 Å surrounding residues are important for stabilizing the complex. The effect of the long-distance range on the interaction energy was not dominant at the MM level. Nevertheless, the method should be used with some proper care. The effect of the boundary resulting from incompatibility between molecular orbital wave functions in the QM part and the MM region may drive unrealistic energy values (Morokuma, 2002).

An effect of solvent environment, which remains unobvious in quantum approach, has been fulfilled with the calculations of binding free energy. The binding free energy of wt-mono25 obtained from MM/PBSA was ~2 kcal mol^{-1} lower than that of the other states (Table 1). The difference was contributed from ΔG_{sol} rather than ΔE^{MM}. Not surprisingly, ΔE^{MM} of the three protonation model were almost equivalent (Table 2). Among all three systems, the only difference, that is the ionizable groups of D25 and D25′, cannot be well described by the empirical force-field energy. In addition, the influence of the solvent to the protonation site was trivial on the basis of the radial distribution function plot (Wittayanarakul et al., 2005). The radial distribution function

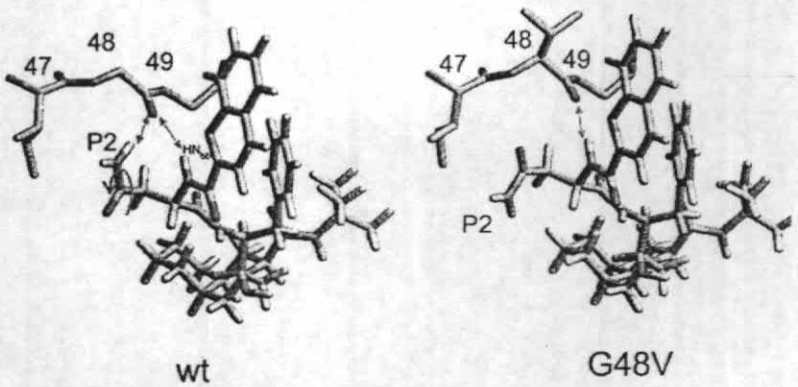

FIGURE 8 Conformational change of SQV at the P2 side chain. The rotation of the P2 subsite and the hydrogen bonds are illustrated.

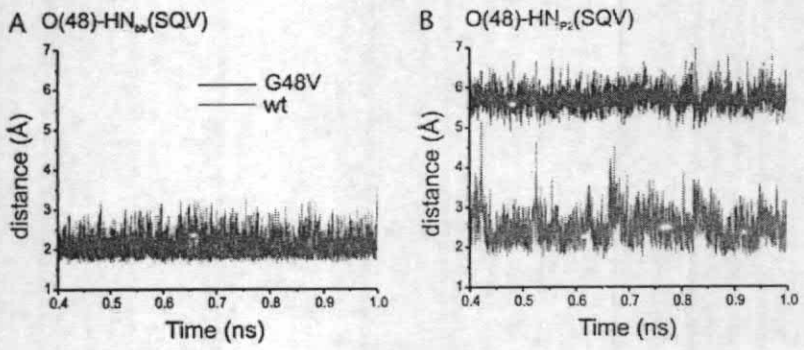

FIGURE 9 Distance trajectories of hydrogen bonding involving the CO backbone of residue 48.

of the hydroxylethylene oxygen of SQV showed an exclusion of water molecules from the protonation site. In this case, the energy information obtained from DFT and ONIOM were reliable. We anticipate that a method for the correction of the MM energy term by the QM treatment in MM/PBSA approach will be valuable for biomolecular research.

The binding pattern at the active site of the wt complex was similar that of the G48V as shown by the very low RMSD of residues E21–D30. Importantly, the interaction energy of the triad residues to SQV was insignificantly different between the wt and the G48V complexes. The results indicated the signature residue mutation developed in the primary resistance does not influence the interactions at the active site.

Significant changes were located at the protein flaps. Moreover, the flap structure of chain *A* was different from that of chain *B*. This is caused by different interactions of the enzyme to the asymmetric inhibitor. Particularly, the perturbation adopts heavily on the flap conformation of chain *A* rather than chain *B*. The slide of flap *A* in the G48V mutant seems to overcome a potential steric conflict caused by the substituted valine. As shown in Fig. 6, position 48 was in close contact with the F53 side chain of the enzyme and the P2 and P3 groups of SQV. Since the substituted valine of the mutant cannot be entirely accommodated in the hydrophobic pocket due to steric conflict of the dimethyl groups with the F53 and P3 side chains, the flap, therefore, shifted toward the symmetric axis of the enzyme. This rearrangement additionally destabilizes hydrogen bonding between the backbone CO of residue 48 of the enzyme and the P2 subsite of the inhibitor. In addition to the flap movement, the side chain of hydrophobic F53 became solvent-exposed to avoid steric clashes with V48 and Met-46, whereas an orientation of F53′ in flap *B* of the mutant was not changed dramatically.

The role of the HIV-1 PR mutation at the flexible flap has been considerably debated about whether it would facilitate the binding reaction or reduce stability of the inhibitor, or both (Ermolieff et al., 1997; Hong et al., 1997; Maschera et al., 1996). The crystal structure of the double mutant G48V/L90M complexed with SQV revealed side-chain rearrangement of the P2 subsite and the F53 of the enzyme similar to this study (Hong et al., 2000). Particularly, the missing of hydrogen bonding between the P2 subsite and the backbone C=O of residue 48 was also found in the x-ray structure of the double mutant. The crystal structure of G48H complexed with peptidic inhibitor U-89360E reported a decrease of flap mobility to stabilize the ligand (Hong et al., 1997).

Apparently the conformational change of the P2 subsite was an influence of steric conflict of the mutation at position 48. Importantly, it reduced saquinavir susceptibility to the mutant by interrupting the hydrogen bond interactions. Thus, a new drug with reduced steric repulsion on P2 could be designed to enhance the activity toward this mutant strain.

The x-ray structural data provided relevant information, insight into the molecular mechanism of HIV resistance to the protease inhibitor. Dynamic details of the full-atomic representation of the complex were required for further investigation. Therefore, MD simulation offers a good opportunity to fulfill basic information that could be useful in understanding the drug resistance mechanism and helpful in designing an anti-HIV inhibitor.

CONCLUSIONS

Molecular dynamics simulations of the wt and the G48V HIV-1 protease complexed with SQV were carried out to investigate the molecular basis of drug resistance. The MD

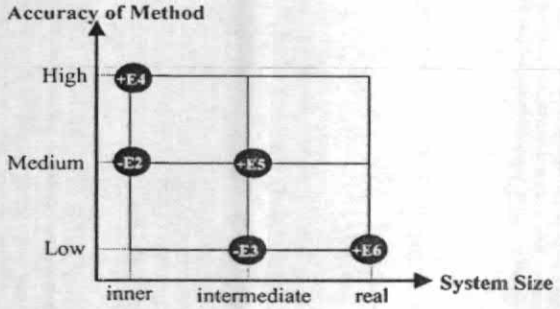

FIGURE 10 Schematic representation of the three-layer ONIOM extrapolation scheme.

