fortune Journals

Review Article

ARCHIVES OF INTERNAL MEDICINE RESEARCH

ISSN: 2688-5654

HIV-1 Gag Gene - Understanding Current Trends in the Development of Promising ARV Treatments

Georges Teto[1*], Pierre Zoelong Emini[2], Beatrice Dambaya[1], Alex Durand Nka[1], Ezechiel Ngoufack Jagni Semengue[1], Desiré Takou[1], Collins Chenwi[1], Aude Christelle Ka'e[1], Grace Angong Beloumou[1], Constant Anatole Pieme[3], Joseph Fokam[1,3,4,5,6], and Alexis Ndjolo

Abstract

Acquired Immune Deficiency Syndrome (AIDS) treatment with combination antiretroviral therapy (cART) has improved the life quality of many patients since its implementation. HIV infection has been incurable till date, and it remains a major public health threat globally. The gag gene, one of the three main HIV-1 genes, occupies a central position in the replication cycle of this virus. This gene encodes for structural proteins and is primarily responsible for assembling viral particles. In addition to this main role, the gag gene and its by-products (Gag proteins) have often been implicated in other stages of the HIV-1 life cycle. Some evidence suggests that this gene can interfere with the function of the three key enzymes, protease, reverse transcriptase and integrase, of the viral replication cycle through interactions with the genes encoding these enzymes. It is particularly well known that the HIV-1 gag gene is subject to numerous mutations that can influence the pathophysiology and treatment of HIV infection. It is also now well established that these mutations can lead to resistance to ARV treatments, particularly treatments including protease or integrase inhibitors. In this review, we will present the gag gene and its implication in the pathophysiology of HIV infection, its implication regarding ARV treatments, and finally we will review the central position that this gene occupies in the research and discovery of new ARV molecules like Gag inhibitors. Gag inhibitors disrupt the assembly and release of new viral particles, thus preventing further infection. Because Gag plays a role in multiple stages of the viral replication cycle, Gag inhibitors can affect both early and late stages of infection, making it a promising therapeutic target.

Keywords: Acquired immune deficiency syndrome (AIDS); Antiretroviral therapy (cART); HIV-1; Gag proteins.

The Gag Gene in HIV/AIDS Infection

HIV infection is a chronic infection due to Human Immunodeficiency Virus. Since its discovery between 1981 and 1983 [1], HIV/AIDS infection remains incurable and widespread throughout the world. In 2024, according to estimates by the Joint United Nations Program on HIV/AIDS (UNAIDS), 40.8 million people were living with HIV worldwide, of whom 31.6 million (77%) had access to antiretroviral therapy, 1.3 million people were newly infected and 630,000 people had died of HIV-related opportunistic infections [2]. This infection remains a major public health concern. To overcome this infection more effectively, it is vital to take a look back on its pathogen.

Affiliation:

[1]Chantal Biya International Reference Centre for Research on HIV/AIDS Prevention and Management, Yaoundé´, Cameroon

[2]Faculty of sciences, University of Yaoundé I, Yaoundé, Cameroon

[3]Faculty of Medicine and Biomedical Sciences, University of Yaoundé I, Yaoundé, Cameroon

[4]Faculty of Health Sciences, University of Buea, Buea, Cameroon

[5]National HIV Drug Resistance Working Group, Yaoundé, Cameroon

[6]National AIDS Control Committee, Ministry of Public Health, Yaoundé, Cameroon.

***Corresponding author:**
Georges Teto, Chantal Biya International Reference Centre for Research on HIV/AIDS Prevention and Management, Yaoundé´, Cameroon.

Citation: Georges Teto, Pierre Zoelong Emini, Beatrice Dambaya, Alex Durand Nka, Ezechiel Ngoufack Jagni Semengue, Desiré Takou, Collins Chenwi, Aude Christelle Ka'e, Grace Angong Beloumou, Constant Anatole Pieme, Joseph Fokam and Alexis Ndjolo. HIV-1 Gag Gene - Understanding Current Trends in the Development of Promising ARV Treatments. Archives of Internal Medicine Research. 9 (2026): 145-155.

Received: May 25, 2026
Accepted: June 05, 2026
Published: June 17, 2026

Teto G, et al., Arch Intern Med Res 2026
DOI:10.26502/aimr.0245

HIV-1 is the most widespread as compare to HIV-2, and is responsible for the pandemic [3]. HIV-1 is an enveloped retrovirus with a genome made up of two identical RNA molecules [4], each of which encodes for the virus' nine genes: structural genes (gag, pol, env), regulatory genes (tat, rev) and accessory genes (vif, vpr, vpu, nef). The HIV-1 gag gene encodes the structural proteins of the viral particle and the information required for the assembly of retroviruses. During the viral replication cycle (Figure1), viral RNA first undergoes reverse transcription, using the enzyme reverse transcriptase, resulting in pro-viral DNA. Thanks to the action of viral enzyme integrase, the pro-viral DNA is integrated into the host cell genome and then transcribed to form messenger RNA, which is translated to produce viral proteins. The part of the messenger RNA representing the gag gene codes directly for the Gag polyprotein and, by shifting the reading frame from -1 to the end of the gag gene, the Gag-Pol polyprotein is produced. Under the enzymatic action of the viral protease, these polyprotein precursors are cleaved into mature viral proteins (Figure2). The Gag polyprotein (Pr55Gag) plays a key role in genomic RNA packaging, specifically selecting whole (unspliced) strands of viral genomic RNA from a large number of other RNAs. This process takes place through specific interactions between Pr55Gag and the 5' region of the genomic RNA [5,6]. The Pr55 multimers Gag, in association with HIV-1 genomic RNA molecules, form a ribonucleoprotein complex inside cells [7,8] that travels to the plasma membrane for viral particle assembly [5]. Gag can bind, fuse and reorganize pre-existing lipid domains in the plasma membrane [9,10]. The association of the Gag polyprotein with the plasma membrane depends on the lipid composition of the membrane; studies suggest that electrostatic interactions with acidic lipids result in different lipid concentrations at the membrane surface, and therefore specific hydrophobic interactions; this creates an affinity between Gag and membrane lipids [10]. The HIV-1 Pr55Gag precursor is composed of several structural domains: the matrix (MA), the capsid (CA), the nucleocapsid (NC), the P6 protein and two spacer peptides (P2 and P1). Each of these structural domains and spacer peptides plays a role in the assembly and maturation of the viral particle (Figure3).

The MA domain, formed by P17 proteins, allows interaction with the plasma membrane, thanks to a highly basic zone it contains [11,12,13]. It has been established that the targeting and binding of Gag proteins to the plasma membrane is made possible by interactions between the basic region of the MA domain and acidic phospholipids such as phosphatidylinositol (4,5)- bisphosphate (PI (4,5) P2) in the plasma membrane. Studies have shown that binding between the MA domain and RNA leads to a specific interaction between the Gag polyprotein and the plasma membrane; specifically, oligomerisation of this polyprotein on the plasma membrane[14,15]. The CA domain (P24) is essential for Gag multimerisation during assembly and capsid formation during maturation [16]. During the final stages of viral particle maturation, the CA domain, derived from Gag cleavage by protease, forms a core containing the viral genetic material (RNA) and other proteins (reverse transcriptase, Integrase) essential for replication of the new viral particles [17].

