From 4,5,6,7-Tetrahydro-5-methylimidazo[4,5,1-*jk*](1,4)benzodiazepin-2(1*H*)-one (TIBO) to Etravirine (TMC125): Fifteen Years of Research on Non-Nucleoside Inhibitors of HIV-1 Reverse Transcriptase[†]

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Received July 7, 2004

Introduction

Dr. Paul Janssen was very passionate about the discovery and development of new drugs in many disease areas. Under his leadership, numerous breakthrough drugs in analgesia, anesthesia, psychiatry, fungal infections, gastrointestinal disorders, and anthelmintic remedies were discovered, developed, and introduced into the market place, and his contributions have been recognized around the world. In the past 17 years of his life, Dr. Paul (as he was affectionally called) focused on the search for better treatments for patients with acquired immune deficiency syndrome (AIDS). Beginning in 1987, Dr. Paul and his collaborators pioneered the field of non-nucleoside inhibitors of HIV reverse transcriptase (NNRTIs) with the discovery of the 4,5,6,7-tetrahydro-5-methylimidazo[4,5,1-jk](1,4)benzodiazepin-2(1H)-one (TIBO) series. The original lead compounds emanated from an antiviral screening approach without knowledge of the molecular target(s) involved. However, with the first potent anti-HIV agents of this type in hand, the mechanism of action was elucidated and a new anti-HIV therapeutic approach was born.¹ This Perspective discusses the history of anti-HIV research up to the discovery of etravirine (TMC125) at Janssen Pharmaceutica, the Janssen Research Foundation, the Center for Molecular Design (Vosselaar, Belgium), the Rega Institute for Medical Research (Leuven, Belgium), Tibotec (Mechelen, Belgium), and the Center for Advanced Biotechnology and Medicine (Rutgers University, NJ).

Discovery of the TIBO Series: The First Anti-HIV NNRTIs

In the early 1980s, strong evidence developed for the causative agent of AIDS being an immunologically destructive retrovirus called HIV.² Since this virus depends on RNA to convey its genetic signature, reverse transcriptase is a critical enzyme for its replication. Hence, nucleoside analogues that were known to inhibit reverse transcriptase from other viruses soon appeared as therapeutic agents for the treatment of HIV.^{2–7} Dideoxynucleosides proved to be especially effective in

inhibiting HIV-1 replication and in preventing the associated destruction of infected T cells.^{8–11} In 1987, zidovudine (3'-azido-2',3'-dideoxythymidine; AZT) was approved by the Food and Drug Administration (FDA) for treating AIDS patients in the U.S.

When Janssen Pharmaceutica entered the area of HIV research in 1987, the understanding of the replication cycle of the HIV virus was very limited and the molecular targets that are known today to be central to HIV replication had not been identified. By use of a pragmatic approach, 600 molecules were selected from the Janssen compound collection for screening in the virology laboratories of Prof. Eric De Clercq and Dr. Rudi Pauwels at the Rega Institute at the Catholic University of Leuven.¹² These selected compounds fulfilled two criteria: (1) they covered a wide range of chemical diversity and (2) they did not show significant biological activity in a battery of unrelated pharmacological assays. The compounds were tested for their ability to protect MT-4 cells infected with HIV. This strategy, which obviated the lack of knowledge about the biology of HIV and was unbiased toward specific molecular targets, led to the discovery of R14458 (1), a TIBO derivative (Figure 1).¹ Although the potency of 1 was rather weak, with an EC_{50} of 62 μ M, the activity was specific, as determined by a cytotoxicity screen. The enantiomers of 1 were prepared via a stereoselective synthesis,¹³ and it was established that the anti-HIV activity resided almost exclusively in the (+)-(S) isomer.

Since the biological target was unknown, the lead optimization program was conducted by a conventional medicinal chemistry approach under the direction of Dr. Michael Kukla. This effort led to a much more potent compound against HIV-1, R82913 (2).¹ Mechanistic studies established that the potent TIBO compounds did not mask the CD4/HIV receptor on MT-4 cells, and effects on binding of HIV-1 to MT-4 cells were also excluded. By use of detergent-disrupted virus particles, it was found that the TIBO compounds markedly inhibited poly(rA)·oligo(dT)₁₂₋₁₈-directed reverse transcriptase (RT) activity. At that point, the TIBO compounds became the first NNRTIs with specific inhibition of HIV-1 replication. From further structure–activity relationship (SAR) studies, R86183 (3), a compound

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Figure 1. Prototype TIBO compounds and their inhibition of HIV-1 replication in HIV-infected MT-4 cells.

whose activity equals that of AZT,^{13–19} was discovered and ultimately selected for clinical evaluation.