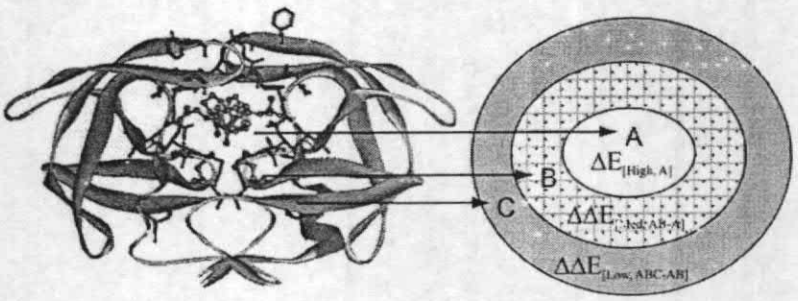

FIGURE 11 Schematic representation for the structure of HIV-1PR-SQV with the three partitioned layers.

results combined with quantum chemical calculations extend the capability of molecular modeling methods to study some biological systems, of which structural information is limited. This study showed that both complexes form the monoprotonation on D25. Overall tertiary structure of the wt and the mutant protease was not significantly altered. Particularly, structure and interactions at the central active site remain unchanged. However, conformational differences between the wt and the G48V mutant were on the protein flap. The conformational change of the P2 subsite decreased the strength of hydrogen bonding of the backbone CO of the residue 48 to SQV. The change in interaction energies was comparable to the experimental K_i data. These observations provide useful information for designing potent HIV-1 PR inhibitors.

APPENDIX: ONIOM CALCULATIONS

The key interactions centered on SQV and the catalytic residues were treated at a high level of calculations, whereas the environmental effect of the entire protein was calculated at a lower level of calculations. In this study, three-layered ONIOM (ONIOM3) was employed (Morokuma, 2002).

On the basis of the ONIOM3 method shown in Fig. 10, the total energy of the system can be obtained from five independent calculations as

$$E^{\text{ONIOM3}} = E[Low, real] + E[Med, intermediate] + E[High, inner] - E[Low, intermediate] - E[Med, inner] \quad (11)$$

or

$$E^{\text{ONIOM3}} = E6 + E5 + E4 - E3 - E2, \quad (12)$$

where *real* denotes the entire system, of which the energy ($E6$) is calculated at the low level. For the *intermediate* layer, the energy is computed at both the *medium* ($E5$) and *low* ($E3$) level. For the *inner* layer, the energy is obtained at both *high* ($E4$) and *medium* ($E2$) level.

As shown by Fig. 11, the structure of the HIV-1 PR-SQV complex was partitioned into three parts represented by *inner* layer (A), *intermediate* layer ($A + B$), and *real* layer ($A + B + C$). The atoms of the enzyme and the inhibitor defined to each layers were described in the Methods section.

To obtain the interaction energy of the HIV-1 PR/SQV complex (ΔE_{cpx}), one can be expressed as

$$\Delta E_{cpx} = E_{cpx} - E_{PR} - E_{SQV}, \quad (13)$$

where E_{cpx}, E_{PR}, and E_{SQV} are the total energy of the HIV-1 PR/SQV complex, HIV-1 PR and SQV, respectively.

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Structure, Dynamics and Solvation of HIV-1 Protease/Saquinavir Complex in Aqueous Solution and Their Contributions to Drug Resistance: Molecular Dynamic Simulations

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As it is known that the understanding of the basic properties of the enzyme/inhibitor complex leads directly to enhancing the capability in drug designing and drug discovery. Molecular dynamics simulations have been performed to examine detailed information on the structure and dynamical properties of the HIV-1 PR complexed with saquinavir in the three protonated states, monoprotonates at Asp25 (Mono-25) and Asp25′ (Mono-25′) and diprotonate (Di-Pro) at both Asp25 and Asp25′. The obtained results support clinical data which reveal that Ile84 and Gly48 are two of the most frequent residues where mutation toward a protease inhibitor takes place. In contrast to the Ile84 mutation due to high displacement of Ile84 in the presence of saquinavir, source of the Gly48 mutation was observed to be due to the limited space in the HIV-1 PR pocket. The Gly48 was, on one side, found to form strong hydrogen bonds with saquinavir, while on the other side this residue was repelled by the hydrophobic Phe53 residue. In terms of inhibitor/enzyme binding, interactions between saquinavir and a catalytic triad of the HIV-1 PR were calculated using the ab initio method. The results show an order of the binding energy of Mono25 < Di-pro ≪ Mono-25′, suggesting that the active site in the HIV-1 PR complexed with saquinavir is monoprotonated states on Asp25. In contrast to the binding energy, 3, 6 and 12 hydrogen bonds between saquinavir and HIV-1 PR were found for the Mono-25, Mono-25′ and Di-pro states, respectively. Discrepancy between the two trends suggests us to conclude that interaction between inhibitor and catalytic residues should be used as a criteria to enhance capability in drug designing and drug screening instead of using the total inhibitor/enzyme interaction which is normally reported in the literature. In addition, the distribution and binding of water molecules, in terms of hydrogen bonding, to the donor atoms of saquinavir were investigated and discussed, referring to that which was reported experimentally.

INTRODUCTION

The protease of human immunodeficiency virus 1 (HIV-1) plays an essential role in maturing infectious HIV particles.[1] Its structure and function have been well characterized, classified into subsite (P1, P1′, P2, P2′, P3, see Figure 1) and widely used to develop potent inhibitors as the therapeutic agent for AIDS.[2] The HIV-1 protease belongs to the class of aspartic proteases which contains a pair of catalytic Asp residues. In the active homodimeric HIV-1 protease (HIV-1 PR),[3] the catalytic aspartyl dyad (Asp25 and Asp25′) is located at the subunit-subunit interfacial region which is at the base of the substrate binding site. The active site is within a largely hydrophobic cavity capped by two flexible flaps (Figure 1). The specific task of the flaps is guarding the entrance to the active site cleft. The development of new and powerful HIV-1 PR inhibitors is relied strongly on the enzyme/inhibitor interactions. Therefore, the understanding of basic properties such as structure, dynamics and solvation of the complex helps directly in drug designing and drug discovery. To obtain the above-mentioned information experimentally, especially in solution, it is rather complicated. Therefore, theoretical methods such as molecular dynamics simulations proved to be a powerful tool for such propose.