Containing several basic residues, the NC domain (P7) is highly important for specific interaction with genomic RNA. It is also involved in reverse transcription, thanks to its ability to facilitate the incorporation of transfer RNA, the tRNALys3, which then serves as a primer [18]. This domain behaves like nucleic acid chaperone proteins [19]. The P6 domain contains binding motifs involved in interaction with the host cell, and budding of the viral particle for release from the host cell [20,21]; it makes use of the endosomal sorting complex required for transport (ESCRT) system to perform this activity, which is its primary one [22,23]. However, it has multiple implications in the viral replication cycle: it plays a role in viral replication through a series of post-translational modifications such as sumoylation, ubiquitination and phosphorylation; it mediates the incorporation of Vpr accessory proteins into virions, thereby promoting Vpr-induced replication. The P6 domain of the Gag gene would therefore be a promising therapeutic target [22]. The two spacer peptides (P2 and P1) are involved in the maturation kinetics of the Pr55 Gag precursor [5].

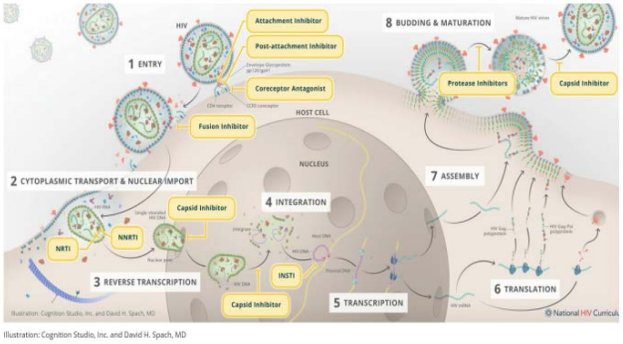


Figure 1: HIV life cycle and site of inhibitors of viral replication [24].

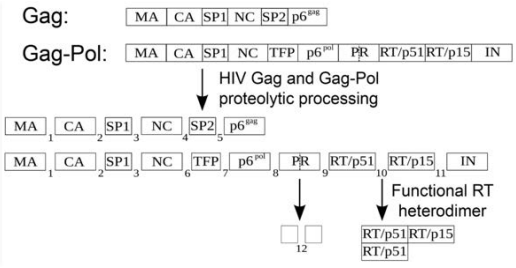


Figure 2: The scheme of Gag and Gag-Pol processing by HIV-1 PR [25].

Abbreviations: MA – matrix, CA – capsid, SP1 – spacer peptide 1, NC – nucleocapsid, SP2 – spacer peptide 2, TFP – transframe peptide, PR – protease, RT – reverse transcriptase, IN – integrase. Boxes representing individual domains are not drawn to scale.

Citation: Georges Teto, Pierre Zoelong Emini, Beatrice Dambaya, Alex Durand Nka, Ezechiel Ngoufack Jagni Semengue, Desiré Takou, Collins Chenwi, Aude Christelle Ka'e, Grace Angong Beloumou, Constant Anatole Pieme, Joseph Fokam and Alexis Ndjolo. HIV-1 Gag Gene - Understanding Current Trends in the Development of Promising ARV Treatments. Archives of Internal Medicine Research 9 (2026): 145-155.

Teto G, et al., Arch Intern Med Res 2026
DOI:10.26502/aimr.0245

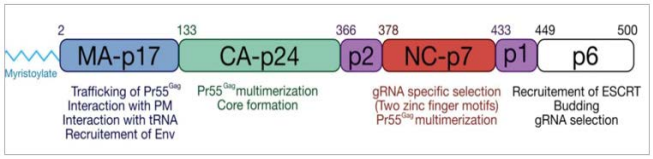


Figure 3: Gag proteins and their main functions.

HIV/AIDS and Antiretroviral Treatment

Research studies carried out since the beginning of the pandemic have led to significant advances in the management of the disease, resulting in the gradual disappearance of the term AIDS. These studies have enabled us to learn more and more about the virus and its pathophysiology, opening the way to various therapeutic approaches. As a result of this research, antiretroviral treatments (ART) have proved highly effective in the fight against HIV and in improving patients' quality life. Starting with the first discovery of an anti-HIV molecule (Zidovudine) in 1987, several other ARV molecules have been developed, including nucleoside reverse transcriptase inhibitors (NRTIs), non-nucleoside reverse transcriptase inhibitors (NNRTIs), protease inhibitors (PIs), integrase inhibitors (INs), entry inhibitors [26] , and newly developed ones, namely capsid inhibitors, nucleoside reverse transcriptase translocation inhibitor, maturation inhibitors, broadly neutralising antibodies and in some extend, the pharmacokinetic enhancers.

Triple therapies are combinations of three antiretroviral molecules that inhibit the multiplication of the virus by at least two mechanisms of action [27]. Generally, this involves a combination of two NRTIs with one PI or one NNRTI or one IN. The ARV treatments currently in use help to reduce the viral load to undetectable levels. Thanks to these treatments, progression to AIDS is on the way out, and HIV infection is no longer perceived as a disaster or an inevitability. However, ART does not eradicate or cure HIV infection. The factors explaining this are mainly the existence of multidimensional viral reservoirs where the virus remains in a latent state and escapes the action of ART and the immune system [28], the loss of ART efficacy due to viral resistance, limited access to ART particularly in Low and Middle Income Countries (LMICs), among others. [29,30]. In addition, these antiretroviral are also responsible of numerous adverse effects [30, 18, 31]. There was a need to find out the above mentioned new therapeutics that would provide an option for people living with HIV who have limited treatment options due to comorbid conditions, side effects, or drug–drug interactions.

Ideally new drugs should exhibit robust HIV-1 antiviral activity against a broad range of subtypes without cross-resistance to currently used therapies, have few drug interactions, and an excellent side effect profile. In addition, simplified dosing regimens, especially having long-acting formulations and being used in two-drug combinations. All these characteristics are the reason why more attention should be paid to the development of new drugs research. In this context, new classes of ARV drugs have been particularly targeted these recent years, like the capsid inhibitors, maturation inhibitors and broadly neutralizing antibodies among others.

