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Entangled MAGAZINE

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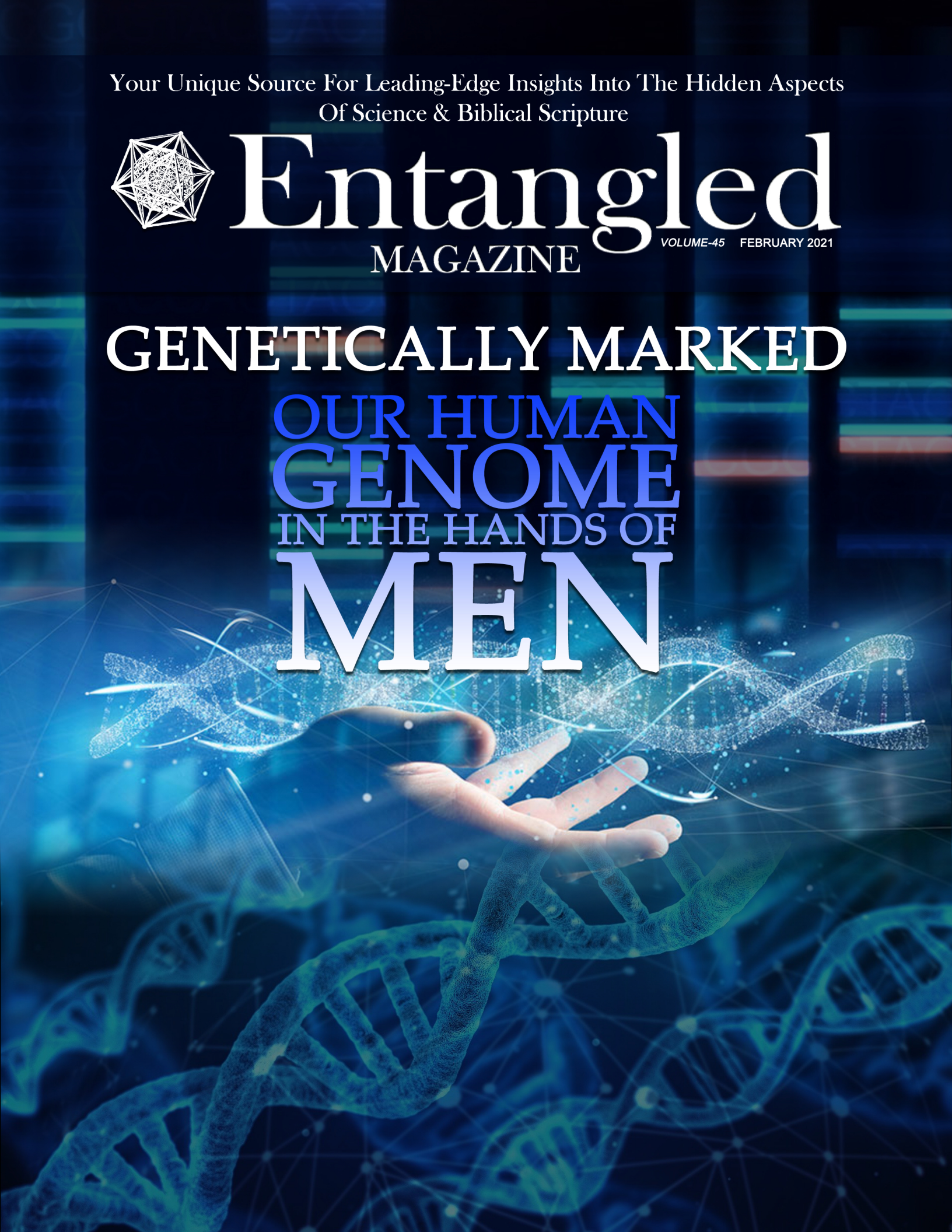
GENETICALLY MARKED

OUR HUMAN GENOME IN THE HANDS OF MEN



Genetically Marked

By Kathleen M. Urquhart

<u>Mechanism of mRNA Transport in the Nucleus</u>

"We found that the rate of Messenger RNP (mRNA-protein) diffusion is so fast that mRNP complexes are dispersed throughout the nucleus soon after their synthesis and well before the onset of significant export into the cytoplasm."

*"Using **molecular beacons** to track single mRNA molecules in living cells, we have characterized the diffusion of mRNP (mRNA-protein) complexes in the nucleus. The mRNP complexes move freely by Brownian diffusion at a rate that assures their dispersion throughout the nucleus before they exit into the cytoplasm, even when the transcription site is located near the nuclear periphery."*

Diana Y. Vargas, Arjun Raj, Salvatore A. E. Marras, Fred Russell Kramer, Sanjay Tyagi

Proceedings of the National Academy of Sciences Nov 2005, 102 (47) 17008-17013; DOI: 10.1073/pnas.0505580102

Please read: https://www.pnas.org/content/102/47/17008.long

Abstract -Recent Advances in the Molecular Beacon Technology for Live-Cell Single-Molecule Imaging

Nucleic acids, aside from being best known as the carrier of **genetic information**, are versatile biomaterials for constructing nanoscopic devices for biointerfacing, owing to their unique properties such as specific base pairing and predictable structure. For live-cell analysis of native RNA transcripts, the most widely used nucleic acid-based nanodevice has been the molecular beacon (MB), a class of stem-loop-forming probes that is activated to fluoresce upon hybridization with target RNA.

Mao S, Ying Y, Wu R, Chen AK. **Recent Advances in the Molecular Beacon Technology for Live-Cell Single-Molecule Imaging**. iScience. 2020 Nov 13;23 (12):101801. doi: 10.1016/j.isci.2020.101801. PMID: 33299972; PMCID: PMC7702005.

https://pubmed.ncbi.nlm.nih.gov/33299972/

Wiki: **Molecular beacons**, or **molecular beacon probes**, are oligonucleotide hybridization probes that can report the presence of specific nucleic acids in homogenous solutions.

https://en.wikipedia.org/wiki/Molecular_beacon

Wiki: (mRNA-protein) Messenger RNP: **Messenger RNP** (**messenger ribonucleoprotein**) **is mRNA with bound proteins**. mRNA does not exist "naked"*i n vivo* but is always bound by various proteins while being synthesized, spliced, exported, and translated in the cytoplasm.

https://en.wikipedia.org/wiki/Messenger_RNP

Wiki: **RNA Vaccine -** An **RNA vaccine** or **mRNA (messenger RNA) vaccine** is a type of vaccine that uses a **copy** of a natural chemical called messenger RNA (mRNA) to produce an immune response.[1] The vaccine transfects molecules of **synthetic RNA** into immunity cells.

mRNA vaccines introduce a short-lived [32] **synthetically created fragment of the RNA sequence** of a virus into the vaccinated individual.

https://en.wikipedia.org/wiki/RNA_vaccine#:~:text=mRNA%20vaccines%20operate%20in%20a,to%20have%20antigens)%20into%20muscles.

RNA Biol. 2016 Sep; 13(9): 760–765.
Published online 2016 Jun 28. doi: 10.1080/15476286.2016.1203504
PMCID: PMC5014007
PMID:27351916

mRNA modifications: Dynamic regulators of gene expression?

