

Structural Basis for Coevolution of a Human Immunodeficiency Virus Type 1 Nucleocapsid-p1 Cleavage Site with a V82A Drug-Resistant Mutation in Viral Protease

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Maturation of human immunodeficiency virus (HIV) depends on the processing of Gag and Pol polyproteins by the viral protease, making this enzyme a prime target for anti-HIV therapy. Among the protease substrates, the nucleocapsid-p1 (NC-p1) sequence is the least homologous, and its cleavage is the rate-determining step in viral maturation. In the other substrates of HIV-1 protease, P1 is usually either a hydrophobic or an aromatic residue, and P2 is usually a branched residue. NC-p1, however, contains Asn at P1 and Ala at P2. In response to the V82A drug-resistant protease mutation, the P2 alanine of NC-p1 mutates to valine (AP2V). To provide a structural rationale for HIV-1 protease binding to the NC-p1 cleavage site, we solved the crystal structures of inactive (D25N) WT and V82A HIV-1 proteases in complex with their respective WT and AP2V mutant NC-p1 substrates. Overall, the WT NC-p1 peptide binds HIV-1 protease less optimally than the AP2V mutant, as indicated by the presence of fewer hydrogen bonds and fewer van der Waals contacts. AlaP2 does not fill the P2 pocket completely; PheP1' makes van der Waals interactions with Val82 that are lost with the V82A protease mutation. This loss is compensated by the AP2V mutation, which reorients the peptide to a conformation more similar to that observed in other substrate-protease complexes. Thus, the mutant substrate not only binds the mutant protease more optimally but also reveals the interdependency between the P1' and P2 substrate sites. This structural interdependency results from coevolution of the substrate with the viral protease.

Human immunodeficiency virus type 1 (HIV-1) matures after the viral protease processes (35) the Gag and Pol polyproteins at 10 substrate locations (3, 15). Therefore, inhibition of HIV-1 protease represents an important avenue for antiviral therapy (13, 48). The substrate sequences cleaved by the protease are nonhomologous (3), with the sequence of the nucleocapsid-p1 (NC-p1) substrate being the most different. In spite of the poor sequence homology among the substrate sites, a series of substrate-protease crystal structures led us to hypothesize that substrate specificity in HIV-1 protease results from the enzyme's recognizing an asymmetric shape (or envelope) rather than a particular amino acid sequence (40). This shape results from the conformation that a particular substrate sequence can adopt, implying that an interdependency necessarily exists among the different substrate residue sites.

All of the protease inhibitors whose designs were structure based bind competitively (8, 18, 28, 52, 53) at the active site. Since these inhibitors bind at the same site as the substrates, many protease residues contact both substrates and inhibitors. Drug resistance, which often develops in the presence of therapeutic protease inhibitors, results from high viral turnover, the infidelity of the viral reverse transcriptase (16, 42, 43), and selective pressure on the virus. With drug resistance, the protease no longer binds as tightly to inhibitors but retains the ability to recognize and cleave its substrate sites.

The first drug-resistant mutation that often occurs in patients, V82A (47), is frequently associated with indinavir or zidovudine therapy (5, 9, 11, 30). Our previous studies have shown that V82A is a prime site for drug resistance to occur, as the valine at residue 82 is not critical for substrate recognition but does extensively contact many of the commonly used inhibitors (39). However, the apparent coevolution of the NC-p1 cleavage site (AP2V) with the V82A mutation in the protease (1, 10, 20, 55) implies that Val82 plays an important role in the protease's recognition of the NC-p1 substrate, a role that is lost when the V82A mutation occurs.

Within the viral context, the NC-p1 cleavage site is the slowest (50), final (37, 54), and, therefore, rate-determining site in HIV-1 Gag to be processed by the viral protease (6, 37). NC-p1 has a polar Asn at the P1 position, while a hydrophobic or aromatic residue is found at the same location in the other substrate sequences. An Ala occupies the P2 position of the NC-p1 substrate, while a branched side chain (14) exists at P2 in the other substrate sequences. The rate and order in which NC-p1 is cleaved may be dictated by its unusual sequence as well as by the location of this site within the Gag polyprotein.

In several studies of drug-experienced patient viral sequences, the NC-p1 substrate cleavage site has been seen to mutate (1, 6, 10, 24, 44, 55). The most frequently observed change occurs at P2, where the alanine mutates to a valine in viral sequences that also contain the V82A drug-resistant protease mutation. Selection for a valine at this site makes sense as valine is the wild-type (WT) residue at P2 in another substrate sequence, the capsid-p2 cleavage site. In fact, the WT HIV-1 protease cleaves AP2V in the NC-p1 cleavage site more efficiently than it cleaves the WT NC-p1 sequence (12).

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The present study focuses on elucidating the structural rationale for HIV-1 protease recognition of the NC-p1 cleavage site. We determined the crystal structures of both the WT and V82A HIV-1 proteases in complex with their respective NC-p1 substrates. As seen in our previous studies (40), there is an interdependency between the substrate subsites throughout the cleavage site sequence that allows for the sequence to be recognized as a substrate sequence by HIV-1 protease.

MATERIALS AND METHODS

Nomenclature. HIV-1 protease variants (WT or V82A), the nucleocapsid-p1 (NC-p1) WT substrate, and its AP2V mutant substrate will be distinguished throughout this article by subscript and superscript acronyms. For example, ^{WT}NC-p1_{WT} denotes the WT substrate NC-p1 in complex with the WT protease, and ^{AP2V}NC-p1_{V82A} denotes the AP2V mutant substrate in complex with the V82A mutant protease.