Interactions between HIV-1 Gag and reverse transcriptase, Protease, Integrase, and entry inhibitors

Reverse transcriptase (RT) is a viral enzyme that acts during the HIV-1 replication cycle by means of DNA polymerase activity, which allows reverse transcription of single- stranded RNA into double- stranded proviral DNA, and endonuclease activity, which results in hydrolysis of the RNA strand contained in the RNA/DNA hybrid molecule. Reverse transcriptase inhibitors are molecules that bind competitively (NRTI) or non-competitively (NNRTI) to this enzyme [32]. Studies have shown that treatment with Efavirenz, a non-nucleoside reverse transcriptase inhibitor, results in significantly lower virus yields due to increased Gag cleavage by the protease [33]. RT instability has been correlated with impaired Gag cleavage by the protease, suggesting that RT stability is critical for protease activation [34]. Mutations in the RT gene can therefore have a significant impact on protease activation; certain mutations in the RT gene can considerably reduce virus production rates or the release of inadequately processed virions due to enhance or reduce Gag cleavage [35]. It should also be noted that several studies have shown that mutations in the HIV-1 gag gene are associated with treatment failure (ARV combinations) including reverse transcriptase inhibitors. mutations in the Gag cleavage sites can increase viral infectivity and resistance to NRTIs [36]

Interactions between HIV-1 Gag and Protease inhibitors

Protease inhibitors (PIs) block the action of the viral protease. The gag and polgenes are flanking sequences, and when the viral mRNA is translated, they are translated into Gag polyproteins and then, thanks to a change in the -1 reading frame, into Gag-Pol polyproteins. Viral protease is an enzyme that catalyzes the hydrolysis of these polyprotein precursors into mature viral proteins (Figure4). Gag and Gag-Pol are significantly associated with the final stages of the viral replication cycle, in particular, assembly, genome packaging, budding, release and maturation of viral particles [32]. Viral protease therefore plays a major role in the maturation and acquisition of infectivity of viral particles. PIs are antiretroviral molecules whose main function is to prevent the cleavage of these polyprotein precursors and consequently the maturation of viral particles. However, treatment of HIV infection with PIs is often confronted with

Teto G, et al., Arch Intern Med Res 2026
DOI:10.26502/aimr.0245

cases of HIV-1 resistance to these drugs. Several studies have reported that this resistance is due to mutations that may be located not only in the protease gene, but also in other HIV-1 genes, in this case, the gag gene [37, 38, 39]. Studies of HIV-1, namely subtype B, showed that mutations on Gag or Gag cleavage sites can induce resistance to antiretroviral drugs and treatment failure, independent of mutations in other segments of the viral genome, and directly contribute to resistance to PIs [36,40,41,42,43,44]. However, the mechanisms by which these mutations in the Gag gene lead to failure or resistance to ARV treatments are not yet well understood. Studies by teto and collaborators in 2022, Abdullahi and collaborators in 2023, found a correlation between some protease mutations and the Gag mutations, for instance the correlation between the mutation V82A, M46I, L10F and the mutations L449F, P453L, D480E in gag gene [38,45,46], of course, the mechanism explaining the above mentioned correlation has not yet been explained, future studies should focus on such mechanism.

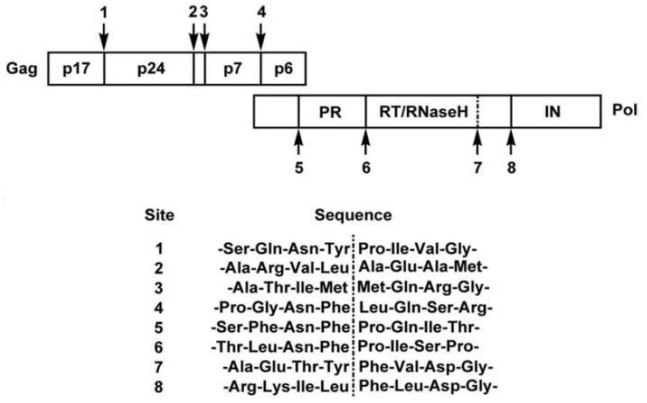


Figure 4: Cleavage site of HIV protease in the Gag and Pol polyproteins

Interactions between HIV-1 Gag and Integrase inhibitors

Integrase inhibitors block viral integrase action, an enzyme essential for HIV replication in target cells. Following their identification as innovative medicines, remarkable progress has been made in the development and approval of several compounds belonging to this class of ARVs, including dolutegravir, raltegravir, elvitégravir, cabotegravir and bictegravir. The latter, also known as integrase strand transfer inhibitors (INSTI), not only effectively block HIV-1 replication, but also have a higher genetic barrier to resistance than reverse transcriptase inhibitors [47]. In recent years, treatments including dolutegravir have demonstrated much greater efficacy and are recommended by the WHO as the treatment of first choice, especially in countries with limited resources. However, there have been cases of antiretroviral resistance in patients receiving treatment protocols including integrase inhibitors such as dolutegravir [47; 48]. There is strong evidence that viral integrase may be involved in assembly and maturation, in addition to its primary role in pro-viral DNA integration [49, 50]. Indeed, mutational analyses have shown that mutations in the integrase gene prevent the correct formation of the virion, leading to the condensation of ribonucleoproteins outside the capsid and thus an empty capsid; this alters the infectivity of viruses that have undergone such mutations [51, 49]. It has been shown that patients receiving integrase strand transfer inhibitors have been reported to experience virologic failure in the absence of resistance mutations in integrase gene. These mutations are selected in the viral nucleocapsid of the Gag rather than integrase. It has been shown that these nucleocapsid mutations accelerate the kinetics of viral DNA integration, suggesting that they limit the window of time available for integrase inhibitors to block viral DNA integration. Moreover, the selected nucleocapsid and integrase mutations act in concert to reduce the susceptibility of the virus to integrase inhibitors. This underscores the importance of genotypic analysis outside IN in patients experiencing failure on integrase inhibitors-containing drug regimens [52, 53, 54, 55, 56, 57].

Interactions between HIV-1 Gag and entry inhibitors

Entry inhibitors are molecules that prevent the virus from entering the high cell. These entry inhibitors can be grouped into three groups according to their target: those that prevent binding between the glycoprotein gp120 and the CD4 receptor, those that target binding between gp120 and coreceptors, and fusion inhibitors [32]. It has been suggested that incorporation of the envelope into forming viral particles (budding) is facilitated by the interaction between glycoprotein GP41 and the MA domain of polyprotein Gag. A good understanding of the mechanisms of interaction between Gag, GP41 and the plasma membrane would help in the development of new molecules to prevent the assembly of viral particles [58].

Gag Based Inhibitors and Novel Developed Antiretroviral Therapies

Capsid Inhibition: Lenacapavir

The HIV-1 capsid is a crucial structural component of the virus, forming a conical protein shell that encases the viral RNA and essential enzymes for replication. Primarily composed of the capsid protein, this complex structure plays a pivotal role in various stages of the viral life cycle, including assembly, uncoating, and nuclear import of the viral genome [59]. Lenacapavir (figure 5), represents the first-in-class HIV-1 capsid inhibitor, a novel mechanism that targets multiple stages of the viral lifecycle (figure 6) [60,61]. By binding to a conserved pocket at the interface of capsid protein (p24) monomers, it allosterically disrupts the delicate processes of viral core assembly, a late-stage event and disassembly, an early-stage event [32, 62]. This

dual mechanism confers picomolar potency and activity against all major HIV-1 subtypes, with no cross-resistance to existing antiretroviral classes [63]. The pivotal evidence for Lenacapavir in treatment comes from the CAPELLA trial, a Phase 2/3 study in heavily treatment-experienced individuals with multidrug-resistant virus [32]. After a functional monotherapy period, participants were switched to an optimized regimen plus subcutaneous Lenacapavir every 26 weeks. At week 52, 83% of participants achieved virologic suppression (HIV-1 RNA <50 copies/mL) [64]. These high rates of suppression were durable, with 82% of those remaining on study maintaining suppression at week 104, accompanied by a robust mean increase in CD4 count of 122 cells/μL [65]. The unique pharmacokinetic profile of Lenacapavir, characterized by a very long half-life, enables its semi-annual subcutaneous dosing and its use as a long acting drug. Studies have also confirmed that an oral dose of 300 mg once weekly can be used effectively as a bridging therapy if a subcutaneous injection is missed [66]. Furthermore, a new intramuscular formulation has shown potential for once- yearly administration [67]. Resistance to Lenacapavir is primarily associated with mutations in the Gag protein at or near the capsid binding site, such as M66I [64,68]. While highly effective, the relatively low genetic barrier to resistance for lenacapavir is a key clinical consideration. A low genetic barrier implies that a small number of viral mutations, sometimes just a single nucleotide change, can confer a significant reduction in susceptibility to the drug.