Difficulty takes place in dealing with HIV-1 PR in which protonation equilibria in the active site depends on the three possible protonated states of the dyad residues, monoprotonated at each Asp25 or Asp25′ and diprotonate. The knowledge of the ionization state of the two catalytic aspartates is extremely important for drug design in a way to optimize the interactions between the inhibitor and the enzyme. Considerable efforts have been spent on this problem.[4−7] These studies reported different protonation models depending upon the local environment of the enzyme−inhibitor complex.[8] Ky-Youb Nam et al.[9] performed ab initio calculations and the free energy pertubation to determine the protonated state of HIV-1 protease complexed with inhibitor, A74704. The results show the significant implication that the protonated state of the active site of the complex is monoprotonated on Asp25. Plane wave-based ab initio molecular dynamics calculations[10] as well as NMR measurements[11] of the active site region of the HIV-1 PR

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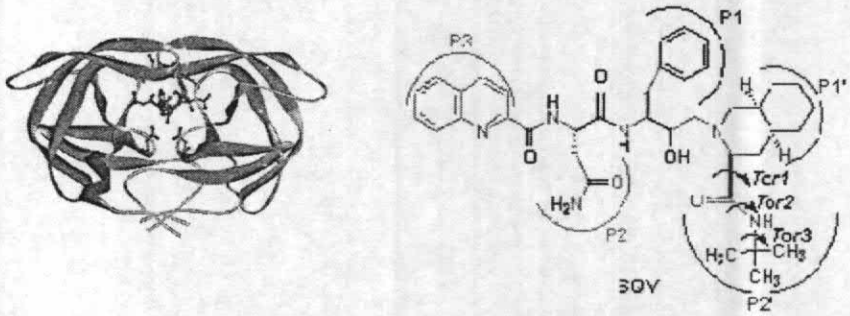

Figure 1. HIV-1 protease complexed with saquinavir, classification of P1, P1′, P2, P2′ and P3 subsites and definition of torsional angles (*Tor1-Tor3*), where catalytic dyad, Asp25 and Asp25′, are displayed as ball-and-stick and the two Ile50 and Ile50′ at the flap regions were also labeled.

complexed with pepstatin suggest that the system is at least monoprotonated, i.e., one of the two catalytic oxygens on an Asp residue is protonated.

This paper aims to investigate the structure, dynamics and solvation of HIV-1 PR complexed with saquinavir (Figure 1), the first HIV-1 PR inhibitor licensed for clinical use.[12] The contribution of such properties to drug resistance was also taken into consideration. The simulations were performed for the three protonated states. The unprotonated one was excluded due to the literature.[9-11]

METHODS

The Initial Structure. The structure of HIV-1 protease complexed with saquinavir (SQV) was taken from the Brookhaven Protein Data Bank (PDB code: 1HXB). The preparation of the initial structure starts by adding hydrogen atoms to the complex using AMBER 7.0 program.[13] The RESP charges were applied to all atoms of the HIV-1 protease, while the atomic charges of atoms of saquinavir, which are not available in the program, were prepared by fitting the electrostatic potentials around the molecule to the standard model using the RESP method.[14] The electrostatic potential was obtained by the Hartree−Fock single point calculation with 6-31G(d,p) basis set using Gaussian 98 program.[15]

Molecular Dynamic Simulations. Three simulations have been performed for the three protonated states of binding of HIV-1 PR/saquinavir complexes: monoprotonates at Asp25 (Mono-25) and 25′ (Mono-25′) and diprotonate at both Asp25 and Asp25′ (Di-Pro). To examine detailed information on the changes of the structure and dynamical properties of the HIV-1 PR via complexation, additional simulation was performed for the HIV-1 PR in its free from in the Mono-25 state. The simulated systems were neutralized by 7 Na+ and additional 11 Cl- and 12 Cl- for mono- and diprotonation, respectively. All models were solvated by TIP3P water molecules in the 74.52 Å × 77.38 Å × 66.26 Å box. Prior to MD simulations, each system was energy minimized. The total atoms of these simulations are 32946 and 32945 for mono- and diprotonation, respectively. The MD simulations were carried out for 1 ns. All simulations and energy minimization were performed using the AMBER 7.0 program[13] with all atomic force field developed by Cornell et al.[16] The simulations were performed with a time step of 2 fs and with a cutoff radius of 12 Å for the nonbonded interactions. The temperature was maintained at 298 K. The Particle Mesh Ewald (PME) method was employed for correcting electrostatic interaction. Periodic boundary conditions were applied, and the pressure was maintained at 1 atm by adjustment of the volume of the periodic box.[17]

Quantum Chemical Calculations. To investigate precise interaction energy in the different protonated states, the complexes were represented by 2 triads, Asp25-Thr26-Gly27 of both chains and saquinavir. The selected residues were obtained from the MD simulation using the following steps: *(i)* calculate the average structure from the whole trajectory, *(ii)* perform geometry optimization using energy minimization from AMBER 7.0 program, *(iii)* remove coordinates of the nonselected residues, keep only those of the 6 residues at the active site triad of the two chains and the saquinavir, *(iv)* terminate the C- and the N-termini at the ends of the selected residues by CH_3NH- and $-COCH_3$ groups, and *(v)* optimize geometry of the newly added hydrogen atoms using ab initio calculations at the second-order Møller−Plesset perturbation level with 6−31 G(d,p) basis set. Then, interaction between the selected residues and saquinavir for the three simulated systems were calculated using the density functional theory B3LYP/6-31G(d,p) with the extended 6-31+G-(d,p) basis sets. Calculations were performed using the Gaussian 98 program.[15]

RESULTS AND DISCUSSION

Flexibility of Saquinavir in the Complex. To explore flexibility of saquinavir's subsites (defined in Figure 1) in the complex, root-mean-square displacement (RMSD) of each subsite, relative to the initial MD (X-ray) structure, was calculated and shown in Figure 2. The RMSD plots through the simulation time, after equilibration, indicate very clearly that conformations of all subsites in the three protonated states are almost unchanged, except that of P2′.

Detailed discussion is centered on the conformational changes of P2′ subsite in which that of each protonated state exhibits different characters. Significant and permanent changes were observed for the Mono-25 state where the RMSD of approximately 1.1 Å starts to be detected through the whole range of the simulation, after equilibration (Figure 2a).

This fact indicates the single preferential conformation of the P2′ subsite of saquinavir in the complex with HIV-1 PR in the Mono-25 state. Situations are different for the Mono-25′ and Di-pro states where fluctuations of the RMSD were obviously detected. Figure 2b suggests two preferential conformations of the P2′ subsite of saquinavir in the

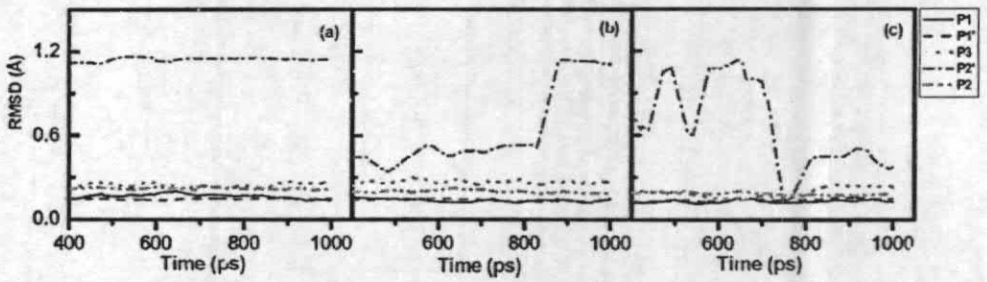

Figure 2. RMSD for the three protonated states, Mono-25 (a), Mono-25′ (b) and Di-pro (c), of saquinavir's subsites (defined in Figure 1) relative to the initial MD (X-ray) structure.