Thomas Philipp Hoernes,Alexander Hüttenhofer, and Matthias David Erlacher

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5014007/

The expression of a gene is a tightly regulated process and is exerted by a myriad of different mechanisms. Recently, RNA modifications located in coding sequences of mRNAs, have been identified as potential regulators of gene expression. N6-methyladenosine (m6A), 5-methylcytosine (m5C), pseudouridine (Ψ) and N1-methyladenosine (m1A) have been found within open reading frames of mRNAs. The presence of these mRNA modifications has been implicated to modulate the fate of an mRNA, ranging from maturation to its translation and even degradation. However, many aspects concerning the biological functions of mRNA modifications remain elusive. Recently, systematic in vitro studies allowed a first glimpse of the direct interplay of mRNA modifications and the efficiency and fidelity of ribosomal translation. It thereby became evident that the effects of mRNA modifications were, astonishingly versatile, depending on the type, position or sequence context. The incorporation of a single modification could either prematurely terminate protein synthesis, reduce the peptide yield, or alter the amino acid sequence identity. These results implicate that mRNA modifications are **a powerful mechanism to post-transcriptionally regulate gene expression**.

Post-transcriptional mRNA modifications might even possess the potential to expand the diversity of proteins through recoding. Therefore, it is of utmost importance to elucidate all mechanisms behind. mRNA modifications not only affect translation, but can also act as **markers** to provide landing platforms for proteins 61,62,85,86 or stimulate other regulatory processes like mRNA degradation 60 or localization. 87 Their role as **markers** is reminiscent of the regulation of gene expression through epigenetic DNA and histone modifications. In line with that, **not single modifications but a combination thereof might collectively mediate biological functions**.

WIKI: Viral Vectors: Viral vectors [edit]

Main article: Viral vector

Viral vectors are generally genetically engineered viruses carrying modified viral DNA or RNA that has been rendered noninfectious, but still contain viral promoters and also the transgene, thus allowing for translation of the transgene through a viral promoter. However, because viral vectors frequently are lacking infectious sequences, they require helper viruses or packaging lines for large-scale transfection. Viral vectors are often designed for permanent incorporation of the insert into the host genome, and thus leave distinct genetic markers in the host genome after incorporating the transgene. For example, retroviruses leave a characteristic retroviral integration pattern after insertion that is detectable and indicates that the viral vector has incorporated into the host genome.

Anthony and I are frequently asked if this vaccine is "The Mark of the Beast". If taken, does it change your DNA? Is your name removed from the "Lamb's Book of Life? I'd like to take this opportunity to share with you information that we have that, to us, makes these points unmistakably clear. It addresses the biological as well as our faith-based system of belief. Acknowledging this vaccination agenda as the beginning or "roll-out" of the Mark of the Beast System (MOBS) will only resonate with those who are true children of God and are in tune/close communication with his Holy Spirit. Sadly, we are discovering that many Christian pastors are not sharing this vital information with their congregations. They will be accountable to God for withholding such soul-saving knowledge.

The word "mark" has many meanings. It can mean dot, spot, blemish, or smear. It can mean sign, token, symbol, or badge. It can mean a level,stage, or degree. It can mean grade, score, or percentage. It can mean target, goal, or objective. It can mean to certify, name, initial, label, seal, or signature. It can mean observe, recognize, acknowledge, or scrutinize. It can mean separate, characterize, distinguish, or identify. It can mean assess, evaluate, or appraise (as in a grade). It can mean heed, listen to, or take notice of.

Ephesians 5:27,KJV: "That he might present it to himself a glorious church, not having spot, or wrinkle, or any such thing; but that it should be holy and without blemish."

With respect to “Mark of the Beast” as worded in Revelation, it takes on the form of a **charagma** (in the Greek –**charax**– meaning a pointed stake or palisade), an engraving (tool) or sharp pointed object, stamp, or imprint/impression. It is the badge of the followers of Antichrist, engraved/stamped/impressed on the right hand or forehead. (See Revelation: 13:16 & 17; 14:9 & 11; 16:2; 19:20; and 20:4).

Ephesians 5:27,KJV: "That he might present it to himself a glorious church, not having spot, or wrinkle, or any such thing; but that it should be holy and without blemish."

◄5480. charagma►

Strong's Concordance

charagma: a stamp, impress

Original Word:χάραγμα, ατος, τό
Part of Speech: Noun, Neuter
Transliteration:charagma
Phonetic Spelling:(khar'-ag-mah)
Definition:a stamp, impress
Usage:sculpture; engraving, a stamp, sign.

We have maintained, based on science, biology, technology, and study of scripture, that this inoculation delivers into the human body an “operating system” encompassing all of the disciplines mentioned. See Moderna’s own mRNA science and technology platform and professed “Operating System”
-https://www.modernatx.com/mrna-technology/mrna-platform-enabling-drug-discovery-development

mRNA **WILL** impact the human genome/body leaving its “mark” within our genetic code. Believing that the human body is the temple of God’s Holy Spirit (1 Cor. 6:19), we conclude that this is the “abomination that causes desolation” spoken of in Matthew 24:15 & 16 and in Daniel Chapter 8.

This scientific/biological/technological “vector” will deliver, disrupt, and permanently alter our divinely created and unique designed genome. It will modify the entire molecular structure of the human body from one thoughtfully and purposefully created by God to a yet-unknown entity that Satan, with the help of science and technology, fatally manipulates. This mRNA vaccine has never been used in human trials.

Wiki: The **vector** itself is generally a DNA sequence that consists of an insert (transgene) and a larger sequence that serves as the "backbone" of the **vector**. The **purpose of a vector** which transfers genetic information to another cell is typically to isolate, multiply, or express the insert in the target cell.

https://en.wikipedia.org/wiki/Vector_(molecular_biology)#:~:text=The%20vector%20itself%20is%20generally,insert%20in%20the%20target%20cell.

Rolled out much like a new software program, this first round of mRNA administration (We will call it Distribution 1.0) will begin with an ultra cold mRNA fabrication delivered by way of a syringe and hypodermic needle. In version 2.0, the look, feel, and ease of dispensing the vaccine will change dramatically allowing for a self-administered microneedle array patch that can be mailed to your door. It will come front-loaded with not only a new and improved mRNA Covid cocktail, but will also house bio-sensing quantum dots, a bioluminescent “tattoo” utilizing an oxidative enzyme called ***Luciferase***. This biological tattoo/**CHARAGMA** is needed in order to mark, track, and identify those who have taken the vaccine. Highly sensitive scanners from a mobile phone or stationary tracking system can read the quantum dot tattoo that, though not visible to the human eye, is under near-infrared light.

The “patch” will be billed as so simple that child could apply it. Simply unseal, press, and hold for a few minutes. The keenly (coincidentally??) designed “**snake fang–inspired stamping patch”** (This is the actual medical term), See:

https://stm.sciencemag.org/content/11/503/eaaw3329?intcmp=trendmd-stm

will painlessly deliver a state-of-the-art operating system into your body that will connect you to the technological “beast” system. There will then be the “seamless” transition into the block chain system (Internet of Things) whereby all of your personal financial, educational, medical, social, and professional information will be conveniently and “confidentially” housed in a cloud. Congratulations! You and your computer have now become ONE in the sentient world simulation!
See: https://www.krannert.purdue.edu/academics/mis/workshop/ac2_100606.pdf

Does any of this sound familiar? It should. Satan does and says nothing original or unique.