For lenacapavir, several key mutations (e.g., M66I, Q67H, K70N) have been identified that can reduce its activity [68]. The emergence of resistance during functional monotherapy in trials underscores the critical need for it to be paired with other active agents, especially given its long pharmacokinetic tail, which can create extended periods of low-level drug exposure if adherence is suboptimal or if a follow-up dose is missed. This long tail is a double-edged sword: while it provides forgiveness for slightly delayed doses, a significantly late or missed dose can result in a prolonged period of sub- therapeutic drug concentrations, an ideal scenario for the selection and amplification of pre-existing resistant variants. Recent analyses from clinical trials have further characterized these resistance pathways, emphasizing that the risk of resistance emergence is highest when lenacapavir is not combined with at least one other fully active agent in the regimen [69]. In vitro studies have shown no cross-resistance between Lenacapavir and other antiretroviral classes, including entry inhibitors, underscoring its value in salvage therapy [70]. Beyond treatment, Lenacapavir has demonstrated transformative potential in HIV prevention (PrEP). [71,72]. A study evaluated subcutaneous twice-yearly lenacapavir for HIV prevention in cisgender women yielded impressive results, with no participants in the lenacapavir arm acquiring HIV infection. This trial established that HIV incidence with lenacapavir was significantly lower than both background HIV incidence and the incidence observed with daily oral emtricitabine/tenofovir disoproxil fumarate (F/TDF) [73]. The PURPOSE 1 trial showed that twice-yearly lenacapavir achieved 100% efficacy in preventing HIV among young women in sub-Saharan Africa. It outperformed both emtricitabine/tenofovir alafenamide (F/TAF) and F/TDF, with no infections observed over 52 weeks [74]. This represents a significant advance in HIV prevention for at risk young women. Additionally, a report detailed the first case of lenacapavir administration during pregnancy to prevent mother-to-child HIV transmission (PMTCT) in a woman with multi-drug resistance HIV. Despite her resistance and high viral load, the newborn was HIV-negative, and lenacapavir was cleared from the infant, suggesting its potential as a safe treatment for pregnant women with adherence issues [75, 76].

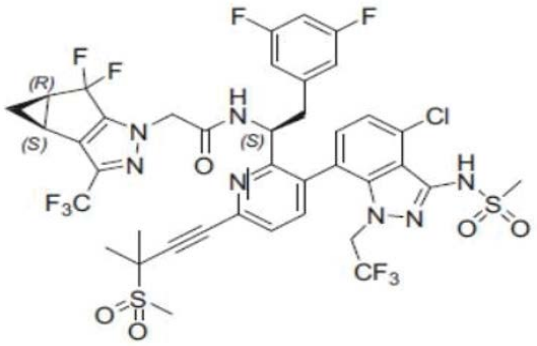


Figure 5: Lenacapavir's chemical structure

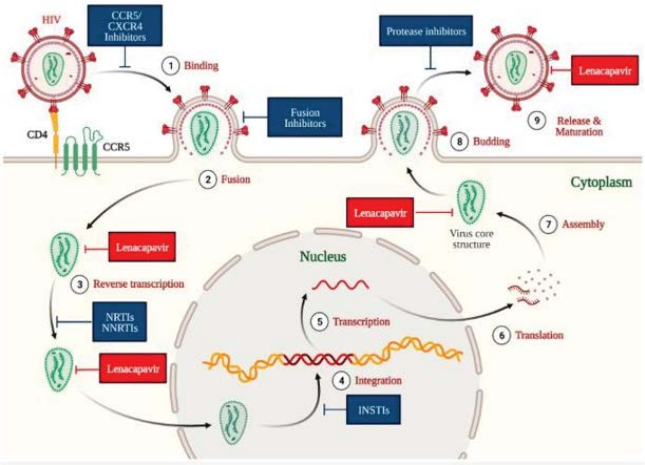


Figure 6: The mechanism of action of capsid inhibitor, lenacapavir at the multiple stages of the HIV life's cycle [77].

Lenacapavir and Broadly Neutralizing Antibodies

Broadly neutralizing antibodies (bNAbs) are a form of immunotherapy for HIV [78]. They are selected for clinical development based on their potency and breadth, with combinations chosen to target distinct, non-overlapping epitopes on the viral envelope protein. This multi-target

Teto G, et al., Arch Intern Med Res 2026
DOI:10.26502/aimr.0245

strategy creates a higher barrier to resistance, forcing the virus to mutate at several sites to escape neutralization. The HIV envelope is highly variable, and the virus can rapidly mutate to escape the pressure of a single antibody. However, by combining two or three bNAbs that target conserved regions—for example, the CD4 binding site, the V3 loop, and the MPER region—the virus would need to accumulate multiple simultaneous mutations to evade neutralization, a far less probable event. This strategy mimics the principles of combination ART. Combinations of two or three bNAbs have demonstrated the ability to maintain virologic suppression in individuals who pause ART [79,80,81], though success is highly dependent on baseline viral sensitivity [82]. Indeed, overcoming the challenges of pre-existing viral resistance and subsequent viral escape remains a primary hurdle for bNAb therapy, requiring the development of more potent and broader antibody combinations or engineered antibodies to increase the barrier to resistance [83]. Their role in cure strategies when combined with latency- reversing agents (LRAs) has shown modest results in trials like TITAN (LRA lefitolimod) and ROADMAP (LRA romidepsin), where no significant additional benefit was observed [84,85]. For prevention, the AMP trials provided proof-of-concept that bNAbs can prevent acquisition of sensitive HIV strains [86]. The future lies in improved combinations, including long acting drugs like lenacapavir [87].

Maturation Inhibitors: Zabofiravir

Maturation inhibitors target the final step of Gag polyprotein cleavage. Zabofiravir (figure 7) (GSK3640254) also known as Fipravirimat is a second-generation agent with potent activity across diverse HIV-1 subtypes and baseline Gag polymorphisms [88]. A Phase IIa monotherapy study confirmed its dose-dependent antiviral activity [89], and it has shown no clinically significant pharmacokinetic interaction when co-administered with dolutegravir [90]. Resistance to this class typically involves mutations in Gag at the cleavage site between capsid (p24) and spacer peptide 1 (SP1). A key advantage of this mechanism is its novel resistance profile, which is not expected to show cross-resistance with existing antiretroviral classes, making it a potentially important component of future combination regimens for both treatment-naïve and experienced individuals. For heavily treatment-experienced patients who have accumulated extensive resistance mutations to protease inhibitors, NRTIs, NNRTIs, and even integrase inhibitors, the availability of a new class with a completely distinct resistance pathway is of paramount clinical value. It offers a new tool to construct a viable, suppressive regimen where options were previously exhausted.