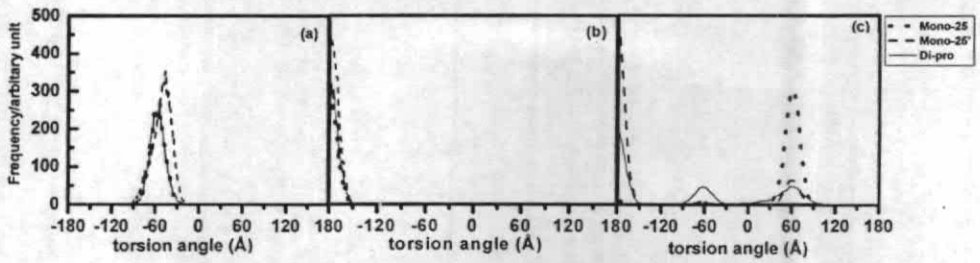

Figure 3. Changes of P2′ torsional angles, *Tor1-Tor3* (a−c) defined in Figure 1, of saquinavir complexed with HIV-1 PR.

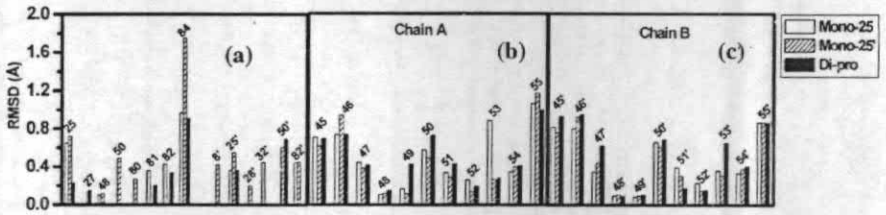

Figure 4. Comparison of RMSD for the Mono-25, Mono-25′ and Di-pro states with respect to their average structure for the residues located within 3 Å around saquinavir (a) and in the flap region, residues 45−55 (b).

monoprotonated state on Asp25′ of HIV-1 PR with the RMSDs of approximately 0.5 and 1.1 Å. Furthermore, the Di-pro state favors two major conformations at the RMSDs of about 0.4 and 1.1 Å and two additional minor probabilities at RMSDs of about 0.6 and 0.1 Å (Figure 2c).

To look into a detailed source of the above findings, changes of P2′ torsional angles, *Tor1-Tor3* defined in Figure 1, of saquinavir were analyzed and displayed in Figure 3. The plots show pronounced and sharp peaks indicating rigidity of the three angles, i.e., they are slightly flexible in a narrow range. No significant difference of the *Tor1* and *Tor2* angles was found for the three protonated states of the HIV-1 PR (Figures 3a-3b). For the angle *Tor3* (Figure 3c), the changes are consistent with the RMSD plots for P2′ at the three states shown in Figure 2 leading to the following conclusions. Single preferential conformation of P2′ subsite for the Mono-25 states (Figure 2a) was represented by the single sharp peak at *Tor3* = 60° (dot line, Figure 3c). Furthermore, the two peaks at *Tor3* = −180° and 60° (broken line) in Figure 3c are due to the two conformations of the Mono-25′ state where RMSDs = 0.5 and 1.1 Å (Figure 2b), respectively. A sharper and higher peak at *Tor3* = −180° than the other one at *Tor3* = 60° indicate higher rigidity and higher probability of finding of the first conformation (RMSD = 0.5 Å from 400 to 840 ps in Figure 2b) than the other one (RMSD = 1.1 Å from 900 ps to 1000 ps in Figure 2b), respectively. In addition, the three peaks at *Tor3* = −180°, −60° and 60° of the Di-pro state (solid line in Figure 3c) can be assigned to the RMSDs = 0.4, 1.1, and 0.6 Å for the Di-pro state taken place in Figure 2c, respectively.

Flexibility of HIV-1 PR in the Complex. Protein flexibility is known to play a role not only in the catalytic process but also in the computer-aided drug design. A clear example is the high flexibility of the flaps (residues 45−55) in both monomeric and dimeric forms of unliganded protease reported by both computational[18,19] and experimental[20,21] studies. We now turn our attention to investigate their property quantitatively. Attention is focused on the flexibility of the residues lying in the flap region and those located within 3 Å from all atoms of saquinavir. The RMSD for those residues with respect to the X-ray structure for three states were evaluated and plotted in Figure 4a-4b.

It is interesting to note that within a spherical radius of 3 Å from the saquinavir highest and lowest displacements were observed at Ile84 and Gly48 residues of chain A (Figure 4a-4b), respectively (Gly48 is not within 3 Å limit for Di-Pro state). Surprisingly, these observations support clinical data which reveal that Ile84 and Gly48 are two of the most frequent residues where mutation toward a protease inhibitor[22] takes place. The data lead us to conclude that a conformational change is a primary source of mutation of Ile84. In contrast, Gly48 mutation can be described in terms of indirect displacement of Phe53 in the flap region. As can be seen in Figure 4b that the RMSDs of Phe53 of the Mono-25 chain A and of Di-pro chain B are significantly higher than those of the other two states. A clear description of the mutation of Gly48 was given in the next paragraph.

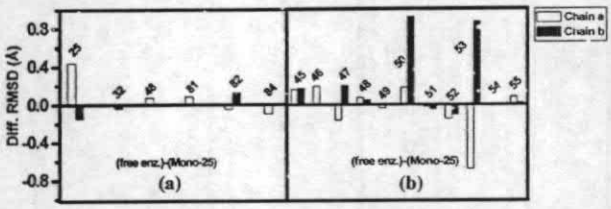

Figure 5. Subtraction between the RMSDs of the free enzyme and complex for the Mono-25 state lying within 3 Å from the atoms of saquinavir (a) and the flap region, residues 45−55 (b).

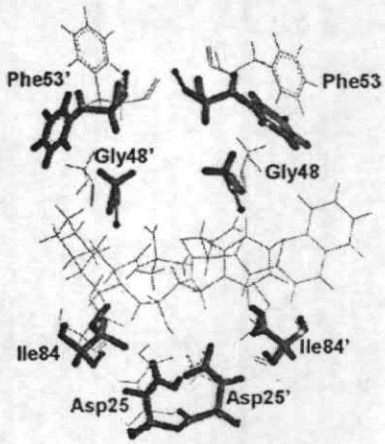

Figure 6. Superimpositon between the average structures of HIV-1 PR in free (stick) and complex forms (line) where only selected residues are displayed.