Non-Nucleoside Reverse Transcriptase Inhibitors

Not surprisingly, the disclosure of the TIBO compounds inspired the search for more potent and selective RT inhibitors in many industrial and academic institutions. More than 30 structurally different classes of NNRTIs have now been identified.^{20–22} Three chemical entities from such series, nevirapine, delavirdine, and efavirenz, have been approved by the FDA for clinical use, while a number of other compounds are in preclinical or clinical development (Figure 2). Emivirine (MKC-442) is the clinically most advanced representative of the pyrimidinedione class.²³ Thiocarboxanilide UC-781 has been identified as a (retro)virucidal agent capable of reducing the infectivity of HIV-1 virions.^{24,25} DPC 083, a close analogue of efavirenz, has proven to reduce the viral load in patients who harbor NNRTI-resistant mutants.^{26,27} Capravirine is also distinguished by its activity against such mutant HIV strains.²⁸ Capravirine is undergoing advanced clinical trials and has proven to be effective in both NNRTI-naive and NNRTI-experienced patients.²⁹

The desire to understand the binding mode of the TIBO compounds with the RT enzyme led Dr. Paul to initiate a collaboration with Prof. Eddy Arnold of the Center for Advanced Biotechnology and Medicine at Rutgers University in Piscataway, NJ. The X-ray crystal structure of HIV-1 RT complexed with 3 was solved at 3.0 Å resolution, and the binding mode was found to be strikingly similar to that previously reported for the complex of nevirapine and HIV-1 RT.³⁰⁻³² Each compound binds in a hydrophobic pocket close to, but distinct from, the substrate binding site, and each compound adopts a butterfly-like shape (Figure 3). In the case of the TIBO compounds, the dimethylallyl substituent interacts with the side chains of Tyr181, Tyr188, and Trp229, and the chlorophenyl group interacts with Leu100, Lys101, and Tyr318. Nevirapine is positioned in the allosteric binding pocket in much the same way; the 4-methylpyridyl fits into the western part of the pocket, and the unsubstituted pyridyl group occupies the eastern part.^{33,34} The thiourea NH group of TIBO forms a critical hydrogen bond with the mainchain carbonyl oxygen atom of Lys101. The latter arrangement is in contrast to that of nevirapine, where no hydrogen bonds occur between the ligand and the HIV-1 RT protein.³⁵

A Second Lead Series: The α-Anilinophenylacetamides (α-APAs)

While the TIBO compounds were being evaluated clinically, high-throughput, cell-based screening systems were installed at the Rega Institute.³⁶ This setup allowed for a more extensive evaluation of the Janssen compound library and led to the identification of a second class of HIV-1 RT inhibitors. As for the TIBO series, the lead compound here, R15345 (4), was originally synthesized in an unrelated medicinal chemistry project (Figure 4). This α -anilinophenylacetamide (α -APA) exhibits an EC₅₀ against HIV-1 of 610 nM.³⁷ The simplicity of its structure and the relative ease of its



Figure 2. Chemical structures of marketed NNRTIs and selected NNRTIs under clinical development.



Figure 3. Molecular surface diagram showing the structure of the non-nucleoside inhibitor binding pocket and the interactions with (A) $\mathbf{3}$ and (B) nevirapine.³⁰



Figure 4. Prototype α -APA compounds and their inhibition of HIV-1 replication.

synthesis made the α -APA series attractive for lead optimization. This effort resulted in loviride (5; R89439), a compound with an EC₅₀ of 13 nM, which became a clinical candidate (Figure 4). X-ray analysis of a cocrystal of loviride analogue R95845 (6) with HIV-RT revealed that the 4-methylacetophenone group occupies the western section of the binding pocket, whereas the 2,6-dihalophenyl substituent is positioned in the eastern section (Figure 5).³⁸ However, the development of loviride was abandoned when it became apparent that it did not offer a sufficient advantage over nevirapine and delavirdine, the two NNRTIs approved for clinical use at that time.³⁹⁻⁴²

From α-APAs to Imidoyl Thioureas (ITUs)

As SAR studies continued with the α -APA series, an unexpected observation was made. In general, increasing the spacer length between the two aryl groups in loviride resulted in a considerable decrease in activity. However, there was one exception with R93514 (**7h**), which did not fit this trend; in fact, **7h** was surprisingly active compared to all other analogues tested (Table 1). Table 1. Activity of Selected $\alpha\textsc{-}Aminophenylacetamides vs} HIV-1$