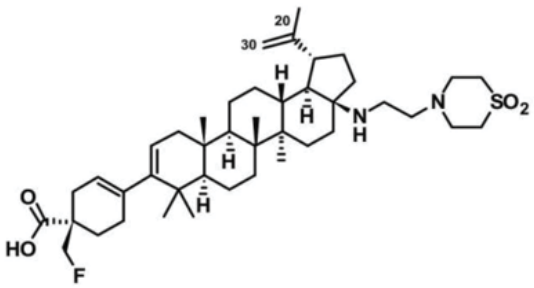
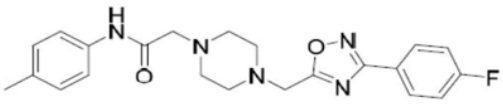


Figure 7: zabofiravir's chemical structure

Matrix inhibitors

The MA domain anchors Gag into the plasma membrane through electrostatic and hydrophobic interactions, but binding is mediated predominantly by dynamic electrostatic interactions. The MA domain is myristoylated on its N terminus and forms ionic interactions with acidic polar heads of phosphatidylinositol-(4,5)-bisphosphate (PI (4,5) P2) through its highly basic region (conserved stretch of lysine and arginine residues). The MA domain is also capable of binding RNA just like NC domain. The specificity of MA binding to PI (4,5) P2 might be attributed to MA-RNA binding because this binding prevents Gag from interacting with other lipid interfaces until it reaches the plasma membrane. It was reported that MA presented a hexamer-of-trimers arrangement for Env incorporation by interacting with the cytoplasmic tail of the Env gp41 protein and some residual mutations hinder this trimeric formation and subsequent Env incorporation for successful virus particle assembly [91,92,93,94,95]. It was shown that both the divalent phosphate groups and the acyl chains of PI (4,5) P2 [95] were essential for strong binding to MA [96]. Zentner et al. 2013 [97] developed compound 7, inhibitor of HIV-1 assembly (Figure8) using a virtual screening method. They further reported that this compound showed potential anti-HIV-1 activity with IC50 values of 7.5–15.6 μM. It was also determined that compound 7 directly interacted with HIV-1 MA, competing with PI (4,5) P2 for MA binding and blocking the generation of new viruses.



Compound **7**

Figure 8: chemical structure of compound 7

In addition, Alfadhli et al. 2013 [98] targeted MA-RNA binding, since RNA binding might protect MA from interacting with other cellular membranes before Gag delivery to the cell surface. They determined four compounds including compound 7 and three thiadiazolanes (TD 1-3) that compete with RNA for MA binding. Thiadiazolanes (figure 9) were found to halt HIV-1 replication but they were subject to toxicity.

Citation: Georges Teto, Pierre Zoelong Emini, Beatrice Dambaya, Alex Durand Nka, Ezechiel Ngoufack Jagni Semengue, Desiré Takou, Collins Chenwi, Aude Christelle Ka'e, Grace Angong Beloumou, Constant Anatole Pieme, Joseph Fokam and Alexis Ndjolo. HIV-1 Gag Gene - Understanding Current Trends in the Development of Promising ARV Treatments. Archives of Internal Medicine Research 9 (2026): 145-155.

Teto G, et al., Arch Intern Med Res 2026
DOI:10.26502/aimr.0245

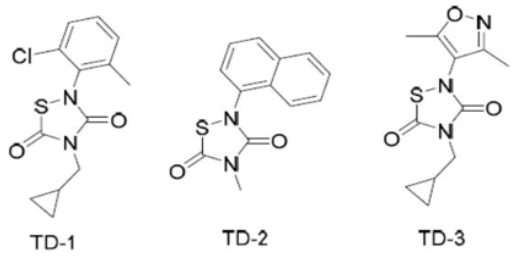


Figure 9: Chemical structure of the three thiadiazolanes TD 1-3

Conclusion

In the search for even more effective and definitive solutions to HIV infection, studies are exploring all possible therapeutic targets. In this context, Gag inhibitors namely capsid inhibitors, maturation inhibitors, matrix inhibitors have been studied. One of these, the capsid inhibitors, lenacapavir has been clinically approved, representing a new and highly promising class of antiretroviral agents, offering excellent potential for reducing viral load, few adverse effects and a long half-life. This long half-life allows twice-yearly administration and greatly improve patient adherence. This ARV class is especially useful for heavily treatment-experienced patients battling multi-drug-resistant HIV. Furthermore, prevention trials showed high efficacy in high-risk groups previously underserved by existing PrEP options. This drug was also effective in preventing mother-to-child HIV transmission of HIV. Despite these advances, several limitations need consideration. The emergence of resistance mutations to lenacapavir highlights the importance of combination therapy to maintain a high genetic barrier to resistance and optimal therapeutic responses. Additionally, concerns regarding potential neurotoxicity through synaptic disruption require ongoing surveillance. Even though pharmacokinetic studies support lenacapavir's use across diverse populations, real-world effectiveness data in resource-constrained settings remains limited. Future research should prioritize developing clinically approved maturation, matrix inhibitors and also second generation capsid inhibitors that maintain potency against emerging lenacapavir-resistant HIV variants while preserving the favourable pharmacokinetic properties that enable long-acting formulations. Working to develop newly long-acting antiretroviral therapy to use in combination with lenacapavir will also be useful to preserve its long term efficacy in the field of HIV infection treatment and prevention.

Ethics and Consent to Participate declarations

Not applicable.

Clinical trial number: Not applicable

Competing interest

Authors declared there is no competing interest.

Funding

No funding has been received for the present work.

Authors' contributions

GT conceived and wrote the manuscript, PZE, BD, AN, ENJS, DT, CC, ACK and GAB reviewed the manuscript, CP, J F and AN reviewed and supervised the work. All authors read and approved the manuscript.

Acknowledgement

We acknowledge all those who participate to the manuscript by sending us useful manuscripts to be considered in the present work.