To explore the conformational changes due to complexation, subtraction between the RMSDs for the residues of the free enzyme and the complex of the Mono-25, lying in the flap region and those located within 3 Å from the atoms of saquinavir were again calculated and plotted in Figure 5a-5b, i.e., a positive value indicates higher rigidity of the complex than the free enzyme. Dramatic changes were detected on the residues Ile50′, Phe53′ (Figure 5b) and Asp25 (Figure 5a) where the RMSD of free enzyme are much higher than those of the complex. This observation can be easily explained in terms of binding between enzyme and inhibitor which leads directly to rigidity of the complex. Surprisingly, residue Phe53 (Figure 5b) in the flap region in the complex form is less rigid than the free form. This is in contrast to what is generally known and reported by Zhongwei Zhu et al.[23] using free energy techniques showing that a barrier to flap opening exists in the presence of an inhibitor while this evidence disappears for the free enzyme. This observation confirms the lower rigidity of Phe53 chain A of Mono-25 state in the complex than the free forms (Figure 5b). To understand the reason for the mutation due to the indirect displacement, superimposition between the enzyme structures in the free and complex forms was examined, and the molecular structure in an area close to Phe53 of both chains was displayed in Figure 6. It can be clearly seen from the plot that the presence of saquinavir leads to dramatic changes of the conformations of Phe53 and Phe53′.

Gly48, on one side, was found to form strong hydrogen bonds with saquinavir (details in HIV-1 PR Binding section), while it was, on the other side, repelled by the hydrophobic Phe53 residue. This leads directly to a very high rigidity of Gly48 (Figure 4b, chain A) as well as a high displacement of Phe53. Such unfavorable conditions were supposed to facilitate the mutation of Gly48. Due to the unsymmetric character of the saquinavir molecule, Gly48′ was not detected to bind to the other end of saquinavir. Therefore, Gly48′ is less interfered by the presence of saquinavir in comparison to Gly48. This can be also a reason for the lower RMSD of Phe53′ than Phe53 (Figure 4b, Mono-25) and the higher degree of drug resistance of Gly48 than Gly48′. This evidence is fully supported by the X-ray crystallographic analysis and molecular modeling experiments.[22] A clear conclusion is that in addition to the I84V mutation due to high displacement of Ile84 in the presence of saquinavir (Figure 4a), cooperation effect can be also due to the limited

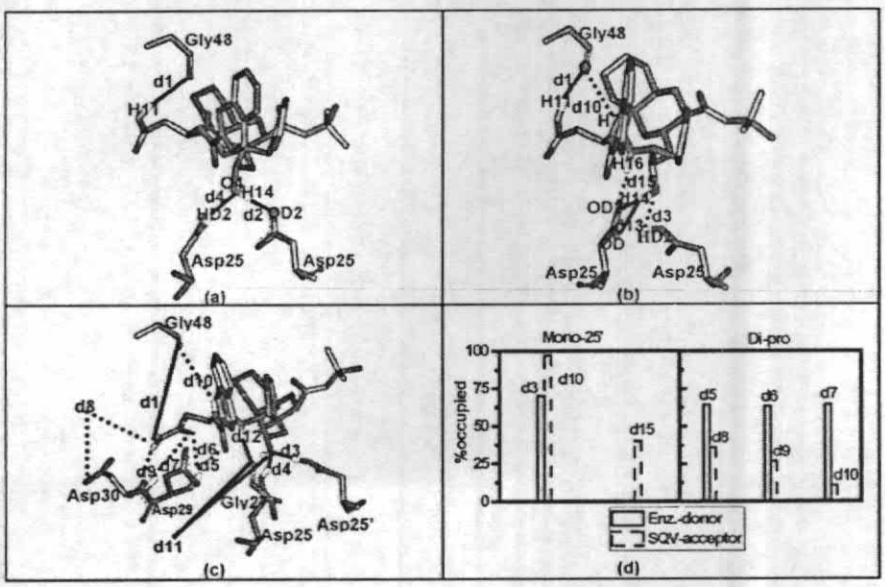

Figure 7. Binding between saquinavir and HIV-1 PR in the Mono-25 (a), Mono-25′ (b) and Di-pro (c) states where solid and broken lines denote hydrogen bonds which were detected 100% and less than 100% of the total configurations (400−1000 ps) after equilibration, respectively. Percentages of occupation were given in a bar graph (d) where roles of saquinavir (SQV) and HIV-1 PR (ENZ) as proton donor/acceptor were separately plotted.

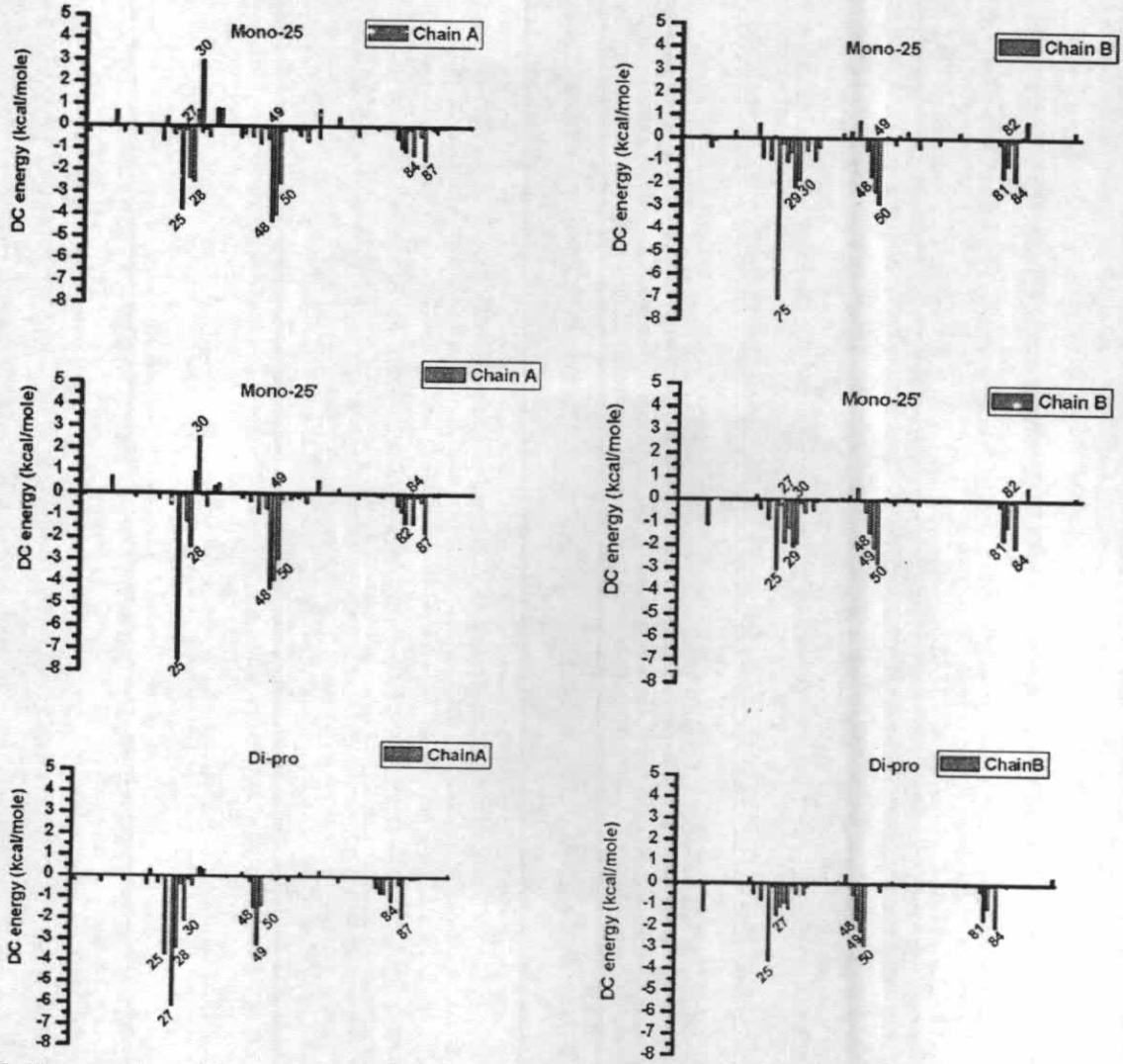

Figure 8. The summations of the van der waal and electrostatic terms are plotted between all residues of HIV-1 PR and SQV.