		-	
compd	Е	Y	$\mathrm{EC}_{50}\left(\mu\mathbf{M}\right)$
7a		o -NO $_2$	0.1
7b		o-Cl	0.4
7c		p-Cl	>50
7d	CH_2	o -NO $_2$	>50
7e	CO	o -NO $_2$	>50
7f	CONH	o -NO $_2$	>50
7g	CSNH	o-Cl	>50
7 h	CSNH	<i>p</i> -Cl	0.16

Further investigation of this anomaly led to a series of imidoyl thioureas (ITUs).⁴³ With proper choice of the substitution pattern on both aryl groups (e.g., R100943, **8a**, Figure 7), these ITUs were potent inhibitors of the wild-type HIV-1. The activity of **8a** was cause for excitement because its activity profile against a number of clinically relevant single mutants compared quite favorably to the profiles of nevirapine, delavirdine, and loviride (Table 2).

The X-ray crystal structure of HIV-1 RT complexed with **8a** explained the apparent anomaly observed with the ITU compounds and revealed that the aryl wings of such compounds were switched compared with compounds in the loviride series (Figure 6).⁴⁴ The RT-bound conformation of **8a** resembles a "U" or horseshoe shape in contrast to the butterfly-like shape of **3**, **5**, or nevirapine. Interestingly, the 2,6-dichlorophenyl sub-







Figure 6. Molecular surface diagram showing the structure of the non-nucleoside inhibitor binding pocket and the interactions with **8a**.⁴⁴



Figure 7. Structures of 8a and metabolite 9.

Table 2. Activity (EC₅₀, μ M) of Nevirapine, Delavirdine, Loviride (5), 8a, and 10 vs HIV-1 and Selected Single Mutants^{*a*}

compd	LAI	L100I	K103N	Y181C	Y188L
nevirapine delavirdine 5 8a 10	$\begin{array}{c} 0.032 \\ 0.063 \\ 0.013 \\ 0.003 \\ 0.006 \end{array}$	$0.32 \\ 2.5 \\ 0.05 \\ 0.51 \\ 0.40$	$egin{array}{c} 6.3 \\ 2.5 \\ 1.3 \\ 0.59 \\ 0.04 \end{array}$	10 2.0 16 0.51 0.20	>100 1.3 50 0.32 0.32

^{*a*} The LAI strain is the wild-type HIV-1. Other infecting viral strains with mutations in the RT enzyme are characterized according to the mutated amino acid position (one-letter codes). The first amino acid is present in the wild-type HIV-1. The second amino acid is present in the mutated strain. For example, Y181C refers to replacement of the tyrosine at position 181 with cysteine.

stituent now resides in the western section of the binding pocket, and the 4-cyanophenyl group resides in the eastern section. In fact, the 4-cyanophenyl group proved to be the optimal eastern-section substituent and was kept constant in the succeeding generations. The in vitro activity profile of **8a** justified consideration of it for clinical development. Unfortunately, oxidative ring closure of the imidoyl thiourea functionality proved to be a major liability. The product of oxidative cyclization, thiadiazole **9**, was inactive (EC₅₀ > 1 μ M vs HIV-1; Figure 7).

The Diaryltriazine (DATA) Series

Soon after the NNRTIs were being used in clinical settings, it became apparent that this class of RT inhibitors is vulnerable to HIV's high mutation rate, which results in a rapid selection of resistant strains.⁴⁵ Mutations in the NNRTI binding pocket render the

Scheme 1. Synthesis of 10

inhibitors inactive without affecting adversely the catalytic competency of the RT enzyme. In response to this clinical reality, Dr. Paul relied on a key collaboration with Dr. Rudy Pauwels at Tibotec. Tibotec had an expanded viral panel available that included all clinically relevant mutants, and it was appreciated that any future NNRTI drug would need to tackle most, if not all, of the clinically relevant mutants.

To improve the metabolic properties of **8a** and protect against the unproductive ring closure, an attempt was made to synthesize the cyanoguanidine isostere as outlined in Scheme 1.⁴⁶ Unexpectedly, the intended cyanoguanidine was never isolated; it presumably was an intermediate that spontaneously cyclized to form diaryltriazine (DATA) **10**.⁴⁷ It was surprising that **10** was equally potent to **8a** given that thiadiazole **9** was inactive (Table 2). A possible explanation may be that the presence of the triazine reduces a number of potentially redundant torsional degrees of freedom.⁴⁴ This entropically favorable restriction of flexibility may explain why the DATA analogues are, in general, more potent than their precursors against both wild-type and NNRTI-resistant HIV-1 mutants (vide infra).