References

1. Sonja Schmid. The discovery of HIV-1. Nature Communications.
2. UNAIDS: Global HIV and AIDS statistics – factsheet (2026).
3. Bbosa N, Kaleebu P, Ssemwanga D. HIV subtype diversity worldwide. Curr. Opin. HIV AIDS 14 (2019): 153-160.
4. Goff SP, Roth MJ. Retroviridae. Fields Virology 3 (2023): 465-526.
5. Bussienne C, Marquet R, Paillart J.-C, et a;. Post-Translational Modifications of Retroviral HIV-1 Gag Precursors: An Overview of Their Biological Role. Int. J. Mol. Sci 22 (2021): 2871.
6. Lu K, Heng X, Garyu L, et al. NMR Detection of Structures in the HIV-15 -Leader RNA That Regulate Genome Packaging. Science 334 (2011): 242-245.
7. Ferrer M, Clerté C, Chamontin C, et al. Imaging HIV- 1 RNA dimerization in cells by multicolor super-resolution and fluctuation microscopies. Nucleic Acids Res 44 (2016): 7922-7934.
8. Kutluay S B, Bieniasz P D. Analysis of the Initiating Events in HIV-1 Particle Assembly and Genome Packaging. PLoS Pathog 6 (2010): e1001200.
9. Tomishige N, Bin Nasim M, Murate M, et al. HIV-1 Gag Targeting to the Plasma Membrane Reorganizes Sphingomyelin-Rich and Cholesterol-Rich Lipid Domains. Nat. Commun 14 (2023): 7353.
10. Denieva Z G, Sokolov V S, Batishchev O V. HIV-1 Gag Polyprotein Affinity to the Lipid Membrane Is Independent of Its Surface Charge. Biomolecules 14 (2024): 1086.
11. Duchon A, Hu W. HIV-1 RNA genome packaging: it's G-rated. mBio 15 (2024): e00861-23.

12. Chukkapalli V, Oh SJ, Ono A. Opposing mechanisms involving RNA and lipids regulate HIV-1 Gag membrane binding through the highly basic region of the matrix domain. Proc Natl Acad Sci USA 107 (2010): 1600-1605.

13. Ono A, Ablan SD, Lockett SJ, et al. Phosphati dylinositol (4,5) bisphosphate regulates HIV-1 Gag targeting to the plasma membrane. Proc Natl Acad Sci USA 101 (2004):14889-14894.

14. Gaines C R, Tkacik E, Rivera-Oven A, et al. HIV-1 Matrix Protein Interactions with tRNA: Implications for Membrane Targeting. J. Mol. Biol 430 (2018): 2113-2127.

15. Thornhill D, Olety B, Ono A. Relationships between MA-RNA Binding in Cells and Suppression of HIV-1 Gag Mislocalization to Intracellular Membranes. J. Virol 93 (2019): 23.

16. Schur F K M, Hagen W J H, Remove M, et al. Structure of the immature HIV-1 capsid in intact virus particles at 8.8 A resolution. Nat. Cell Biol. 517 (2015): 505-508.

17. Rossi E, Meuser M E, Cunanan CJ, et al. Structure, Function, and Interactions of the HIV-1 Capsid Protein. Life 11 (2021).

18. Webb J A, Jones C P, Parent L J, et al. Distinct binding interactions of HIV-1 Gag to Psi and non-Psi RNAs: Implications for viral genomic RNA packaging. RNA 19 (2013): 1078-1088.

19. Rein A. Nucleic acid chaperone activity of retroviral Gag proteins. RNA Biol 7 (2010): 700-705.

20. Dubois N, Khoo K K, Ghossein S, et al. The C-terminal p6 domain of the HIV-1 Pr55Gag precursor is required for specific binding to the genomic RNA. RNA Biol 15 (2018): 923-936.

21. Fossen T, Wray V, Bruns K, et al. Solution structure of the human immunodeficiency virus type1 p 6 protein. J Biol Chem 280 (2005): 42515-42527.

22. Chen X, Wang X. The HIV-1 gag p6: a promising target for therapeutic intervention. Retrovirology BioMed Central (2024).

23. Votteler J, Sundquist WI. Virus budding and the ESCRT pathway. Cell Host Microbe 14 (2013): 232-241.

24. David H. Spach, MD, Brian R. Wood, MD. Antiretroviral Medications and Initial Therapy. National HIV curriculum, (2025).

25. Balázs Könnyű, S. Kashif Sadiq, Tamás Turányi, et al. Gag-Pol Processing during HIV-1 Virion Maturation: A Systems Biology Approach. PloS computational biology 6 (2013) 1- 15.

26. Tedbury PR, Freed EO. HIV-1 gag: an emerging target for antiretroviral therapy.Curr Top Microbiol Immunol 389 (2015): 171-201.

27. Dick A, Cocklin S. Recent Advances in HIV-1 Gag Inhibitor Design and Development. Molecules 25 (2020): 1-25.

28. Steven G. Deeks, Nancie Archin, Paula Cannon, et al. Research priorities for an HIV cure: International AIDS Society Global Scientific Strategy 2021. Nature Medicine 27 (2021): 2085-2098.

29. Chatzidimitriou D, Tsotridou E, Grigoropoulos P, et al. HIV-1: Towards understanding the nature and quantifying the latent reservoir. Acta Virol 64 (2020): 3-9.

30. Menéndez-Arias L, Delgado R. Update and latest advances in antiretroviral therapy. Trends Pharmacol Sci 43 (2022): 16-29.

31. Belgin Sever, Masami Otsuka, Mikako Fujita, et al. A Review of FDA-Approved Anti-HIV-1 Drugs, Anti-Gag Compounds, and Potential Strategies for HIV-1 Eradication.International journal of molecular sciences 25 (2024).

32. Sever B, Otsuka M, Fujita M, et al. A Review of FDA-Approved Anti-HIV-1 Drugs, Anti-Gag Compounds, and Potential Strategies for HIV-1 Eradication. Int. J. Mol. Sci 25 (2024): 3659.

33. Tachedjian G, Moore KL, Goff SP, et al. Efavirenz enhances the proteolytic processing of an HIV-1 pol polyprotein precursor and reverse transcriptase homodimer formation. FEBS Lett 579 (2005): 379-384.

34. Hsieh S, Yu F, Huang K, et al. HIV-1 reverse transcriptase stability correlates with Gag cleavage efficiency: reverse transcriptase interaction implications for modulating protease activation. Journal of Virology 97 (2023): 1-16.

35. Chiang CC, Wang SM, Pan YY, et al. A single amino acid substitution in HIV-1 reverse transcriptase significantly reduces virion release. J Virol 84 (2010): 976-982.

36. Solange Peters, Miguel Muñoz, Sabine Yerly, et al. Resistance to nucleoside analog reverse transcriptase inhibitors mediated by human immunodeficiency virus type 1p6 protein. Journal of virology 75 (2001): 9644-9653.

37. Nka AD, Teto G, Santoro MM, et al. HIV-1 Gag gene mutations, treatment response and drug resistance to protease inhibitors: A systematic review and meta-analysis protocol. PLoS ONE 16 (2021): e0253587.

38. Teto G, Nka A D, Fokam J, et al. Detection of Gag C – terminal mutations among HIV - 1 non - B subtypes in a subset of Cameroonian patients. Scientific Reports (2022): 1-11.

Citation: Georges Teto, Pierre Zoelong Emini, Beatrice Dambaya, Alex Durand Nka, Ezechiel Ngoufack Jagni Semengue, Desiré Takou, Collins Chenwi, Aude Christelle Ka'e, Grace Angong Beloumou, Constant Anatole Pieme, Joseph Fokam and Alexis Ndjolo. HIV-1 Gag Gene - Understanding Current Trends in the Development of Promising ARV Treatments. Archives of Internal Medicine Research 9 (2026): 145-155.