Substrate peptides. Two decameric peptides, ^{WT}NC-p1 (P5 to P5': ERQAN*FLGKI) and ^{AP2V}NC-p1 (P4 to P6': RQVN*FLGKIN), with sequences corresponding to the NC-p1 substrate cleavage site within the Gag polyprotein, were chosen as previously described (40). The slight difference in the regions of the cleavage sites that were crystallized occurred because the ^{AP2V}NC-p1 peptide (P5 to P5': ERQVN*FLGKI) was not very soluble, whereas the decameric peptide (P4 to P6': RQVN*FLGKIN) was. Both peptides were purchased from Quality Controlled Biochemicals Inc., Hopkinton, Mass.

Mutagenesis, protein purification, and crystallization. The protease was expressed from a synthetic gene optimized for *Escherichia coli* codon usage with Q7K to prevent autoproteolysis (45). This gene was used as the starting template for mutagenesis to introduce the D25N (to prevent the protease from cleaving its substrates) and V82A substitutions. Mutations were made by using a Quick-Change site-directed mutagenesis kit (Stratagene, La Jolla, Calif.).

Protein expression, isolation, and purification were carried out as previously described (17). The purified protease, in 50% acetic acid, was then refolded by rapid 10-fold dilution into a mixture of 0.05 M sodium acetate (pH 5.5), 10% glycerol, 5% ethylene glycol, and 5 mM dithiothreitol (refolding buffer). The diluted protein was concentrated on an Amicon ultrafiltration cell and dialyzed to remove any residual acetic acid. Protease used for crystallization was further purified by using a Pharmacia Superdex 75 fast-performance liquid chromatography column equilibrated with refolding buffer.

Crystals were grown by the hanging drop, vapor diffusion method as previously described (38, 39, 49). Stock solutions (25 mM) of substrate peptides used for cocrystallization were dissolved in refolding buffer rather than in dimethyl sulfoxide. The protein concentration was approximately 1 mg ml⁻¹. Small crystals started appearing after 6 to 8 weeks, with the longest length between 0.1 and 0.2 mm.

Data collection. Crystals chosen for data collection were flash frozen in a nitrogen stream. X-ray data on these cryocooled crystals were collected on our in-house Rigaku X-ray generator with an *R*-axis IV image plate system. Approximately 200 5-min frames were collected per crystal with 1-degree oscillations and no overlap between frames. The frames were later integrated and scaled by using the programs DENZO and ScalePack, respectively (29, 34). The ^{WT}NC-p1_{WT} and ^{AP2V}NC-p1_{V82A} complexes diffracted up to 2.1 and 2.0 Å, respectively. Complete data collection statistics are listed in Table 1.

Structure solution and crystallographic refinement. The CCP4i interface to the CCP4 suite and related software modules (4) was used for most of the operations described in this section. The molecular replacement package AMoRe (33) was used to solve the structures. X-ray data within 8.0 to 3.0 Å were used for structure solution by employing a Patterson radius of 25 Å. An inhibitor-protease complex obtained from the Protein Data Bank (PDB code 1MTR) (27) was used as the search model. The molecular replacement solutions had typical correlation function and *R* values of 78 to 81 and 29 to 31%, respectively. After structure solutions were obtained, Refmac5 (32) was used to perform a rigid body refinement of 25 cycles on data to 3.0 Å. Although the *R* values for both complexes decreased slightly, the free *R* dropped considerably to just above 30%. ARP/WARP (31) was used to improve the initial phases. Graphical rebuilding was performed with CHAIN (46), and the substrate peptides were modeled. The real space refinement package RSREF (2) was used to adjust the model to fit the electron density maps. Repeated rounds of Refmac5 and manual rebuilding were performed until the refinement converged. The final refinement statistics are also listed in Table 1.

TABLE 1. Crystallographic statistics for the two NC-p1 complexes

Variable	^{WT} NC-p1 _{WT}	^{AP2V} NC-p1 _{V82A}
Substrate	ERQAN*FLGKI	RQVN*FLGKIN
Data collection		
Space group	P2 ₁ 2 ₁ 2 ₁	P2 ₁ 2 ₁ 2 ₁
a (Å)	51.1	50.8
b (Å)	57.7	57.3
c (Å)	61.5	60.9
Z	4	4
Temperature (°C)	-80	-80
Resolution (Å)	2.1	2.0
Total number of reflections	38149	80252
Number of unique reflections	10450	12492
R _{merge} (%)	9.2	7.5
Completeness (%)	94.1	99.7
I/σ ₁	4.5	9
Crystallographic refinement		
R value (%)	20.6	19.5
R _{free} (%)	23.3	23.1
Sigma cutoff	0	0
RMSD ^a in:		
Bond lengths (Å)	0.004	0.005
Bond angles (°)	1.5	1.3

^a RMSD, root mean square deviation.

RESULTS

Overall structure of the complexes. Two decameric substrate peptides corresponding to the Gag polyprotein cleavage sites of NC-p1 (ERQAN*FLGKI) and its AP2V mutant (RQVN*FLGKIN) were crystallized in complex with inactive (D25N) variants of WT and drug-resistant HIV-1 protease having the V82A mutation (referred to as ^{WT}NC-p1_{WT} and ^{AP2V}NC-p1_{V82A} complexes, respectively). Although the peptides used for crystallization span a slightly different region of the cleavage site (P5 to P5' and P4 to P6'), these differences are likely to have minimal or no effect on the bound conformation of the substrate. From our previous experience with to determine substrate complexes with HIV protease (38, 39, 49), the P5 and P5' residues usually have no contact with the protease and are often disordered in the electron density. Thus, the presence or absence of P5 or P6' is unlikely to impact how the substrate is packed in the active site. The ^{WT}NC-p1_{WT} and ^{AP2V}NC-p1_{V82A} complexes were refined to respective resolutions of 2.1 and 2.0 Å. Their crystallographic statistics are listed in Table 1. Eight substrate residues (P4 to P4') in the ^{WT}NC-p1_{WT} complex and all 10 substrate residues (P4 to P6') in the ^{AP2V}NC-p1_{V82A} complex were identified from the electron density maps. The side chains of GlnP3 in both of these complexes are disordered. Otherwise, residues at P2 to P3' were unambiguously located within the electron density. The ^{WT}NC-p1_{WT} complex has larger temperature factors than the ^{AP2V}NC-p1_{V82A} complex, with average overall temperature factors of 40 and 27 Å², respectively. The higher temperature factors in the ^{WT}NC-p1_{WT} complex could be due to increased thermal motions, possibly resulting from a more dynamic fit between the protein and substrate.