When **10** was identified, Dr. Paul had formally retired from Janssen Pharmaceutica. Now fully convinced of the power of computer-aided drug design, he worked to establish and lead the newly formed Center for Molecular Design (CMD). At the CMD, Dr. Paul, Dr. Paul Lewi, and collaborators employed a variety of computational modeling tools to help advance the NNRTI project. Around this time, efavirenz reached the market place, and this drug was considered to be a secondgeneration NNRTI. The activity of efavirenz against a number of clinically relevant single mutants made it the new "gold standard" in the field. An important challenge now was to equal or improve on the profile of efavirenz. The single greatest weakness facing efavirenz was its lack of efficacy against the K103N mutant.

Synthetic work in the Janssen Research Foundation (JRF) initially focused on exploring the substituents on the triazine core of 10, and it became apparent that the 2,6-dichlorobenzyl group could easily be replaced by 2,6disubstituted or 2,4,6-trisubstituted anilines, phenols, or thiophenols. At the same time, molecular modeling and X-ray crystallography studies suggested that the primary amino group in **10** is probably not interacting with the RT enzyme. This prediction was confirmed when the disubstituted triazines proved to be very potent inhibitors of HIV-1 and several clinically important single mutant strains. Compounds **11a-c** inhibited both wild-type HIV-1 and the clinically important L100I, K103N, Y181C, and Y188L single mutants with low nanomolar potency (Table 3). However, excitement surrounding these disubstituted triazines was some-



Table 3. Activity (EC₅₀, μ M) of Selected Disubstituted Triazines 11 vs HIV-1 and Selected Single and Double Mutants^a

compd	R	Y	LAI	L100I	K103N	Y181C	Y188L	L100I + K103N	K103N + Y181C	
11a 11b 11c	2,4,6-tri-Me 2,4,6-tri-Me 2,6-di-Me-4-CN	NH O NH	$0.0003 \\ 0.0006 \\ 0.001$	$0.013 \\ 0.020 \\ 0.25$	0.003 0.003 0.008	$0.008 \\ 0.02 \\ 0.05$	$0.04 \\ 0.063 \\ 0.05$	1.3 2.5 >10	0.05 0.13 nd	

^a The LAI strain is the wild-type HIV-1. Other infecting viral strains with mutations in the RT enzyme are characterized according to the mutated amino acid position (one-letter codes). The first amino acid is present in the wild-type HIV-1. The second amino acid is present in the mutated strain. For example, Y181C refers to replacement of the tyrosine at position 181 with cysteine. nd = not determined.

Table 4. Activity (EC₅₀, μ M) of Isomeric Pyrimidines 12 vs HIV-1 and Selected Single Mutants^a



compd	Х	Y	Z	LAI	L100I	K103N	Y181C	Y188L
12a	N	CH	N	$\begin{array}{c} 0.001 \\ 0.010 \\ 0.45 \end{array}$	0.30	0.012	0.18	0.071
12b	CH	N	N		>10	>10	>10	>10
12c	N	N	CH		>10	>10	>10	>10

^a The LAI strain is the wild-type HIV-1. Other infecting viral strains with mutations in the RT enzyme are characterized according to the mutated amino acid position (one-letter codes). The first amino acid is present in the wild-type HIV-1. The second amino acid is present in the mutated strain. For example, Y181C refers to replacement of the tyrosine at position 181 with cysteine.

what tempered by the appearance of double mutants of the HIV-1 virus in clinical settings around that time. The prevalent L100I + K103N and K103N + Y181Cdouble mutants were not appreciably affected by these disubstituted triazines.

The Diarylpyrimidines (DAPYs): Discovery of Etravirine

Three isomeric pyrimidines can be generated by replacing any one nitrogen atom in the triazine core of the DATA series with a carbon atom. All three regioisomers, 12a-c, were prepared, but only 12a possessed an anti-HIV activity comparable to that of 10 (Table 4).⁴⁸ Compound 12a is the only isomer that fulfills two critical requirements for binding. First, it has two hydrogen bonds with Lys101: the NH group linking the pyrimidine and the 4-cyanophenyl group interacts with the main-chain carbonyl oxygen of Lys101, and the pyrimidine nitrogen serves as hydrogen acceptor to the Lys101 side chain amine. Second, it has a proper

0.001

0.073

compd

13a

13b

13c

13d

R

Me

Me

CN

CN

0

positioning of the two phenyl rings in the eastern and western hydrophobic binding pockets.