39. Alencar CS, Sabino EC, Diaz RS, et al. Genetic diversity in the partial sequence of the HIV-1 gag gene among people living with multidrug- resistant HIV-1 infection. Rev Inst Med Trop São Paulo 66 (2024): e35.

40. Y M Zhang, H Imamichi, T Imamichi, et al. Drug resistance during indinavir therapy is caused by mutations in the protease gene and in its Gag substrate cleavage sites. Journal of virology 71 (2024): 6662-6670.

41. Chris M Parry 1, Arinder Kohli, Christine J Boinett, et al. Gag determinants of fitness and drug susceptibility in protease inhibitor-resistant human immunodeficiency virus type 1. Journal of virology 83 (2009): 9094-9101,

42. Clavel F, Mammano F. Role of Gag in HIV Resistance to Protease Inhibitors.Viruses 2 (2010): 1411-1426.

43. Soriano V, de Mendoza C. Genetic mechanisms of resistance to NRTI and NNRTI. HIV Clin Trials 3 (2002): 237-248.

44. Dam E, Quercia R, Glass B, et al. Gag mutations strongly contribute to HIV-1 resistance to protease inhibitors in highly drug-experienced patients besides compensating for fitness loss. PLoS pathogens 5 (2009): e1000345.

45. Adam Abdullahi, Ana Garcia Diaz, Olga Mafotsing Fopoussi, et al. A detailed characterization of drug resistance during darunavir/ritonavir monotherapy highlights a high barrier to the emergence of resistance mutations in protease but identifies alternative pathways of resistance. J Antimicrob Chemother (2023): 1-10

46. Garcia Diaz A. An Investigation of the role of HIV-1 Gag mutation in failure of Protease Inhibitors. Doctoral thesis, UCL (University College London) (2012).

47. Mbhele N, Chimukangara B, Gordon M. International Journal of Antimicrobial Agents HIV-1 integrase strand transfer inhibitors: a review of current drugs, recent advances and drug resistance. International Journal of Antimicrobial Agents 57 (2021): 106343.

48. Lübke N, Jensen B, Hüttig F, et al. Failure of do-lutegravir first-line ART with selection of virus carrying R263K and G118R. N Engl J Med 381 (2019): 887-889.

49. Kleinpeter A B, Freed E O. HIV-1 Maturation: Lessons Learned from Inhibitors. Viruses 12 (2020): 940.

50. Kessl J J, Kutluay S B, Townsend D, et al. HIV-1 Integrase Binds the Viral RNA Genome and Is Essential during Virion Morphogenesis. Cell 166 (2016): 1257-1268.

51. Engelman A, England G, Orenstein J M, et al. Multiple effects of mutations in human immunodeficiency virus type 1 integrase on viral replication. J. Virol 69 (1995): 2729.

52. Yuta Hikichi, Ryan C Burdick, Sean C Patro, et al. Elucidating the mechanism by which HIV-1 nucleocapsid mutations confer resistance to integrase strand transfer inhibitors. Sci Adv 11 (2025).

53. Espeseth A S, Felock P, Wolfe A, et al. HIV-1 integrase inhibitors that compete with the target DNA substrate define a unique strand transfer conformation for integrase. Proc. Natl. Acad. Sci, U.S.A 97 (2000): 11244-11249.

54. Levin J G, Mitra M, Mascarenhas A, et al. Role of HIV-1 nucleocapsid protein in HIV-1 reverse transcription. RNA Biol 7 (2010): 754-774.

55. Christensen D E, Ganser-Pornillos B K, Johnson J S, et al. Reconstitution and visualization of HIV-1 capsid-dependent replication and integration in vitro. Science 370 (2020): eabc8420.

56. Buckman J S, Bosche W J, Gorelick R J. Human immunodeficiency virus type 1 nucleocapsid zn2+ fingers are required for efficient reverse transcription, initial integration processes, and protection of newly synthesized viral DNA. J. Virol 77 (2003): 1469-1480.

57. Mori M, Ode H, Kubota M, et al. Nanopore sequencing for characterization of HIV-1 recombinant forms. Microbiol Spectr 10 (2022): e0150722.

58. Murphy R E, Saad J S. The Interplay between HIV-1 Gag Binding to the Plasma Membrane and Env Incorporation. Viruses (2020): 1-23.

59. Dwivedi R, Prakash P, Kumbhar BV, et al. HIV-1 capsid and viral DNA integration. mBio 215 (2024): 1-20.

60. Reed JC, Solas D, Kitaygorodskyy A, et al. Identification of an Antiretroviral Small Molecule That Appears To Be a Host-Targeting Inhibitor of HIV-1 Assembly. J Virol 95 (2021): e00883-20.

61. Zhou J, Yuan X, Dismuke D, et al. Small-molecule inhibition of human immunodeficiency virus type 1 replication by specific targeting of the final step of virion maturation. J Virol 78 (2004): 922-929.

62. Pereira-Montecinos C, Toro-Ascuy D, Ananías-Sáez C, et al. Epitranscriptomic regulation of HIV-1 full-length RNA packaging. Nucleic Acids Res 50 (2022) :2302-2318.

63. Dvory-Sobol H, Shaik N, Callebaut C, et al. A first-in-class HIV-1 capsid inhibitor. Curr. Opin,; HIV AIDS 17 (2022): 15-21.

64. Segal-Maurer S, DeJesus E, Stellbrink H J, et al CapsidInhibition with Lenacapavir in Multidrug-Resistant HIV-1 Infection. N. Engl. J. Med 386 (2022): 1793-1803.

65. Ogbuagu O, Molina J M, Chetchotisakd P, et al. Efficacy

and Safety of Long-Acting Subcutaneous Lenacapavir in Heavily Treatment-Experienced People with Multidrug-Resistant HIV-1: Week 104 Results of a Phase 2/3 Trial. Clin. Infect. Dis 80 (2025): 566-574.

66. Ogbuagu O E, Avihingsanon A, Segal-Maurer S, et al. Efficacy, safety, and pharmacokinetics of lenacapavir oral bridging when subcutaneous lenacapavir cannot be administered. AIDS 39 (2025): 639-648.

67. Jogiraju V, Pawar P, Yager J, et al. Pharmacokinetics and safety of once-yearly lenacapavir: A phase 1, open-label study. Lancet 405 (2025): 1147-1154.

68. Wensing A M, Calvez V, Ceccherini-Silberstein F, et al. Update of the Drug Resistance Mutations in HIV-1. Top. Antivir. Med 33 (2025): 457-473.

69. Gupta S K, Berhe M, Crofoot G, et al. Lenacapavir administered every 26 weeks or daily in combination with oral daily antiretroviral therapy for initial treatment of HIV: A randomised, open-label, active-controlled, phase 2 trial. Lancet HIV 10 (2023): e15-e23.

70. Margot N, Pennetzdorfer N, Naik V, et al. Cross-resistance to entry inhibitors and lenacapavir resistance through Week 52 in study CAPELLA. Antivir. Ther 28 (2023): 13596535231220754.