Jesus stated FIRST in John 14:20:

"In that day you will know that I am in My Father, and you are in Me, and I in you."

Then again in John 17:23:

"I in them, and thou in me, that they may be made perfect in one; and that the world may know that thou hast sent me, and hast loved them, as thou hast loved me."

This mark/stamp/sign/impression/charagma is revealed in the many definitions stated earlier about the word "mark." It is multi-faceted. It can be a "dot" as applied today in "quantum dots" which are used in research and labeling of biological material (in vitro and in vivo). Quantum dots, crystals of a fluorescent semiconductor material with a diameter of as few as 10 to100 atoms (2-10mm), can be inserted into cells and attach to proteins to identify/label/track individual biomolecules due to their very narrow fluorescence spectra, brightness and resistance to photobleaching. (Definition from Nature.com). According to Samsung, and technologically speaking, "A Quantum Dot is a human-made nanoparticle that has semiconductor properties."

Back to Distribution 1.0 – in this beta test, people who have agreed to take the inoculation will be issued a form of proof of vaccination. Some sort of physical pass, paper, or digital record will certify their health compliance and declare them "safe" to enter back into society. In Distribution 2.0, the "MNA" upgrade (Microneedle Array), brings with it technological capabilities that will render paper prehistoric. Now the person carries around in their bodies all of their "records" to be scanned and maintained in "the cloud" instantly accessible by way of quantum dots. The biological tattoo/charagma will certify compliance and thus allow them to enter any store, arena, school, public/government buildings and parks, airlines, hospital, or place of employment. The governments will be quick to say that they will not "mandate" compliance, however, through the strong ties of P3's (Public Private Partnerships) pressure will be placed on businesses, schools, hospitals, restaurants etc. to mandate that one must show proof of vaccination to enter in order to maintain public safety and stop the spread of those dreaded "mutations" which you *know* will be carried around only by those who didn't take the vaccine…TAKE HEED.

A large percentage of the world's population will take this vaccine. Those who don't will be targeted and made to separate from society (See our live stream about us coming out of "Egypt" once again). Governments might not come right out and say that it is mandated at first, but they will cause the private sector to do so through financial coercion.

Revelation 13:16-18 - King James Version

16And he **causeth** all, both small and great, rich and poor, free and bond, to receive a mark in their right hand, or in their foreheads:

17And that no man might buy or sell, save he that had the mark, or the name of the beast, or the number of his name.

We've covered why we believe this is the mark spoken of in Revelation. We have provided you with a great deal of medical, scientific, and technological data over many months of in-depth live streams and insightful Entangled magazines to conclude that this DOES change the human genome.

Concerning the Lamb's Book of Life, I believe scripture will relay it best. If you agree that this new form of medical/technological treatment will change and defile God's original human design and method for fighting sickness and disease, please read below:

Revelation 13:8,KJV:

"And all that dwell upon the earth shall worship him, whose names are not written in the book of life of the Lamb slain from the foundation of the world."

Revelation 17:8, KJV:

"The beast that thou sawest was, and is not; and shall ascend out of the bottomless pit, and go into perdition: and they that dwell on the earth shall wonder, whose names were not written in the book of life from the foundation of the world, when they behold the beast that was, and is not, and yet is."

Revelation 20:12-15, KJV:

"And I saw the dead, small and great, stand before God; and the books were opened: and another book was opened, which is *the book* of life: and the dead were judged out of those things which were written in the books, according to their works. **13** And the sea gave up the dead, which were in it; and death and hell delivered up the dead, which were in them: and they were judged every man according to their works. **14** And death and hell were cast into the lake of fire. This is the second death.**15** And whosoever was not found written in the book of life was cast into the lake of fire."

Revelation 21:27, KJV: “And there shall in no wise enter into it any thing that defileth, neither *whatsoever* worketh abomination, or *maketh* a lie: but they which are written in the Lamb's book of life.”

The body will be “defiled” and rendered “desolate” once the permanent gene changes take place. These modifications begin the moment the mRNA injection enters the body. There is no turning back. mRNA immediately undertakes a replication process that alters our very molecular/cellular structure. It is very different from the attenuated virus’ used in vaccinations of the past. This changes the way your body recognizes and fights infection and disease. The body may very well turn and begin to attack itself.

Please pray in earnest about the decision you make. This is for eternity. The mainstream media will never tell you this. God will! We are “leaving Egypt” or the world’s current system. We will work and live outside of the world’s system of commerce. The physical mark, will put in place an identification and tracking system connected to commerce – buying and selling. The biological/genetic markers permanently alter God’s original human design. This He takes issue with.

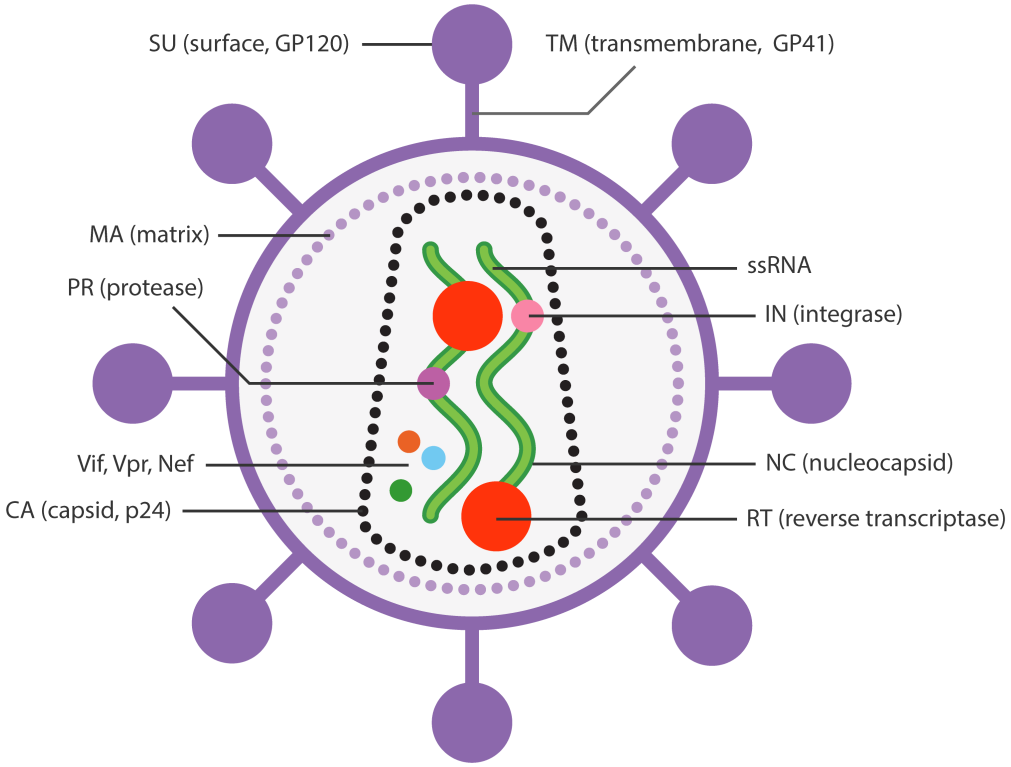
We enjoy and appreciate your friendship. We will face the days ahead together. Utilizing our God-given power through the Holy Spirit, we can and will upset the plans of the enemy in the spiritual realm that has its outworking in our carnal world. We do not ever fight with physical weapons of warfare, but with spiritual knowledge and power that can cripple demonic strongholds!!! You know how to do this...now USE it wisely.