As observed in other HIV-1 protease-substrate complexes (40, 51), the substrates exist in an extended β-strand conformation (Fig. 1). However, a difference between the two complexes is observed in the φ and ψ angles for the P1 and P1' residues that flank the scissile peptide bond (Fig. 1). The φ and ψ angles for the ^{WT}NC-p1_{WT} complex are -60° and 34°, re-

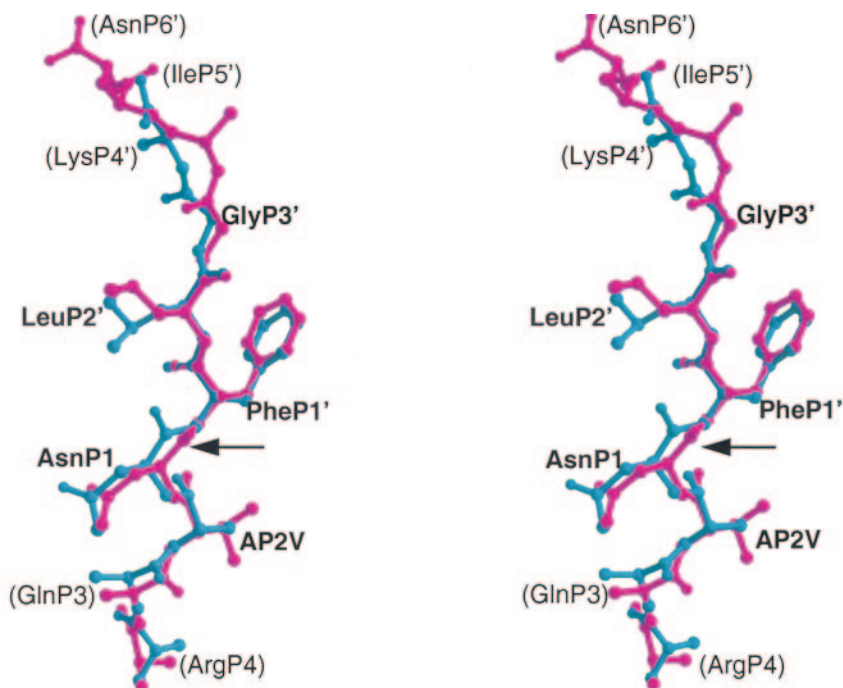


FIG. 1. Conformation of the NC-p1 substrates. Stereo diagram of the superposition of the WT (cyan) and AP2V (magenta) variants of NC-p1 peptides. An arrow indicates the difference in conformation of the scissile bonds between the two structures. The superposition was based on structurally conserved parts of the respective protease structures. Disordered side chains, whose conformation could not be resolved in the electron density, have their names listed in parentheses.

spectively, for P1 and -50° and 152° , respectively, for P1', whereas for the $^{AP2V}NC-p1_{V82A}$ complex, they are -72° and 87° , respectively, for P1 and -102° and 143° , respectively, for P1'. These angles are still in the "generally allowed β -strand region" of the Ramachandran plot (41). Significant shifts are

seen in the ψ angle of P1 (53°) and the ϕ angle of P1' (52°), resulting in a large change in the orientation of the P1 carbonyl oxygen (Fig. 1).

Double difference plots were calculated (39) in order to elucidate regions where changes have occurred between the