71. Bekker L G, Das M, Abdool Karim Q, et al. Twice-Yearly Lenacapavir or Daily F/TAF for HIV Prevention in Adolescent Girls and Young Women. N. Engl. J. Med 391 (2024): 1179-1192.

72. Kelley C F, Acevedo-Quinones M, Agwu A L, et al. Twice-Yearly Lenacapavir for HIV Prevention in Men and Gender-Diverse Persons. N. Engl. J. Med 392 (2025): 1261-1276.

73. Bekker LG, Das M, Karim QA, et al. Twice-yearly lenacapavir or daily F/TAF or HIV prevention in cisgender women. N Engl J Med 391 (2024): 1179-1192.

74. Nozza S, Castagna A. Twice-yearly lenacapavir: a milestone for HIV prevention in young African women. Med 5 (2024): 1200-1202.

75. Lin Y, Ling X, Li L, et al. Lack of Resistance Mutations to the Novel HIV-1 Capsid Inhibitor Lenacapavir Among People Living with HIV in Guangdong, China. Infect Drug Resist 17 (2024): 4271-4277.

76. Hémar V, Bouchet S, Ribeiro E, et al. A case of lenacapavir use for preventing mother-to-child HIV transmission. J Antimicrob Chemother 79 (2024): 3354-3355.

77. Tafadzwa Dzinamarira, Mazen Almehmadi, Ahad Amer Alsaiari, et al. Highlights on the Development, Related Patents, and Prospects of Lenacapavir: The First-in-Class HIV-1 Capsid Inhibitor for the Treatment of Multi-Drug-Resistant HIV-1 Infection. Medicina, review 59 (2023): 1041.

78. Thavarajah J J, Honge B, Wejse C M. The Use of Broadly Neutralizing Antibodies (bNAbs) in HIV-1 Treatment and Prevention.Viruses 16 (2024): 911.

79. Mendoza P, Gruell H, Nogueira L, et al. Combination therapy with anti- HIV-1 antibodies maintains viral suppression. Nature 561 (2018): 479-484.

80. Gaebler C, Nogueira L, Stoffel E, et al. Prolonged viral suppression with anti-HIV-1 antibody therapy. Nature 606 (2022): 368-374.

81. Sneller M C, Blazkova J, Justement J S, et al. Combination anti-HIV antibodies provide sustained virological suppression. Nature 606 (2022): 375-381.

82. Becerra J C, Hitchcock L, Vu K, et al. Neutralizing the threat: Harnessing broadly neutralizing antibodies against HIV-1 for treatment and prevention. Microb. Cell 11 (2024): 207-220.

83. Julg B, Walker-Sperling V E K, Wagh K, et al. Safety and antiviral effect of a triple combination of HIV-1 broadly neutralizing antibodies: A phase 1/2a trial. Nat. Med 30 (2024): 3534-3543.

84. Stephenson K E, Julg B, Tan C S, et al. Safety, pharmacokinetics and antiviral activity of PGT121, a broadly neutralizing monoclonal antibody against HIV-1: A randomized, placebo-controlled, phase 1 clinical trial. Nat. Med 27 (2021): 1718-1724.

85. Gunst J D, Hojen J F, Pahus M H, et al. Impact of a TLR9 agonist and broadly neutralizing antibodies on HIV-1 persistence: The randomized phase 2a TITAN trial. Nat. Med 29 (2023): 2547-2558.

86. Gruell H, Gunst J D, Cohen Y Z, et al. Effect of 3BNC117 and romidepsin on the HIV-1 reservoir in people taking suppressive antiretroviral therapy (ROADMAP): A randomised, open-label, phase 2A trial. Lancet Microbe 3 (2022): e203-e214.

87. Corey L, Gilbert P B, Juraska M, et al. Two Randomized Trials of Neutralizing Antibodies to Prevent HIV-1 Acquisition. N. Engl. J. Med 384 (2021): 1003-1014.

88. Dicker I, Jeffrey J L, Protack T, et al. GSK3640254 Is a Novel HIV-1 Maturation Inhibitor with an Optimized Virology Profile. Antimicrob. Agents Chemother 66 (2022): e01876-21.

89. Spinner C D, Felizarta F, Rizzardini G, et al. Phase IIa Proof-of- Concept of GSK3640254, a Next-Generation Maturation Inhibitor. Clin. Infect. Dis 75 (2022): 786-794.

90. Pene Dumitrescu T, Joshi S R, Xu J, et al. Phase I

Teto G, et al., Arch Intern Med Res 2026
DOI:10.26502/aimr.0245

evaluation of pharmacokinetics and tolerability of the HIV-1 maturation inhibitor GSK3640254 and dolutegravir in healthy adults. Br. J. Clin. Pharmacol, 87 (2021): 3501-3507.

91. Tedbury P R, Novikova M, Alfadhli A, et al. HIV-1 Matrix Trimerization-Impaired Mutants Are Rescued by Matrix Substitutions That Enhance Envelope Glycoprotein Incorporation. J. Virol 94 (2019): e01526-19.

92. Socas L B P, Ambroggio E E. HIV-1 Gag specificity for PIP2 is regulated by macromolecular electric properties of both protein and membrane local environments. Biochim. Biophys. Acta Biomembr 1865 (2023): 184157.

93. Mercredi P Y, Bucca N, Loeliger B, et al. Structural and Molecular Determinants of Membrane Binding by the HIV-1 Matrix Protein. J. Mol. Biol 428 (2016): 1637-1655.

94. Dilley K A, Nikolaitchik O A, Galli A, et al. Interactions between HIV-1 Gag and Viral RNA Genome Enhance Virion Assembly. J. Virol 91 (2017): e02319-16.

95. Ono A, Ablan S D, Lockett S J, et al. Phosphatidylinositol (4,5) bisphosphate regulates HIV-1 Gag targeting to the plasma membrane. Proc. Natl. Acad. Sci 101 (2004): 14889-14894.

96. Anraku K, Fukuda R, Takamune N, et al. Highly sensitive analysis of the interaction between HIV-1Gag and phosphoinositide derivatives based on surface plasmon resonance. Biochemistry 49 (2010): 5109-5116.

97. Zentner I, Sierra L J, Fraser A K, et al. Identification of a small-molecule inhibitor of HIV-1 assembly that targets the phosphatidylinositol (4,5)-bisphosphate binding site of the HIV-1 matrix protein. ChemMedChem 8 (2013): 426-432.

98. Alfadhli A, McNett H, Eccles J, et al. Analysis of small molecule ligands targeting the HIV-1 matrix protein-RNA binding site. J. Biol. Chem 288 (2013): 666-676.

Citation: Georges Teto, Pierre Zoelong Emini, Beatrice Dambaya, Alex Durand Nka, Ezechiel Ngoufack Jagni Semengue, Desiré Takou, Collins Chenwi, Aude Christelle Ka'e, Grace Angong Beloumou, Constant Anatole Pieme, Joseph Fokam and Alexis Ndjolo. HIV-1 Gag Gene - Understanding Current Trends in the Development of Promising ARV Treatments. Archives of Internal Medicine Research 9 (2026): 145-155.