With much love,
Kathleen

Implications of a Third Strand of DNA Within SARS-CoV-2 and Its Vaccines

Within HIV-1, a Lentivirus, a genus (above species and below family) of retroviruses (a type of virus that inserts a copy of its RNA genome into the DNA of a host cell) there exists a third strand of DNA. This is referred to in the literature as a central DNA Flap [Montagnier, et al. 2000]).

Discovered within the mRNA genomic sequence of SARS-CoV-2 is the presence of 16 genomic fragments of HIV-1 (HIV Man-Manipulated Coronavirus Genome Evolution Trends [Montagnier, et al. 2020]).



Video illustrating the basic components of a Lentivirus employing HIV as an example. Click on arrow or the above image of a Lentivirus.

Additional references to the discovery within the mRNA genomic sequence of SARS-CoV-2 of 16 genomic fragments of HIV-1.

Excerpts:

French virologist Luc Antoine Montagnier, who was awarded a Nobel prize in Physiology in 2008 along with Françoise Barré-Sinoussi and Harald zur Hausen for discovering of the HIV virus, has now spoken out. Montagnier was a researcher at the prestigious Pasteur Institute in Paris causes malaria, are found in the coronavirus's genome.

Montagnier said: "We were not the first since a group of Indian researchers tried to publish a study which showed that the complete genome of this coronavirus [has] sequences of another virus, which is HIV."

The research that Montagnier refers to was posted on the science website Biorxiv January 31, 2020, and has since been withdrawn.

The researchers wrote: "We found 4 insertions in the spike glycoprotein (S) which are unique to the 2019-nCoV and are not present in other coronaviruses.

Importantly, amino acid residues in all the 4 inserts have identity or similarity to those in the HIV-1 gp120 or HIV-1 Gag ... The finding of 4 unique inserts in the 2019-nCoV, all of which have identity /similarity to amino acid residues in key structural proteins of HIV-1 is unlikely to be fortuitous in nature." COVID-19 Derives From a Failed HIV Vaccine, Says Montagnier In a separate appearance on the French podcast Pourquoi Docteur, also April 17.

Montagnier said the coronavirus had escaped in an "industrial accident" while Chinese scientists at the Wuhan city laboratory were trying to develop a vaccine against HIV.10 "In order to insert an HIV sequence into this genome, molecular tools are needed, and that can only be done in a laboratory," said Montagnier.

In a paper Montagnier and Perez published on the Center for Open Science in April 2020, they write: "Using our proprietary bio-mathematic approach we are able to evaluate the level of cohesion and organization of a genome; ... we then searched in this genome for possible traces of HIV or even SIV [related simian immunodeficiency virus].

A first publication reports the discovery of 6 HIV SIV RNA pieces." The HIV and SIV elements that Montagnier and Perez detect, called Exogenous Informative Elements, or EIEs, provide the basis of their theory that COVID-19 is not a simple derivative of SARS and bat-related viruses. They write: "A major part of these 16 EIE already existed in the first SARS genomes as early as 2003.

However, we demonstrate how and why a new region including 4 HIV1 HIV2 Exogenous Informative Elements radically distinguishes all COVID-19 strains from all SARS and Bat strains ... ... a contiguous region representing 2.49% of the whole COVID-19 genome is 40.99% made up of 12 diverse EIE originating from various strains of HIV SIV retroviruses ... a novel long region of around 225 nucleotides, appears to us to be totally new: this region is completely absent in ALL SARS genomes, whereas it is present and 100% homologous for all COVID-19 genomes listed in NCBI or GISAID COVID_19 genomic databases."

More About Montagnier and Perez's Theory. After in-depth sequencing of related genomes from many different countries, regions of countries and time periods using their proprietary biomathematic approach, Montagnier and Perez say their research enabled them to: "... demonstrate how and why a new region including 4 HIV/SIV EIE radically distinguishes all COVID-19 strains from all SARS and Bat strains."

Other Researchers Agree With Montagnier and Perez. Since Montagnier's comments to French media, other researchers have agreed that COVID-19 appears manmade, with insertions that hint at lab construction. In June 2020, research published in the Quarterly Review of Biophysics makes similar claims.

Norwegian scientist Birger Sørensen and British oncologist Angus Dalgleish refer to COVID-19 as a "chimeric virus" and write:

"We show the non-receptor dependent phagocytic general method of action to be specifically related to cumulative charge from inserted sections placed on the SARS-CoV-2 Spike surface in positions to bind efficiently by salt bridge formations; and from blasting the Spike we display the non human-like epitopes from which Biovacc-19 has been down-selected."

While conceding the Quarterly Review of Biophysics assertions were controversial, the scientific website Minerva wrote that the science should be pursued.

"Minerva has read a draft of the article, and has after an overall assessment decided that the findings and arguments do deserve public debate, and that this discussion cannot depend entirely on the publication process of scientific journals."

Like Montagnier, Sørensen's background is HIV research work and he launched a new immunotherapy for HIV in 2008 that was acclaimed.

In an interview with Minerva about his recent contentious research, he says:

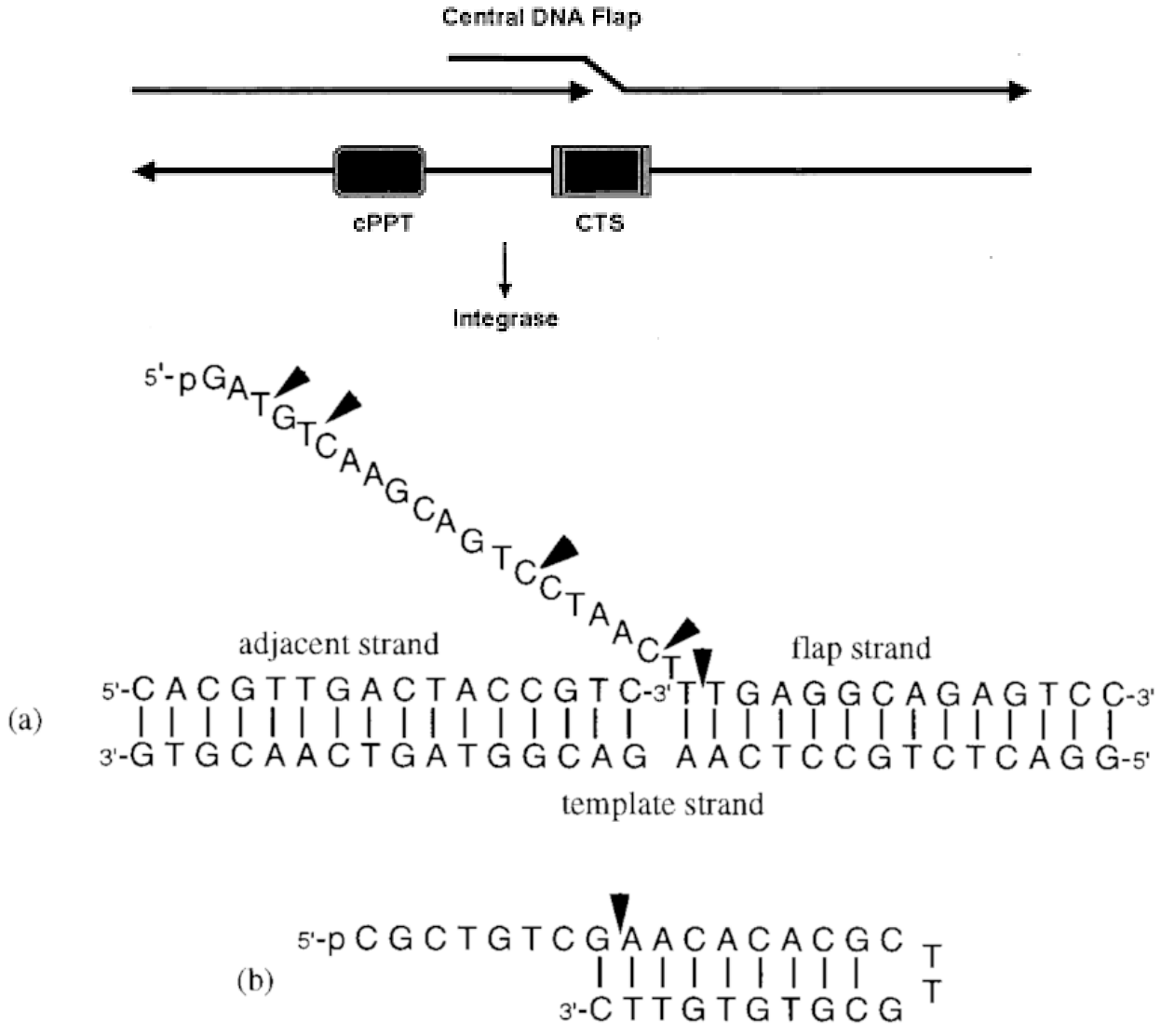
"We have examined which components of the virus are especially well suited to attach themselves to cells in humans. And we have done this by comparing the properties of the virus with human genetics.

End reference article

Significance

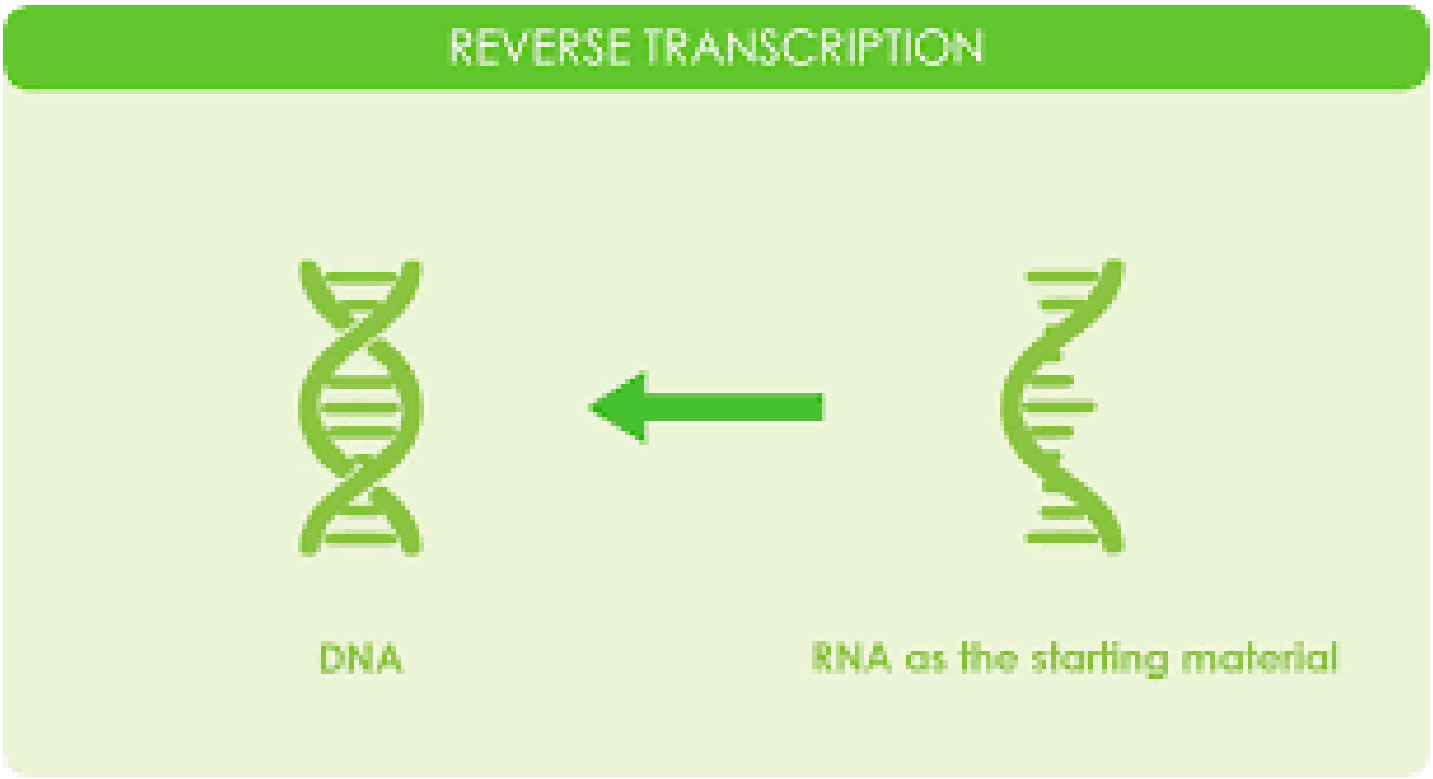
The significance of the central DNA flap is to ensure the entire genome comprising the Lentivirus HIV-1 is successfully imported into the nucleus of the target host cell. There exists however, only 16 fragments of the HIV-1 viral genome within the single strand mRNA of SARS-CoV-2. In this case, the lentiviral traits of nuclear entry and integration with the host cell DNA remain intact as a chimeric genome of SARS-CoV-2 and HIV-1.

Figure 1



Sequence of events

A vaccine consisting of mRNA reverses the normal biological sequence of events known as transcription. Typically, double-stranded DNA transcribes (copies) to single strand molecules of RNA, which in turn translates a proteins.