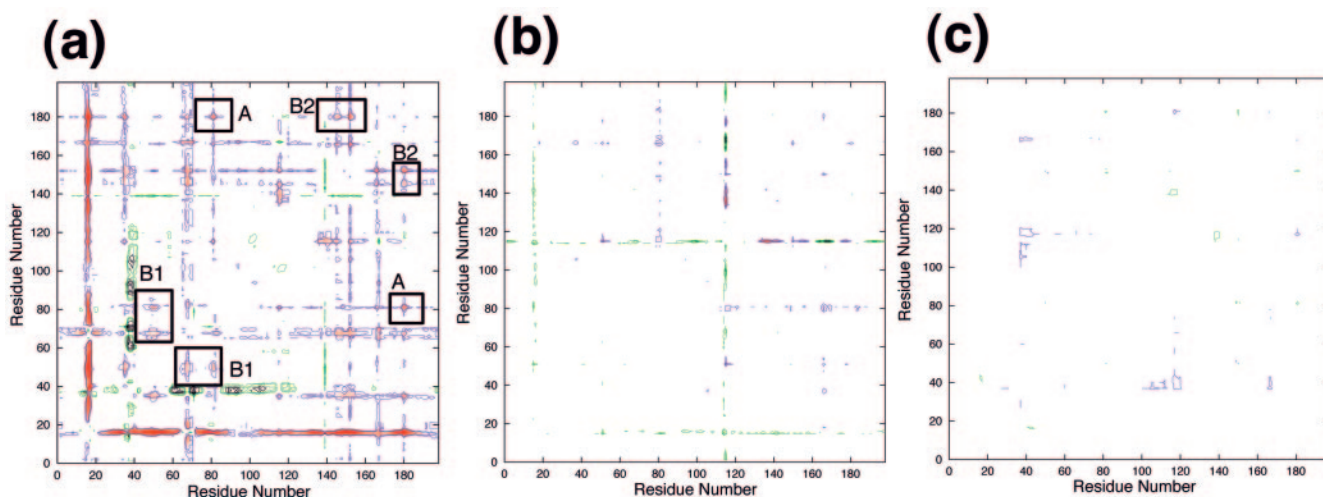


FIG. 2. Double difference plots. Relative shifts in the V82A complexes in reference to the corresponding WT complexes with NC-p1 (a), CA-p2 (b), and p1-p6 (c). Double difference plots contour differences in internal $C\alpha$ - $C\alpha$ distances between two complexes. Each contour line represents a deviation by 0.25 \AA . Black, green, blue, and red distinguish the contour ranges -1.0 \AA and below, -1.0 to -0.5 \AA , 0.5 to 1.0 \AA , and 1 \AA and above, respectively. In panel a, box A corresponds to conformational changes between the P1 loops (Gly78-Asn83) from each of the two monomers, and boxes B1 and B2 correspond to the conformational changes between the P1 loop with respect to the flap (Ile50) within each of the two monomers. All of the boxed regions emphasize internal regions of the protease whose relative conformation has changed by more than 1.0 \AA between the two complexes.

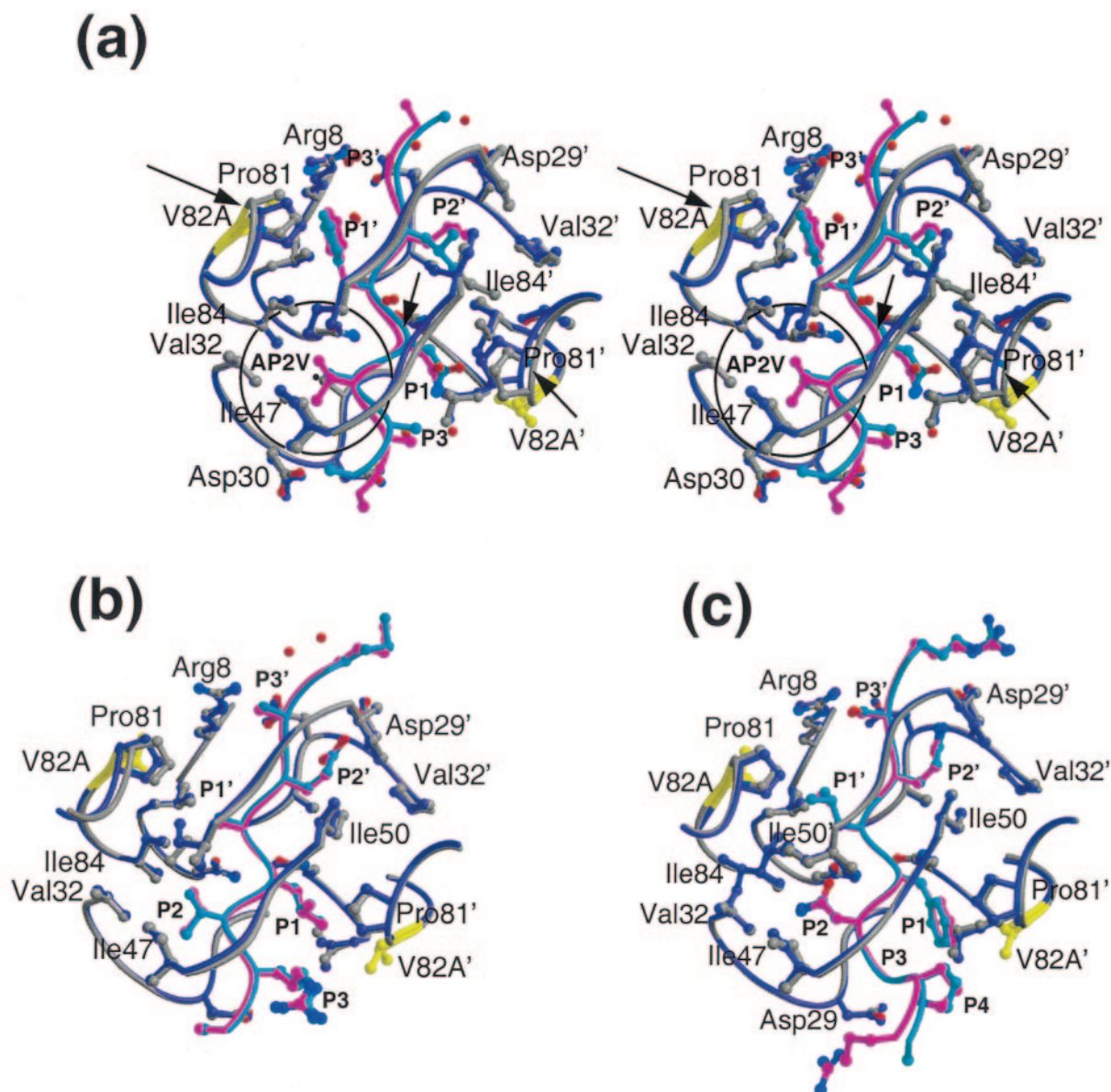


FIG. 3. Superposition of WT and V82A complexes. (a) Stereo diagram of the superimposed active site residues in the $^{WT}NC-p1_{WT}$ (in gray and cyan) and $^{AP2V}NC-p1_{V82A}$ (in magenta and purple) complexes. Protease residues within 4.2Å of the substrate are shown in ball-and-stick representation, and residue 82 is highlighted in yellow. The substrate mutation site (P2) is circled, and regions exhibiting large structural changes are indicated with arrows. Similarly, panels b and c show the superposition of CA-p2 and p1-p6, respectively, in complex with the WT and V82A protease variants. Note that there are virtually no conformational changes seen between the WT and V82A complexes in these two complexes.