When the primary amino group was omitted from the pyrimidine nucleus, potency was maintained, supporting the observation made with the disubstituted triazines that the exocyclic NH₂ group is not intimately involved in binding. Compounds 13a-d were very potent inhibitors of both HIV-1 and a number of clinically important single mutant strains. Although the activity of the 2,4-disubstituted pyrimidines against the K103N + Y181C double mutant was encouraging, the activity against the L100I + K103N double mutants was not significant (Table 5). Pyrimidine 13a (TMC120, R147681) is currently being evaluated as a topical microbicide for the prevention of vaginal HIV transmission.49,50

Replacement of the triazine core in the DATAs with a pyrimidine also allowed for exploration of the impact of substitution at the 5-position of the pyrimidine ring. Introduction of a bromine atom in the 5-position of the pyrimidine proved to be the secret to obtaining potent inhibitors of the L100I + K103N and K103N + Y181C double mutants (Table 6). In particular, the activity of 14b and 14c against the very recalcitrant L100I + K103N double mutant was reason for excitement.

Finally, introduction of an amino group at the 6-position afforded etravirine (15, TMC125, R165335), a compound with low-nanomolar potency against wildtype HIV-1 and a large panel of clinically relevant HIV single and double mutants. Etravirine is a potent, nextgeneration NNRTI. The first-generation NNRTIs, nevirapine and delavirdine, owe their clinical utility largely to activity against the HIV-1 wild-type strain. The second-generation NNRTI efavirenz possesses a much-improved activity profile against wild-type HIV-1 and several clinically relevant HIV-1 mutants. Etravirine is extraordinary by virtue of its potency against

0.80

K103N + Y181C

0.044

0.037

0.094

1.1

Table 5. Activity (EC₅₀, μ M) of Selected 2,4-Disubstituted Pyrimidines 13 vs HIV-1 and Selected Single and Double Mutants^a

0.003

Y	LAI	L100I	K103N	Y181C	Y188L	L100I + K103N				
NH	0.001	0.018	0.004	0.008	0.048	>10				
0	0.003	0.022	0.003	0.038	0.055	8.2				
NH	0.0004	0.034	0.002	0.007	0.008	1.1				

^a The LAI strain is the wild-type HIV-1. Other infecting viral strains with mutations in the RT enzyme are characterized according to the mutated amino acid position (one-letter codes). The first amino acid is present in the wild-type HIV-1. The second amino acid is present in the mutated strain. For example, Y181C refers to replacement of the tyrosine at position 181 with cysteine.

0.037

0.019

Table 6. Activity (EC₅₀, μ M) of Selected 2,4,5-Trisubstituted Pyrimidines 14 vs HIV-1 and Selected Single and Double Mutants^a



					DI				
compd	R	Y	LAI	L100I	K103N	Y181C	Y188L	L100I + K103N	K103N + Y181C
14a	Me	NH	0.006	0.011	0.007	0.036	0.027	0.35	0.28
14b	CN	0	0.001	0.007	0.001	0.022	0.006	0.049	0.025
14c	CN	NH	0.0004	0.007	0.0004	0.010	0.003	0.037	0.032

^{*a*} The LAI strain is the wild-type HIV-1. Other infecting viral strains with mutations in the RT enzyme are characterized according to the mutated amino acid position (one-letter codes). The first amino acid is present in the wild-type HIV-1. The second amino acid is present in the mutated strain. For example, Y181C refers to replacement of the tyrosine at position 181 with cysteine.

Table 7. Activity (EC₅₀, μ M) of Marketed NNRTIs and 15 (Etravirine) vs HIV-1 and Selected Single and Double Mutants^a

compd	LAI	L100I	K103N	Y181C	Y188L	L100I + K103N	K103N + Y181C
nevirapine delavirdine ofaviranz	$0.032 \\ 0.063 \\ 0.001$	0.32 2.5 0.04	$6.31 \\ 2.5 \\ 0.04$	$10 \\ 2.0 \\ 0.002$	>10 1.3 0.16	nd^b nd^b >10	>10 >10 0.040
	0.001	0.004	0.04	0.002	0.005	0.019	0.004
15 (etravirine)							

^{*a*} The LAI strain is the wild-type HIV-1. Other infecting viral strains with mutations in the RT enzyme are characterized according to the mutated amino acid position (one-letter codes). The first amino acid is present in the wild-type HIV-1. The second amino acid is present in the mutated strain. For example, Y181C refers to replacement of the tyrosine at position 181 with cysteine. ^{*b*} nd = not determined.