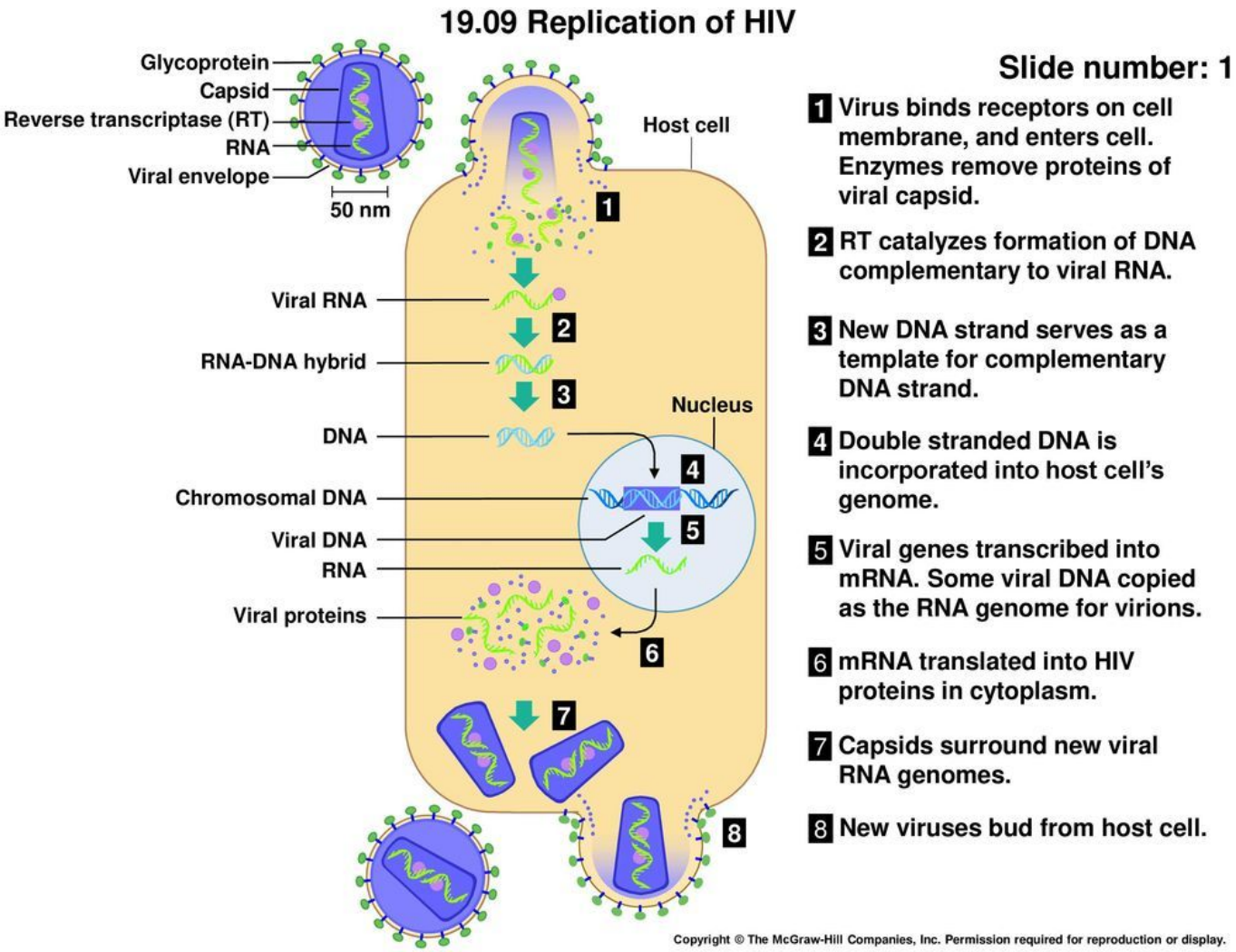


By way of reverse transcription (RT), a mRNA based vaccine for SARS-CoV-2 transcribes two strands of DNA, referred to as complementary DNA (cDNA). Then, in translating a protein, the mRNA molecules leave the cell nucleus and enter the cytoplasm to synthesize individual proteins.

Replication of HIV slideshow.

Click on arrow to begin. Opens in a new browser, click through slides using arrows at the bottom of the new page.

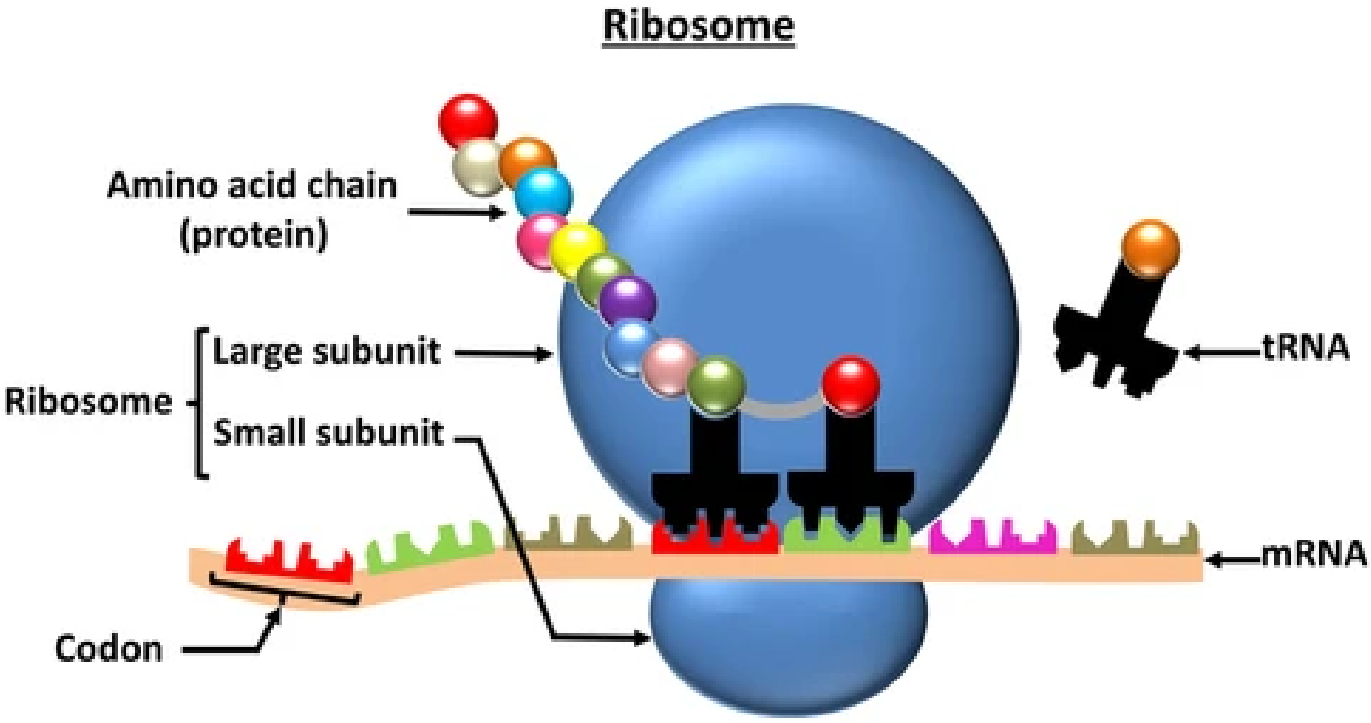
The presence of 16 genomic fragments of HIV-1 provides the gain of function to the viral genome of SARS-CoV-2 as illustrated within this slideshow. The actions of SARS-CoV-2 are now the same as for HIV itself.