α -carbon backbones of the $^{WT}NC-p1_{WT}$ and $^{AP2V}NC-p1_{V82A}$ complexes (Fig. 2a). Double difference plots allow for comparison of two complexes without superimposing them and, thus, are unbiased by which residues are chosen for the superposition. To compute these plots, the distances between all the C α atoms within each of the complexes are calculated, and the difference in these C α -C α distances between the two complexes is mapped as a contour plot. The contour plot indicates that the P1 loops (Gly78-Asn83) in the two monomers are more than 1Å farther apart in the $^{WT}NC-p1_{WT}$ complex than in the $^{AP2V}NC-p1_{V82A}$ complex (Fig. 2a, box A). Similarly, the distances between the P1 loops and the flaps within the monomers are larger in the $^{WT}NC-p1_{WT}$ complex (Fig. 2a, boxes B1

and B2). These two observations suggest that the P1 loops in the $^{AP2V}NC-p1_{V82A}$ complex have moved closer to each other in response to amino acid modifications at position 82 and at P2 in the substrate (Fig. 3a). Calculation of the shape complementarity (21) between the two substrates and their respective proteases shows that the complementarity is much better for the $^{AP2V}NC-p1_{V82A}$ complex (0.71) than for the $^{WT}NC-p1_{WT}$ complex (0.58). Thus, the AP2V substrate appears to fit more tightly within the V82A HIV-1 protease than the WT substrate within its protease.

We have previously determined the crystal structures of the WT and V82A protease variants with three other Gag polyprotein substrates: MA-CA, CA-p2, and p1-p6 (39, 40). Based on

TABLE 2. Substrate-protase hydrogen bonds formed by the two NC-p1 substrates

Substrate atom	Protein atom	Length (Å) of hydrogen bond		D1 – D2 ^a	Average bond length (Å) ^b
		^{WT} NC-p1 _{WT} (D1)	^{AP2V} NC-p1 _{V82A} (D2)		
AlaP4 O	Gly48 N	3.2	3	+	3
AlaP4 N	Asp30 OD2		2.9	+	
AlaP3 N	Asp29 OD2	3.5	3.3	+	2.9
AlaP3 O	Asp29 N	3.6	2.8	+	3
Ala/ValP2 N	Gly48 O	3.2	2.8	+	2.9
AsnP1 N	Gly27 O	3.2	2.8	+	2.8
AsnP1 ND2	Gly27 O		3.5	+	
AsnP1 O	Asn25 ND2	3.2	2.5	+	2.7
LeuP2' N	Gly27' O	3.2	2.9	+	3
LeuP2' O	Asp29' N	3.1	2.9	+	3.2
LeuP2' O	Asp29' OD2	3.6		–	
GlyP3' N	Gly48' O	3.1	2.8	+	2.8
GlyP3' O	Gly48' N	3.1	2.8	+	3
GlyP3' O	Asp30' OD2		3.3	+	
AlaP4' N	Asp29' OD2	3.6	3	+	2.9
AlaP4' N	Asp30' OD2	3.5		–	
AlaP4' O	Asp30' OD2	2.4		–	
AlaP5' N	Asp30' OD2		3.3		
AlaP6' N	Met46' O		2.5		
AlaP6' O	Met46' N		2.8		

^a +, hydrogen bond is longer in the ^{WT}NC-p1_{WT} complex than in the ^{AP2V}NC-p1_{V82A} complex; –, hydrogen bond is shorter in the ^{WT}NC-p1_{WT} complex than in the ^{AP2V}NC-p1_{V82A} complex. Note that if no distance is listed for a particular interaction, it is because that distance is well beyond hydrogen bonding distance.

^b Average length of corresponding hydrogen bonds found in six substrate-protase WT complexes (40) and three substrate-protase V82A complexes (39).

their crystallographic statistics, the latter two were chosen for double difference distance analysis. Only minor changes were previously observed between these WT and V82A variant structures (Fig. 2b and c and Fig. 3b and c) (39). The previous study, which also analyzed WT and V82A variant protease complexes with two protease inhibitors (saquinavir and ritonavir) approved by the Food and Drug Administration, found that Val82 is more crucial for inhibitor binding than for substrate recognition. However, the large structural deviations we find in the present study between the ^{WT}NC-p1_{WT} and ^{AP2V}NC-p1_{V82A} complexes, along with the coevolution of AP2V, implicate Val82 as important for the recognition of the NC-p1 cleavage site.

Hydrogen bonds. All of the substrate complexes of HIV-1 protease show an extensive network of 12 to 18 hydrogen bonds between the proteases and their respective substrates. This network also exists in the two NC-p1 substrate-protase structures (Table 2). Three hydrogen bonds seen in the ^{AP2V}NC-p1_{V82A} structure but not in the ^{WT}NC-p1_{WT} complex were compensated by two new hydrogen bonds in the latter. However, the lengths of the hydrogen bonds conserved between the two complexes differ by 0.2 to 0.8 Å, with the hydrogen bonds in the ^{WT}NC-p1_{WT} complex almost always being longer. The lengths of the conserved hydrogen bonds in the ^{AP2V}NC-p1_{V82A} complex agree well with the average hydrogen bonding distances for corresponding interactions in the other substrate-protase complexes (40) (39) (Table 2). Only two hydrogen bonds in the ^{AP2V}NC-p1_{V82A} complex are longer by 0.1 Å, and six others are shorter by 0.2 Å than the average distance. In the ^{WT}NC-p1_{WT} complex, on the other hand, the hydrogen bond lengths are generally longer by 0.2 to 0.8 Å from the average hydrogen bond lengths found in the other

nine protease-substrate structures. Rearrangement of the ϕ and ψ angles near the scissile bond in the ^{AP2V}NC-p1_{V82A} complex (Fig. 1) may be attributed to improved hydrogen bonding in that structure relative to the ^{WT}NC-p1_{WT} complex.

