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Marita Högberg,* Christer Sahlberg, Per Engelhardt, Rolf Noréen, Jussi Kangasmetsä, Nils Gunnar Johansson, Bo Öberg, Lotta Vrang, Hong Zhang, Britt-Louise Sahlberg, Torsten Unge,* Seved Lövgren, Kerstin Fridborg, and Kristina Bäckbro: Urea−PETT Compounds as a New Class of HIV-1 Reverse Transcriptase Inhibitors. 3. Synthesis and Further Structure−Activity Relationship Studies of PETT Analogues.

Page 4154. Figure 1 was incorrectly published as a halftone. Figure 1 in color, along with its legend, appears below.

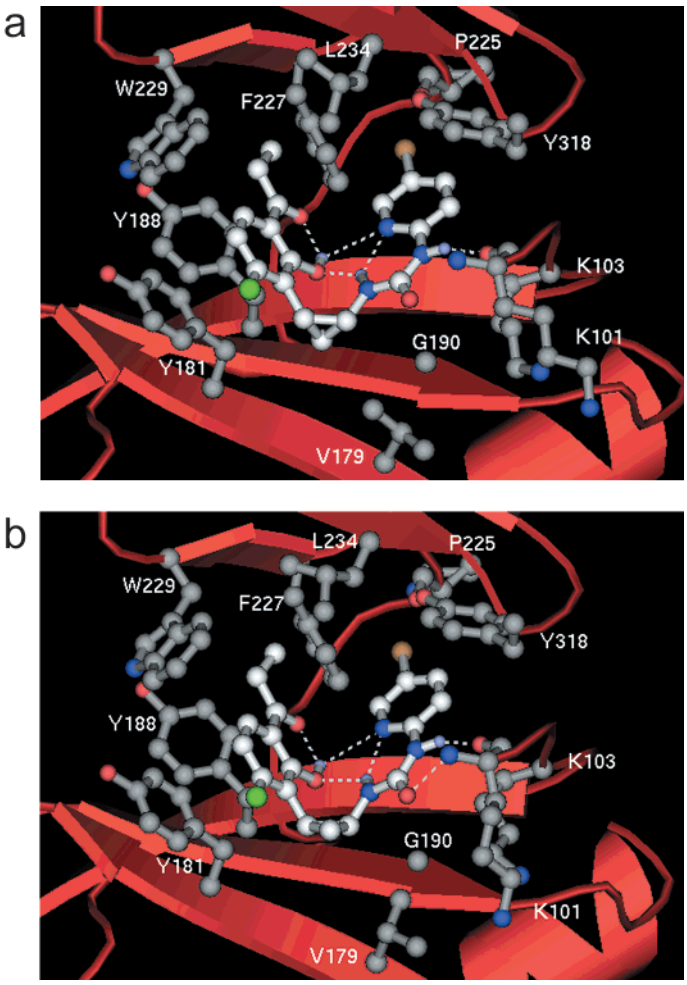

Figure 1. Three-dimensional structure of the complex between HIV-1 RT and (a) **17** and (b) **18**. Positioning of HIV-1 RT inhibitors **17** and **18** in the NNI binding site of the palm subdomain. In order to make the figure less complex, the residues L100, E1138 (residue 138 in the p51 subunit), H235, and P236 have been excluded, though they are important ligands. The two inhibitors bind similarly. The striking features of the binding mode of these inhibitors are the internal stabilizing hydrogen bond network, the hydrogen bonds between the inhibitor urea moiety and the main chain atoms of K101, and the efficient utilization of the van der Waals interactions with the propionylphenyl moiety of the inhibitor and the aromatic amino acid residues Y181, Y188, and W229. Moreover, there is an extensive utilization of close-packing interactions of predominantly hydrophobic nature between these inhibitors and the protein. The program Molscript was used for drawing the figures.[33]

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