space (Figure 6) in the HIV-1 PR pocket, especially for the G48V where saquinavir requires more space on the Gly48 than the Gly48′ sides.

Saquinavir-HIV-1 PR Binding. Most enzymes are highly specific for their substrate; therefore, an inhibitor of a similar shape and chemical nature is usually supposed to be recognized by the enzyme. This approach was widely used to design inhibitors for diverse enzymatic targets, including HIV-1 protease. To further explore the binding between saquinavir and HIV-1 PR, hydrogen bonds of the three protonated states were analyzed based on the donor−acceptor distance criteria. The results were illustrated in Figure 7a−7c. Percentages of occupation in which saquinavir and HIV-1 PR play a role as proton donor/acceptor were separately given in Figure 7d. The plots (Figure 7a−7c) show 3, 6 and 12 hydrogen bonds between saquinavir and HIV-1 PR in the Mono-25, Mono-25′ and Di-pro states, where 3, 3 and 6 of them are 100% occupied, respectively. Detailed comparison is concentrated on the different binding between saquinavir and HIV-1 PR in the two monoprotonated states, Mono-25 and Mono-25′. In the first system, saquinavir was held in the cavity of the HIV-1 PR by the three hydrogen bonds with 100% occupation, via Gly48 and the two catalytic residues, Asp25 and Asp25′ (Figure 7). The other three bonds were additionally detected for the Mono-25′ state. In this case, Gly48 forms one more pronounced hydrogen bond with H7 (95% occupation), while Asp25 forms one more pronounced bond with H14 (100% occupation) and another weak bond with H14 (30% occupation). Note that binding between Asp25′ and the OH group of saquinavir in the Mono-25′ state is slightly weaker (70% occupation) than that in the Mono-25 state. For the diprotonated state, saquinavir forms several hydrogen bonds with not only Gly48, Asp25 and Ap25′ as in the monoprotonated one but also to Gly27, Asp29 and Asp30. The corresponding percentages of fully and partial occupations were shown in Figure 7c and 7d.

To seek for the fundamental basis of protein-drug interactions, the interaction energy between individual protease residue and saquinavir were calculated using the decomposition energy module of Amber 7 and, then, plotted as shown in Figure 8. The decomposition of the energy shows that the *per residue* interaction energy varies in the range 3 to −8 kcal/mol for all three protonation states. These plots suggested that the relatively significant interaction between the enzyme and SQV was due to the residues in the 3 regions of both chains, those in the catalytic site, the flaps and the

Table 1. Interaction between Saquinavir and the Catalytic Triad Residues, Asp25-Thr26-Gly27 of Both Chains of HIV-1 PR at the Three Protonated States Yielded from QM and MM Calculations[a]

protonated state	QM (kcal/mol)	MM (kcal/mol)	MM/QM × 100 (%)
Mono-25	−66.9	−34.84	52
Mono-25′	−49.7	−28.09	56
Di-pro	−59.3	−25.11	42

[a] For the QM, the density functional theory B3LYP/6-31G(d,p) with the extended 6-31+G(d,p) basis sets were applied (see text for more details).

C-terminus (Pro81-Ile84). The fact that these three regions are recognized as the binding sites for SQV.

As discussed above, the significant conformational changes are associated with the mutation of Gly48 and Ile84. The decomposition of the SQV-enzyme interaction energy in Figure 8 provides a strong support in terms of energy contributions from those two residues. With an exception of the catalytic residues, which must be highly conserved in the aspartyl protease family, the mutation of Gly48 and Ile84 in the HIV-1 protease is, therefore, an optimal choice for the virus to achieve drug resistance.

To separate interaction between saquinavir and the catalytic site of the enzyme from the total enzyme/saquinavir interaction, ab initio calculations were performed (more details in the Quantum Chemical Calculations section). Table 1 shows the interaction energy between saquinavir and the catalytic triad residues, Asp25-Thr26-Gly27 of both chains, of HIV-1 PR. An unexpected result is an order of stability in which the interaction energy of −66.9 kcal/mol for Mono-25 is significantly deeper than that of −59.3 kcal/mol and −49.7 kcal/mol for the Di-pro and Mono-25′, respectively, i.e., Mono-25 < Di-pro ≪ Mono-25′.

In addition to the QM interaction energy, the energy derived from the force field implemented in the Amber program was also computed to estimate the MM potential quality (Table 1). The MM interaction energy was obtained by adding up the decomposed energy data (Figure 8) of the catalytic triad residues, in which the model is analogously used in the QM calculation. The results in Table 1 show that the MM interaction energies for the three states are approximately 50% lower than those yielded from the QM approach. In addition, the MM results suggest an order of the stability of Mono-25 ≪ Mono-25′ < Di-pro. This is different from that predicted from the QM calculation where Mono-25 ≪ Di-pro < Mono-25′. Nevertheless, both approaches suggest the Mono-25 is the most energetically favorable configuration where the predicted energies are significantly lower than the other two states. It should be noted that the MM potential energy surface is usually generalized to be applicable for a wide range of molecular systems, leading to a lack of some specific details, especially for the present study where hydrogen bonding and ion−molecule interactions are known to a play role. These effects can be quantum mechanically taken into account.