In general, the hydrogen bonds between the substrates and HIV-1 protease involve the peptide backbones (40, 51). This is also the case in the NC-p1 complexes, where only one substrate side chain is involved in hydrogen bonds. AsnP1 ND2 makes a weak hydrogen bond (3.5 Å) with Gly27 O in the ^{AP2V}NC-p1_{V82A} complex. This is the only substrate complex structure where a hydrogen bond is observed between the protease and the side chain of P1. This hydrogen bond, however, is absent in the ^{WT}NC-p1_{WT} structure. Although the side chains of ArgP4, GlnP3, and LysP4' could possibly be making hydrogen bonds, they are disordered in both complexes and so cannot be observed. Hence, apart from the lone and weak AsnP1 ND2-Gly27 O hydrogen bond, there appears to be no stable side chain hydrogen bond in either complex.

In addition to direct substrate-protase hydrogen bonds, water-mediated hydrogen bonds were also examined, as they can be relevant in rational drug design (22). Out of the five water sites conserved among HIV-1 protease complexes (23, 25, 40), only four are observed in the ^{WT}NC-p1_{WT} complex (Fig. 4). However, all five of the water molecules are found in the ^{AP2V}NC-p1_{V82A} complex. The water molecule that is absent in the ^{WT}NC-p1_{WT} complex (Fig. 4, W3) directly mediates substrate backbone (GlnP3 O) with the protease (Gly27 O, Asp29 OD1, and Arg8 NE). Absence of this water bridge, in the ^{WT}NC-p1_{WT} complex may be a direct consequence of the poor substrate-protase hydrogen bonding.

In addition to the five conserved water molecules, three other water molecules stabilize the ^{AP2V}NC-p1_{V82A} complex. The side chain of AsnP1 forms a hydrogen bond with W2 (Fig. 4 and Table 3), which itself forms a hydrogen bond with the conserved W3. W7 mediates interactions between the backbone atoms of Gly48' (N) and LysP4' (O) in the ^{AP2V}NC-p1_{V82A} complex. The third water site, W8, bridges the side chain oxygens of Asp30' with IleP5'N. Thus, these three additional water molecules appear to further stabilize the ^{AP2V}NC-p1_{V82A} complex, whereas the absence of the W3 water site may be indicative of the higher level of disorder in the ^{WT}NC-p1_{WT} complex.

van der Waals interactions. Both V82A and AP2V mutations involve changes in the size of their hydrophobic side chains. A detailed examination of the substrate residues P2 to P2' (GlnP3 is disordered in both complexes and GlyP3 has no side chain) reveals several rearrangements in packing between the two complexes. At residue 82, the site of the protease mutation, packing between PheP1' and residue 82 is lost with the V82A mutation (Fig. 5a and Table 4). For each substrate residue, the closest van der Waals contact made by each atom in that residue with the protease atoms was measured, and an average contact distance was calculated for the residue. PheP1', which makes four additional van der Waals contacts to Gly27', Leu23, Pro81, and Val82 in the ^{WT}NC-p1_{WT} complex is an average of 0.3 Å closer relative to its contact distance in the ^{AP2V}NC-p1_{V82A} complex. The remaining substrate side chains within P2 to P2', AsnP1, ValP2, and LeuP2', are significantly closer to the protease in the ^{AP2V}NC-p1_{V82A} complex by 0.5, 0.4, and 0.4 Å, respectively (Fig. 5b and c and Table 4),

TABLE 3. Water-bridging network involving substrates and protease

Water site	^{WT} NC-p1 _{WT}			^{AP2V} NC-p1 _{V82A}		
	Substrate atom(s)	Water	Protein atom(s)	Substrate atom(s)	Water	Protein atom(s)
W1	Ala P2 O Phe P1' O	Wat25	Ile50 N Ile50' N	ValP2 O PheP1' O	Wat33	Ile50 N Ile50' N
W2		Disordered		AsnP1 ND2	Wat93	Arg8' NE Wat27
W3		Disordered		GlnP3 O ^a	Wat27	Gly27 O Asp29 OD1 Arg8' NE Wat93, Wat4
W4		Wat6	Thr26 O Asp29 OD1 Arg87 NE		Wat4	Thr26 O Asp29 OD1 Arg87 NE Wat27
W5	LeuP2' O	Wat9	Gly27' O Asp29' OD1 Wat1	LeuP2' O	Wat55	Gly27' O Asp29' OD1 Arg8 NE Wat9
W6		Wat1	Thr26' O Arg87' NE Wat9		Wat9	Thr26' O Asp29' OD1 Arg87' NE Wat55
W7				LysP4' O ^a	Wat112	Gly48' N
W8				IleP5' N ^a	Wat50	Asp30' OD1 and OD2

^a These residues are currently modeled as alanines due to lack of electron density.

and make 14, 7, and 10 additional van der Waals contacts, respectively. These additional contacts occur because of a change in the conformation of AsnP1 (Fig. 1) that enables it to fit within the pocket formed by Gly27, Pro81', and Asn25' (Fig. 5c). LeuP2' also changes conformation (Fig. 1) and forms closer van der Waals contacts with Gly27', Ala28', and Asp30' (Fig. 5c). The two added methyl groups in ValP2 allow it to make new contacts with Val32 CG2 and Ile50 CD. (However, in the ^{WT}NC-p1_{WT} complex, the side chain of Ile50 is disordered in the electron density map.) However, no change is seen in the conformation of residues Val32, Ile47, and Ile84', which line the corresponding P2 pocket (Fig. 3a). Thus, except for the PheP1' Val82 interaction, the overall van der Waals packing in the ^{AP2V}NC-p1_{V82A} complex is better than in the ^{WT}NC-p1_{WT} complex. The loss of contact from the V82A mutation is compensated by the gain of contacts throughout the ^{AP2V}NC-p1_{V82A} complex due to the AP2V substitution, implicating a subtle balance of interdependency between the different residues within the substrate. These results support the previous observation that the P2 substrate site for HIV-1 protease is preferentially a β -branched amino acid (14) and, in particular, a valine (7).