the single mutants K103N and Y181C and the double mutants K103N + Y181C and L100I + K103N (Table 7). In fact, etravirine retains meaningful activity (EC₅₀ < 100 nM) against 97% of 1081 clinically derived recombinant viruses resistant to at least one of the currently marketed NNRTIs.⁵¹

The exceptional spectrum of activity of etravirine might be attributed to its ability to bind the RT enzyme in more than one conformationally distinct mode.^{52–54} This hypothesis may explain why X-ray diffraction of the wild-type HIV-1 RT/etravirine crystals has only been obtained with poor resolution (6–8 Å). It is thought that the structures of etravirine and closely related DAPY compounds can adapt to changes in the NNRTI binding pockets. The torsional flexibility of the DAPY structure permits access to numerous conformational variants, and their compact structure permits repositioning and reorientation when mutations in the binding pocket are present.⁴⁴

Preliminary clinical investigations have confirmed the therapeutic potential of etravirine.⁵⁵ Treatment of patients harboring NNRTI-resistant HIV-1 variants with etravirine (900 mg, b.i.d. for 7 days) results in a median decrease in the plasma HIV-1 RNA of $-0.89 \log_{10}$ units.⁵⁶ This observation challenges the existing belief that resistance to NNRTIs is a class phenomenon and that resistance to one particular NNRTI will result in resistance to all the members of this class of RT inhibitors. Thus, etravirine has the potential for use in individuals infected with NNRTI-resistant HIV-1.⁵⁷

Beyond Etravirine. The Discovery of Rilpivirine (TMC278)

Drug discovery efforts have continued since the discovery of etravirine. The primary goal of further analogue work has been to improve the pharmacokinetic properties of etravirine while maintaining its activity profile against wild-type HIV-1 and clinically relevant HIV-1 mutants. This effort has led to the discovery of rilpivirine, a novel DAPY NNRTI with an exceptional activity profile and very desirable druglike properties. The discovery and attributes of rilpivirine are the subject of another manuscript.⁵⁸

Conclusion

During the 17 years of HIV research, under the leadership of Dr. Paul Janssen, several new classes of NNRTIs were discovered. The TIBOs were the first inhibitors of the HIV-1 virus to be identified as belonging to the NNRTI class. Shortly thereafter, loviride, a representative of the α -APA family of NNRTIs, was discovered. SAR studies around the α -APAs produced the ITUs, a third class of promising NNRTIs. An effort to improve the metabolic stability of the ITUs led to the serendipitous discovery of 10, the first DATA compound. Structural modification of the DATA compounds eventually provided 15 (etravirine), a prototypical DAPY compound that is highly potent and effective against wild-type and drug-resistant HIV-1 variants. Thus, etravirine has the potential for use in individuals infected with NNRTI-resistant HIV-1. A common thread throughout these notable achievements was Dr. Paul's scientific brilliance, creativity, and perseverance. To be sure, the memory of Dr. Paul will remain a constant inspiration for all of us.

Acknowledgment. The discovery of the TIBOs, α -APAs, DATAs, and DAPYs under the leadership of Dr. Paul Janssen was the result of a collaboration between scientists from many different backgrounds who shared a common goal of scientific excellence. Without their contributions, etravirine would never have been identified. Special thanks go to Eddy Arnold and Kalyan Das for providing the X-ray crystallography

Perspective

pictures and to Bruce Maryanoff, Donald Ludovici, Robert Kavash, Henry Breslin, Paul Lewi, Eddy Arnold, Karen Manson, Marie-Pierre de Béthune, and Robert Galemmo, Jr. for helpful suggestions and critical review of this manuscript.

Biography

Bart L. De Corte is a native of Belgium. He completed his undergraduate education in the Department of Agricultural and Chemical Engineering at the State University of Gent, Belgium. After receiving a Diplome d'Etudes Approfondies at the Université de Rennes in France, he obtained his Ph.D. in 1992 under the guidance of Prof. John Welch at the University at Albany, State University of New York. He performed postdoctoral research in the laboratory of Prof. Tom Harris at the Center of Molecular Toxicology at Vanderbilt University in Nashville, TN. He joined Janssen Research Foundation and the Johnson & Johnson family of companies in 1993. He is currently a Principal Scientist at Johnson & Johnson Pharmaceutical Research & Development in Spring House, PA.

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JM040127P