Consequently, the trend suggested by the QM results is in contrast to an order of a number of hydrogen bonds between saquinavir and HIV-1 PR in which Dipro ≫ Mono-25′ > Mono-25 (Figure 7). This can be due to structural changes of both saquinavir and catalytic residues via complexation in order to allow a better conformational fit

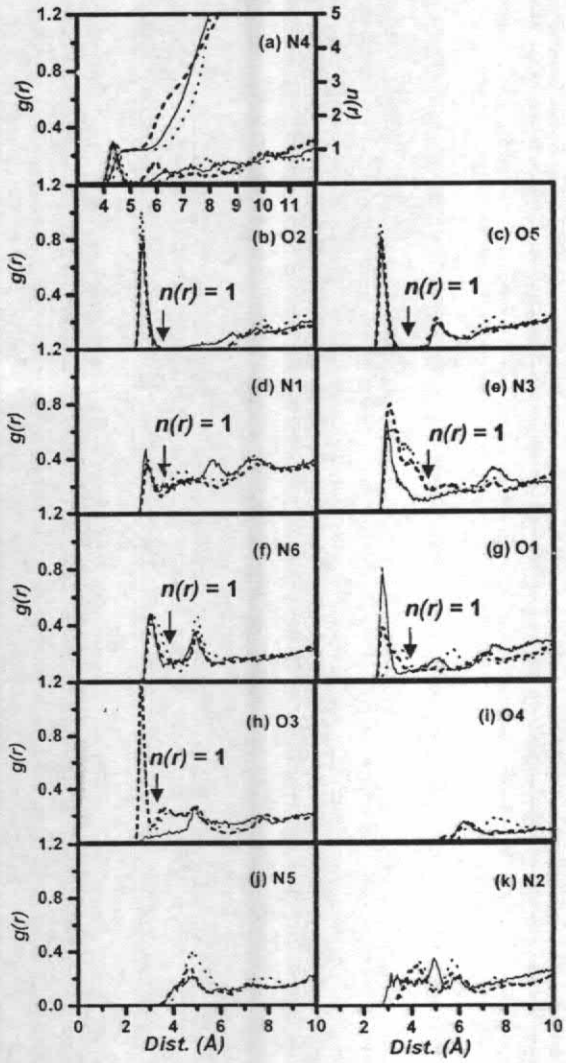

Figure 9. Radial distribution function, $g(r)$, and corresponding integration numbers (right axis for Figure 8a and marked by number and arrow for the other) from acceptor atoms of saquinavir (labeled as an inset and in Figure 9) to oxygen atom of water molecule for the three protonated states, Mono-25 (dot line), Mono-25′ (short dash line) and Di-pro (solid line).

between saquinavir and HIV-1 PR in the catalytic than the other regions. The above finding has potentially significant implications that the protonated state of the active site in HIV-1 PR complexed with saquinavir inhibitor is a mono-protonated state on Asp25. However, since the protease has C_{2V} symmetry, the proton-transfer mechanism is much faster than reorientation of the inhibitor at the active site.[24] Therefore, the proton transfer is associated with the Asp25/Asp25′ conversion. In addition, interaction between the inhibitor and the catalytic region of the enzyme is supposed to relate directly to the activity of the inhibitor in the catalytic process. Therefore, interaction between the inhibitor and the catalytic residues should be used as a criteria to enhance capability in drug designing and drug screening instead of using the total inhibitor/enzyme interaction which is normally reported in the literatures.

Some comments should be made concerning contributions of the environment to the free energy of binding as well as the QM interaction energy shown in Table 1. These effects

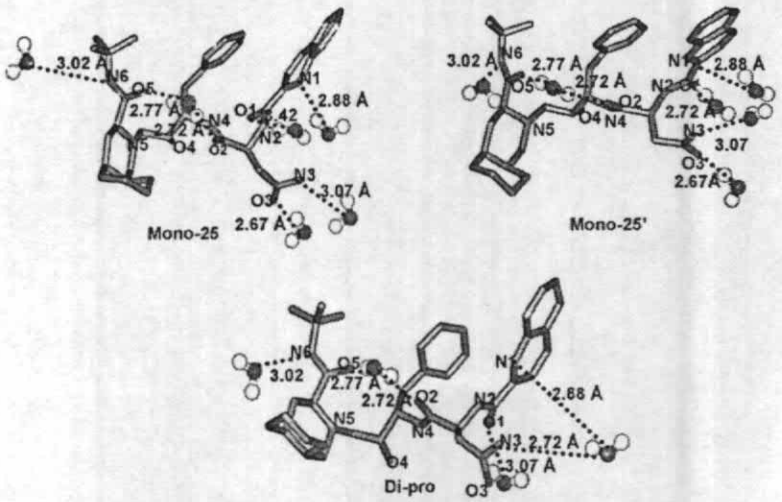

Figure 10. Snapshot which accumulates water molecules lying in the first hydration shell of saquinavir inhibitor in the three protonated states.

were taken into account in our previous work[25] using ONIOM and MM/PBSA methods embedded in the Gaussian 98 the AMBER programs, respectively.

Characteristic of Water Molecules in the Cavity of HIV-1 PR. An important question that arises in the context of drug binding studies involves the distribution of water molecules in the cavity region. To seek for such information the plot of radial distribution function (RDF, $g_{xy}(r)$)—the probability of finding a particle of type x in a spherical radii, r, around the particle of type y—from acceptor atoms of saquinavir (see labels in Figure 10) to an oxygen atom of water was used. The results, for the three protonated states were calculated, were shown in Figure 9 together with the corresponding running integration numbers.

Investigation was primarily focused on N4 of saquinavir since it was, topologically, located almost at the center of the binding pocket of the HIV-1 PR (see labels in Figure 9). The plots for the three states (Figure 9a) show the first sharp peak centered at 4.3 Å with the running coordination number of 1 water molecule, integrated up to the first minimum of 4.8 Å. Although the peak is very sharp and well pronounced but with the distance of 4.3 Å, it can be concluded very clearly that no water molecule is bound directly to the N4 atom. The plots of the coordination number (right scale of Figure 9a) start to increase exponentially between 6 and 7 Å indicating the boundary between the water inside the cavity and bulk water. This distance is consistent with half of the estimated diameter (from the tips of the flap to the active site residues) of the HIV-1 PR pocket of 13.5 Å.[23] To estimate the total number of water molecules in the pocket of the HIV-1 PR, an oxygen atom of a water molecule lying within the spherical radius of 3.0 Å (distance to the first minimum of the RDFs from donor atoms of saquinavir to oxygen atoms of saquinavir to oxygen atom of water as shown in Figure 9 around the atoms of saquinavir were counted and averaged using the water-shell option in the Amber program). The Mono-25, Mono-25′ and Di-pro pockets were found to contain 17, 15 and 15 water molecules, respectively.

The RDF plots in Figure 9b-9k can be classified into 3 types, i.e., the RDFs exhibit *(i)* the first sharp peak at ~3 Å where the minimum approaches zero (Figure 9b-9c); *(ii)* the first sharp peak at ~3 Å where the minimum is above zero (Figure 9d-9h exclude Di-pro of O3) and *(iii)* the first broad peak either at ~3 Å or > 3 Å (Figure 9i-9k). The first type RDF with the corresponding coordination number of one indicates that O2 and O5 of saquinavir are solvated by one water molecule in terms of hydrogen bonding (O−O distance = 3.0 Å) with 100% occupation (the first minimum approaches zero). For the second type RDF, the coordination number of one indicates a single hydrogen bond, almost 100% occupation, between a saquinavir and a water molecule, while the nonzero minimum demonstrates solvent exchange, hydrogen bond breaking and forming, between the first and the second peaks (second solvation shells). In contrast, O4, N5 and N2 were observed to be free form solvation, third type RDF (Figure 9i-9k). To visualize the above-mentioned hydration, a snapshot which accumulates water molecules lying under the first peak at 3 Å of the RDFs was displayed in Figure 10.