DISCUSSION

The NC-p1 cleavage site is the rate-determining step in the processing of the Gag polyprotein (7, 37, 54). The amino acid sequence of this site, with an Asn at P1 and an Ala at P2, is also the least homologous compared with the other HIV-1 protease substrates sites, which have hydrophobic residues at P1 and branched residues at P2. If either P1 or P2 is replaced with Phe, Leu, Met, and Tyr or with Val, respectively, the site is cleaved more efficiently (36). Peptide library screens find that the P2 site within NC-p1 is preferentially a Val (7). However, these substitutions are not seen in WT virus, implying that a

more efficient and presumably premature cleavage of this site may be detrimental to viral maturation (19, 26, 36).

The NC-p1 cleavage site has been seen to coevolve in response to the V82A drug-resistant mutation in HIV-1 protease, with the Ala residue at P2 mutating to a Val (1, 10, 20, 55). Previous studies on the kinetics of substrate cleavage have shown that this mutation results in the substrate's being

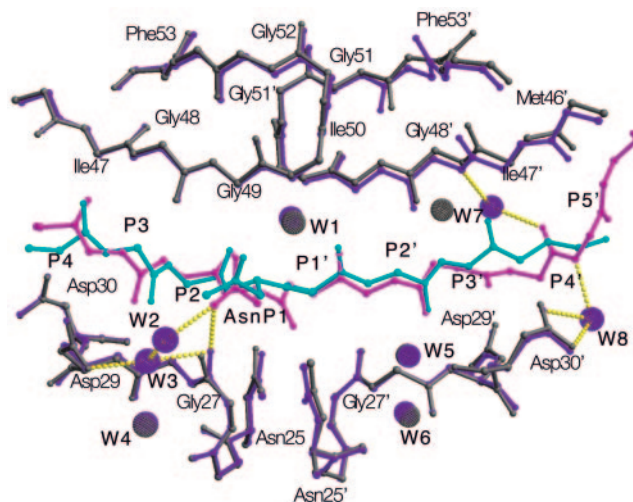


FIG. 4. Variations in the substrate-protease hydrogen bonds between the ^{WT}NC-p1_{WT} and ^{AP2V}NC-p1_{V82A} complexes. In the superimposed active site regions of the ^{WT}NC-p1_{WT} (gray and cyan) and the ^{AP2V}NC-p1_{V82A} (magenta and purple) complexes, only those side chains that form protease-substrate hydrogen bonds are explicitly shown (Asn 25, 25'; Asp29, 29'; Asp30, 30'; and AsnP1). Water molecules are shown with van der Waals surfaces. The ^{AP2V}NC-p1_{V82A} complex forms additional hydrogen bonds compared with the ^{WT}NC-p1_{WT} complex. These are highlighted with dotted yellow lines (Tables 2 and 3).