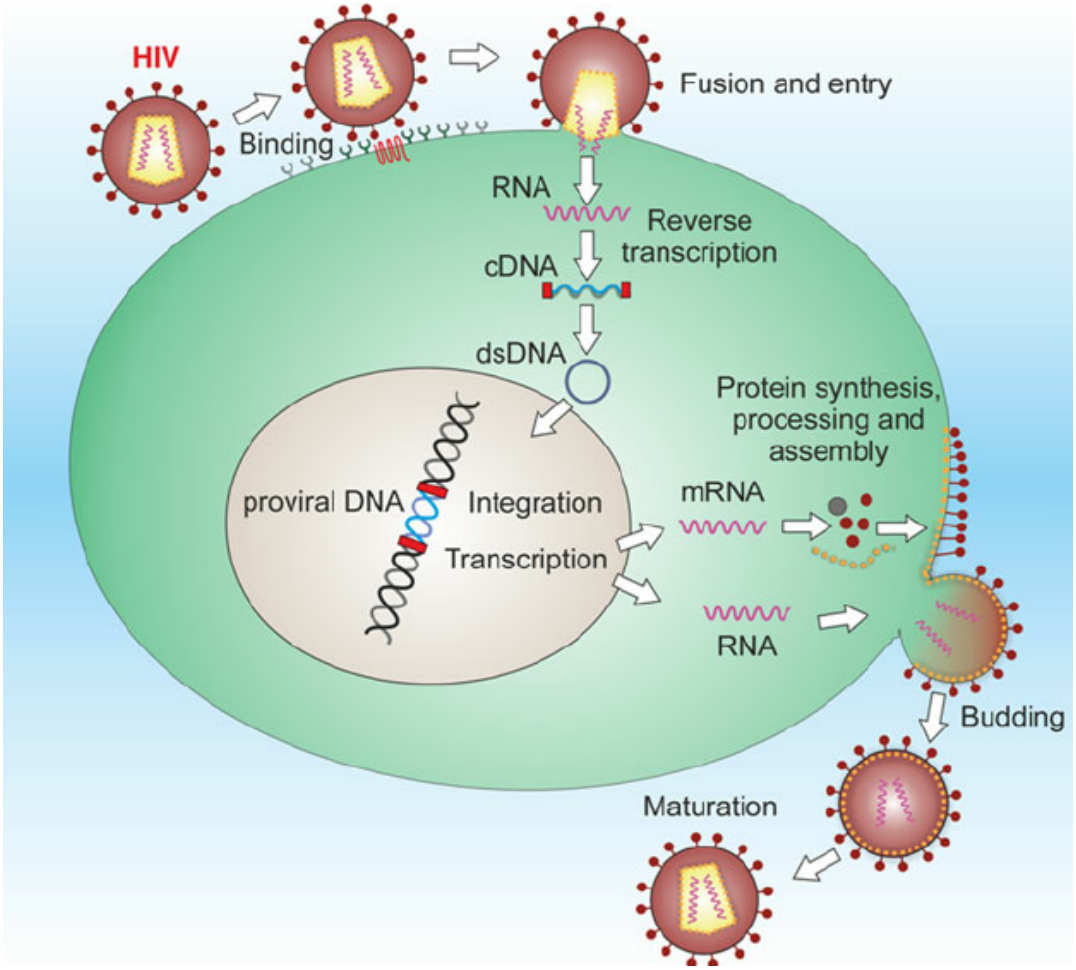
Central DNA flap

Due to the inclusion of 16 HIV-1 fragments within this double strand cDNA, a third strand manifests as a central DNA flap. Additionallly, codons of 3 DNA bases, represent the genetic code that transfers information from genes to mRNA within the nucleus, and then within the cytoplasm tRNA (transfer RNA) transfers the genetic code for the translation of proteins within the ribosome.

Additionally, HIV envelope and Gag (Group-specific antigen) genes in SARS-CoV-2 have been codon optimized (optimize protein expression) to improve the expression of viral antigens. Antigens are a foreign substance which induces an immune response in the body.



Lastly, published scientific research states the RNA of the *virus* SARS-CoV-2 itself, reverse-transcribes and integrates into the human genome.