Comprehensive investigation has been made to seek for the precise orientation of the one water molecule in the nearest of O2 and O5. It is interesting to note that O2 and O5 were observed to solvate by the same water molecule in the configuration shown in Figure 9. This water molecule was, at the same time, found to form a hydrogen bond with the flap residues, Ile50 and Ile50′ (see Figure 1). This is in good agreement with the experimental observation where these unique water molecules are commonly detected to hold the molecular structure in the peptidomimetic inhibitor complexes.[26] Interest is also focused on the solvation of O4 which is the OH group of saquinavir known to bind to the catalytic dyad residues of the HIV-1 PR and to take part in inhibiting the catalytic process.[23] Within a spherical radius of 5 Å around O4, no water molecule was detected (Figure 9h).

This fact supports the previous finding which states that inhibition of the catalytic mechanism of the protease is most likely a combination of favorable binding of a particular compound and exclusion of water from the active site.[23] In contrast, a single water molecule, known as catalytic water,[27] is required in the catalytic mechanism of the HIV-1 PR. However the HIV-1 PR mechanism was also proposed to involve the nucleophilic attact.[28]

CONCLUSIONS

MD simulations of the HIV-1 PR complexed with saquinavir in the three protonated states, monoprotonates at Asp25 and Asp25′ and diprotonate at both Asp25 and Asp25′, provide information on structural and dynamical characteristics in term of flexibility, saquinavir/HIV-1 PR binding and hydration structure of the complexes. The simulation results report good evidence that deal with questions related to the basic mutation and solvation data. With reference to the molecular structure of the HIV-1 PR in free form, the presence of saquinavir leads to dramatic changes of the conformations of Phe53 and Phe53′. In terms of the flexibility of saquinavir in the complexes, significant changes of the conformation of P2′ subsite were obviously detected. For the enzyme, the highest and lowest displacements were observed at Ile84 and Gly48 residues of chain A, respectively. These observations support clinical data which reveal that Ile84 and Gly48 are two of the most frequent residues where mutation toward a protease inhibitor takes place. The detected data suggest us to conclude that conformational change is a primary source of mutation of Ile84. In contrast, Gly48 mutation can be described in terms of indirect displacement of Phe53 in the flap region. Furthermore, 3, 6 and 12 hydrogen bonds between saquinavir and the HIV-1 PR were observed in the Mono-25, Mono-25′ and Dipro states, where 3, 3 and 6 of them are 100% occupied, respectively. To separate interaction between saquinavir and the catalytic site of enzyme from the total enzyme/saquinavir interaction, ab initio calculations were performed. An unexpected result was found in terms of complex stability in which an interaction energy of −66.9 kcal/mol for Mono-25 is significantly more favorable those of −59.3 kcal/mol and −49.7 kcal/mol for the Di-pro and Mono-25′, respectively, i.e., Mono-25 < Di-pro ≪ Mono-25′. This trend is in contrast to an order of number of hydrogen bonds between saquinavir and HIV-1 PR in which Di-pro ≫ Mono-25′ > Mono-25. The interaction data suggest to us to conclude that the protonated state of the active site in HIV-1 PR complexed with saquinavir inhibitor is a monoprotonated state on Asp25. In addition, the solvent effect was taken into consideration in terms of radial distribution functions and corresponding integration numbers. It was found that the HIV-1 PR pocket contains 17, 15, and 15 water molecules, coordinated in the first hydration of saquinavir.

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1. Publication for this thesis

1.1 Wittayanarakul, K., Aruksakulwong, O., Saen-oon, S., Chantratita, W., Parasuk, V., Sompornpisut, P. and Hannongbua, S. Insights into saquinavir resistance in the G48 HIV-1 protease: quantum calculations and molecular dynamic simulations. J. Bio. Phys. 88 (2005): 867-879.

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1.3 Wittayanarakul, K., Feig, M., Hannongbua, S. On the correlation between drug-resistant pattern of HIV-1 protease inhibitors and binding free energy and structural changes. BMC System Biology. (2007) *in press*. (Abstract)

1.4 Wittayanarakul, K., Hannongbua, S., Feig, M. Accurate prediction of protonation state as a prerequisite for reliable MM-PB(GB)SA binding free energy calculations of HIV-1 protease inhibitors. J. Comput. Chem. (2007) submitted.

2. Publication for related work

2.1 Aruksakunwong, O., Promsri, S., **Wittayanarakul, K.**, Nimmanpipug, P., Lee, V., Wijitkosoom, A., Sompornpisut, P., and Hannongbua, S. Currently developed HIV-1 protease inhibitors. Current Computer-Aided Drug Design (2006) accepted.

2.2 Sanen-oon, S., Aruksakunwong, O., **Wittayanarakul, K.**, Sompornpisut, P., and Hannongbua, S. Insight into analysis of onteractions of saquinavir with HIV-1 protease in comparison between wild-type, G48V and G48V//L90M mutant: based on QM and QM/MM calculations. (2006) submitted.

3. Publication for other contributions

3.1 Lee, V. S., **Wittayanarakul, K.**, Remsungnen, T., Parasuk, V., Sompornpisut, P., Chantratita, W., Sangma, J., Vannarat, S., Sricchaisakul, P, Hannongbua, S., Saparpakorn, P., Treesuwan, W., Aruksakulwong, O., Pasomsub, E., Promsri, S., Chuakheaw, D., and Hannongbua, S. Structure and dynamics of SARS coronavirus proteinase: the primary key to the designing and screening for anti-SARS drugs. ScienceAsia 29 (2003): 181-188.

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3.3 Lee, V. S., **Wittayanarakul, K.**, Remsungnen, T., Parasuk, V., Sompornpisut, P., Chantratita, W., Sangma, J., Vannarat, S., Sricchaisakul, P, Hannongbua, S., Saparpakorn, P., Treesuwan, W., Aruksakulwong, O., Pasomsub, E., Promsri, S., Chuakheaw, D., and Hannongbua, S. Dimer of SARS coronavirus main protease as studied by

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PUBLICATIONS

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2. **Wittayanarakul, K.**, Aruksakulwong, O., et al. J. Bio. Phys. 88 (2005): 867-879.
3. **Wittayanarakul, K.**, Aruksakunwong, O., et al. J. Chem. Inf. Model. 45 (2005): 300-308.
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6. Aruksakunwong, O., **Wittayanarakul, K.**, et al. Current Computer-Aided Drug Design (2006) accepted.
7. Sanen-oon, S., **Wittayanarakul, K.**, et al. (2006) submitted.
8. **Wittayanarakul, K.**, Feig, M., and Hannongbua, S. BMC System Biology. (2007) *in press*. (Abstract)
9. **Wittayanarakul, K.,** Hannongbua, S., and Feig, M. J. Comput. Chem. (2007) submitted.

PRESENTATIONS

3 INTERNATIONAL (2 Oral Presentations and 1 Poster) AND 4 NATIONAL PRESENTATIONS (4 Oral Presentations)