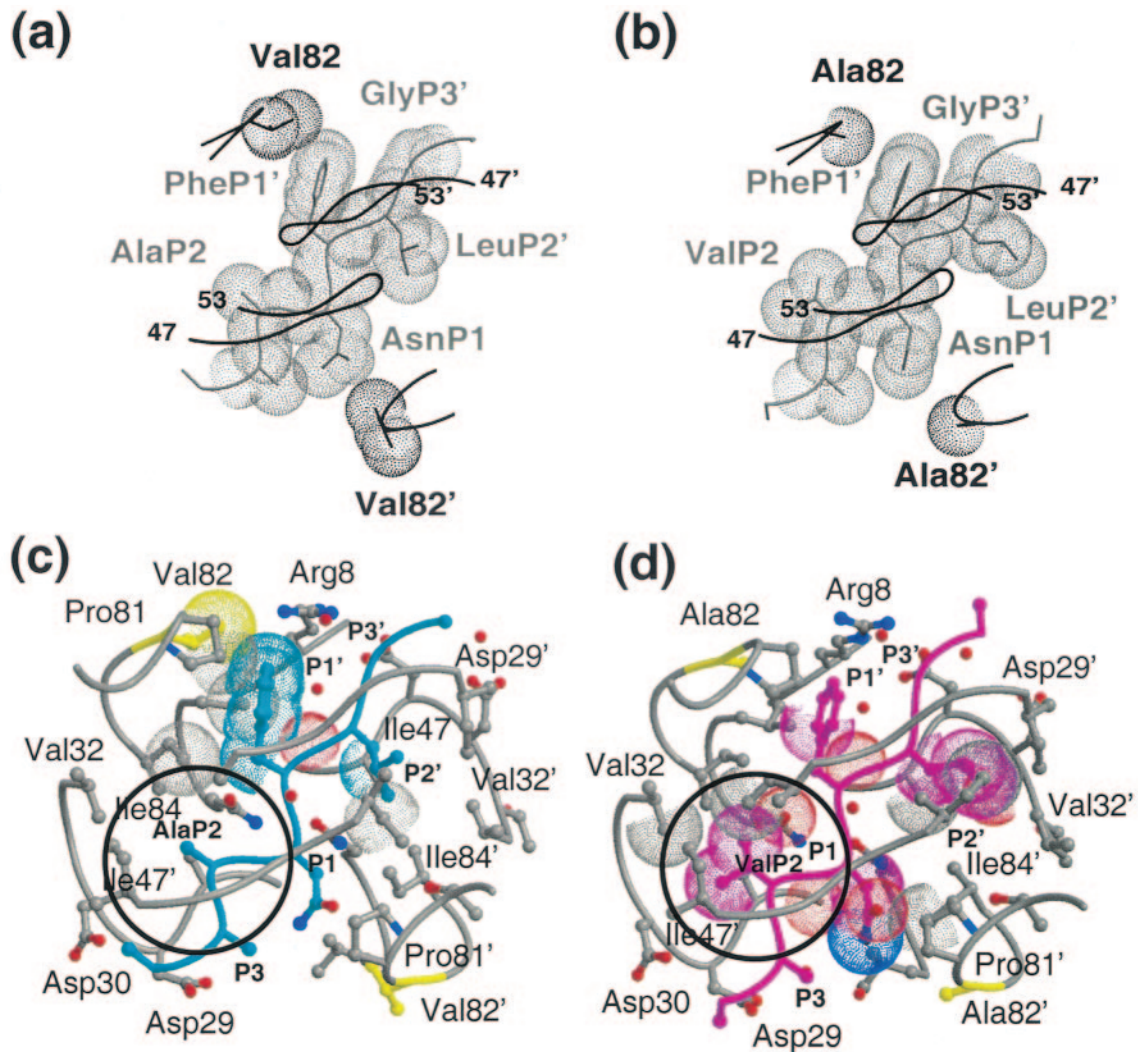


FIG. 5. Variations in the substrate-protease van der Waals interactions between the $^{WT}NC-p1_{WT}$ and $^{AP2V}NC-p1_{V82A}$ complexes. van der Waals surfaces of protease residue 82, viewed down the dimer twofold axis, and neighboring atoms of the corresponding NC-p1 substrate: (a) $^{WT}NC-p1_{WT}$ complex (note that Val82 contacts PheP1') and (b) $^{AP2V}NC-p1_{V82A}$ complex (note that no contact is made between Ala82 and the substrate). Substrates and proteases are distinguished in gray and black, respectively. A $C\alpha$ trace of the overlying flaps is also shown. (c) Active site residues in the $^{WT}NC-p1_{WT}$. The protease is shown in gray and the substrate in cyan. Protease residues within 4.2Å of the substrate are shown in ball-and-stick representation, and residue 82 is highlighted in yellow. van der Waals contacts that are lost compared with the $^{AP2V}NC-p1_{V82A}$ complex are highlighted with dotted surfaces and the P2 site is circled. (d) Active site residues in the $^{AP2V}NC-p1_{V82A}$. The protease is shown in gray, and the substrate is shown in magenta; protease residues within 4.2Å of the substrate are shown in ball-and-stick representation, and residue 82 is highlighted in yellow. van der Waals contacts that are lost compared with the $^{WT}NC-p1_{WT}$ complex are highlighted with dotted surfaces, and the P2 site is circled.

cleaved 2.1 times more efficiently (ratios of k_{cat}/K_m [mutant substrate/WT substrate]) for the V82A protease variant and 2.6 times more efficiently for WT HIV-1 protease (12). However, despite the enzymatic advantage, the AP2V mutation is not observed in sequences of the WT virus. In this study we have determined the crystal structures of two NC-p1 substrate complexes, the $^{WT}NC-p1_{WT}$ complex and the $^{AP2V}NC-p1_{V82A}$ complex, in order to understand the structural basis for this coevolution. Residue 82 is not in direct van der Waals contact with the P2 site of the substrate, so the coevolution is not as simple as a decrease in the size of one residue corresponding to an increase in the size of a neighboring residue. However, unlike what we have observed in other substrate complexes (CA-p2, MA-CA, and p1-p6), where the substrates make no or

minimal contact with Val82 (39), in the $^{WT}NC-p1_{WT}$ complex Val82 does make contact with both AsnP1 and PheP1'. Thus, in comparison with the other WT substrate complexes, residue 82 appears to be more important for recog-

TABLE 4. Total number of van der Waals contacts among substrate residues between P2-P2' and HIV-1 protease

Substrate residue	No. of contacts	
	$^{WT}NC-p1_{WT}$	$^{AP2V}NC-p1_{V82A}$
Ala/ValP2	10	24
AsnP1	19	26
PheP1'	29	25
LeuP2'	28	34

niton of the NC-p1 substrate cleavage site, and when the drug-resistant V82A mutation occurs, the interactions at P1 and P1' are perturbed.

The question remains of why the loss of contact at P1 and P1' would affect the residue at P2. Compared with the other substrate complexes where the P2 residue usually makes van der Waals contacts with protease residues in its surrounding pocket, in the ^{WT}NC-p1_{WT} complex, the Ala at P2 is unable to do so. In addition, the hydrogen bonds in the ^{WT}NC-p1_{WT} complex (Table 2) between the substrate and the protease are longer than those observed in other substrate complexes. The lack of interactions at the P2 site and the lengthening of the hydrogen bonds possibly indicate that NC-p1 binds in the active site of HIV-1 protease less optimally than in the other substrate cleavage sites.

In the ^{AP2V}NC-p1_{V82A} complex, the PheP1' and, to a lesser extent, the AsnP1 lose contact with residue 82. This loss of contact at residue 82 would probably cause the NC-p1 substrate to fit even more poorly within the active site of HIV-1 protease. However, the Val substitution at P2 fills the protease pocket, allowing van der Waals interactions to occur with the surrounding protease residues, thereby apparently stabilizing the conformation of the substrate within the active site. Additional evidence of stabilization is demonstrated in the hydrogen bonding pattern in the ^{AP2V}NC-p1_{V82A} complex, which is more comparable, in terms of both the greater numbers of hydrogen bonds and shorter hydrogen bonding distances, to those seen in other substrate complexes (Table 2) than it is to the ^{WT}NC-p1_{WT} complex. The ValP2, therefore, appears to compensate for the V82A mutation by restabilizing the NC-p1 substrate site through alternative interactions within the active site cavity. This suggests that for optimal HIV-1 protease recognition of the NC-p1 substrate site, a possible interdependency exists between the P1' and P2 positions. This interdependency thereby accounts for the seemingly unusual coevolution of the NC-p1 substrate site (AP2V) with the V82A drug-resistant mutation within HIV-1 protease. This coevolution is necessary as the HIV-1 protease drug resistant mutation, V82A, directly impacts the recognition and cleavage of the NC-p1 site, a rate-determining step in viral maturation.

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