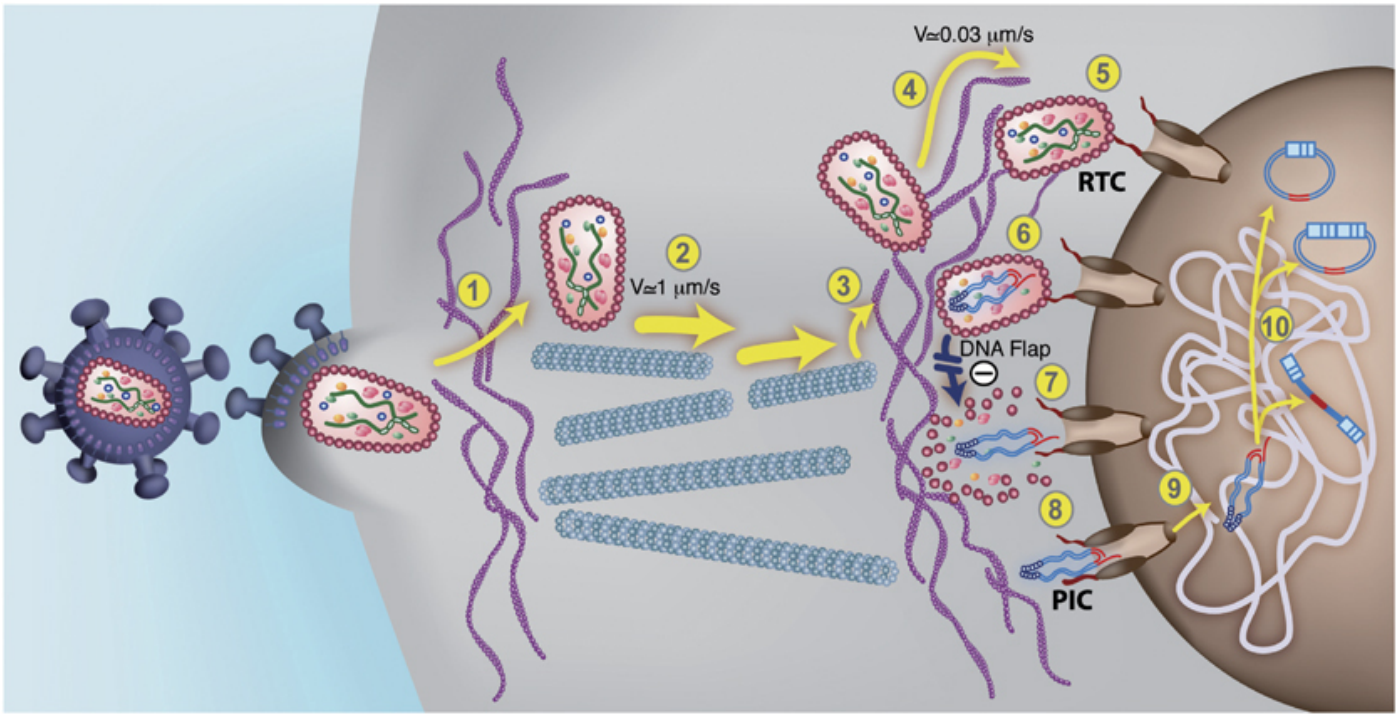


Two Integration Mechanisms

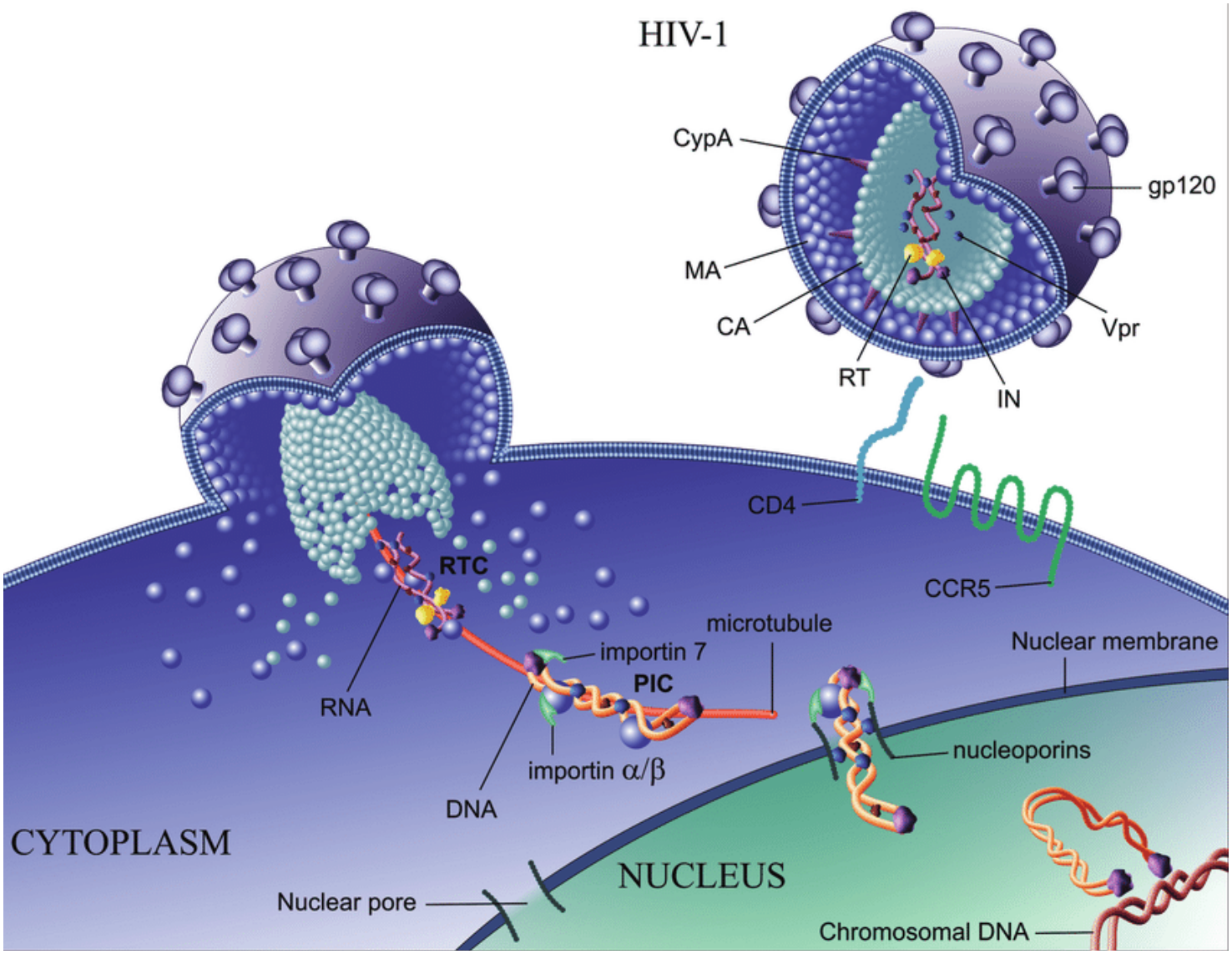
The enzyme retroviral integrase, produced by a Lentivirus such as HIV-1, plays an important role integrating the viral DNA into the nucleus. Covalent links (a chemical bond that involves the sharing of electron pairs between atoms) are formed between the viral and host DNA, resulting in a permanent alteration referred to in the literature as "a point of no return" for the host cell. This forms a provirus, a permanent carrier of the virus. Thus, two primary mechanisms are at work in the changing of the host DNA. The central DNA flap and the enzyme retroviral integrase.

A Third Integration Mechanism

Lentiviruses possess a unique capacity, among retroviruses, to replicate efficiently in nondividing cells. They can of course, enter cells undergoing cell mitosis. Another mechanism at work in HIV-1 are pre-integration complexes (PIC), which are able to cross the double nuclear membrane of host cells. This is a pivotal event ensuring Lentiviruses are able to replicate in nondividing cells.



Uncoating of the pre-integration complex at the nuclear pore. Note the presence of the DNA flap mediating the folding of 2 complementary strands of DNA (cDNA). These reverse transcribed from the Lentivirus SARS-CoV-2 containing the 16 genomic fragments of HIV-1. The cDNA enters through the nuclear pore complex (NPC) and into the nucleus to the right in this image.

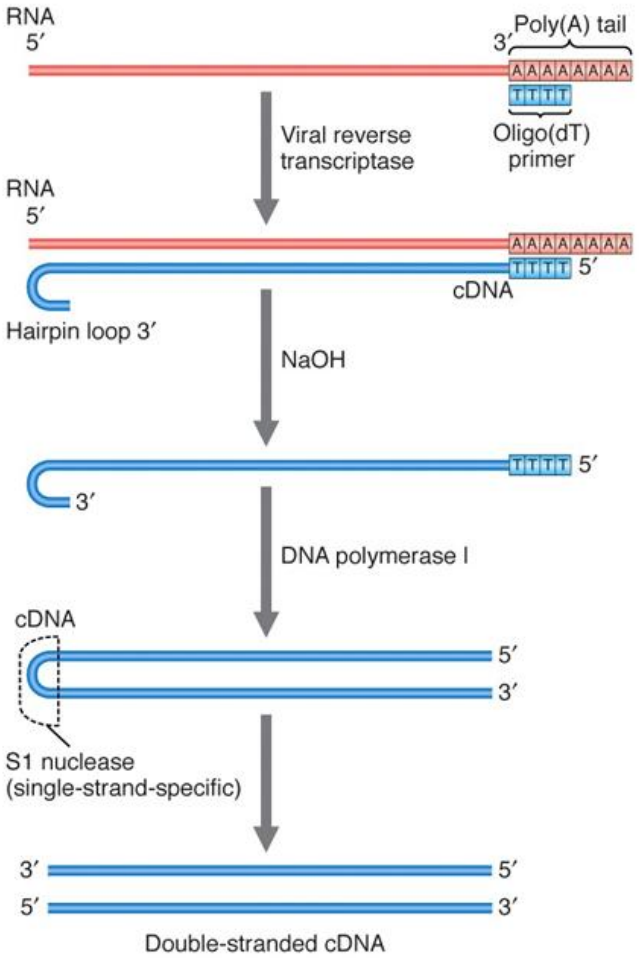


Pre-integration steps of HIV-1 replication. Events starting with HIV-1 binding to its main receptors on the target cell, CD4 and CCR5, and ending with viral integration into the host cell's genome are shown. Proteins packaged into virions are shown; some of these proteins (MA, RT, IN, and Vpr) find their way into the reverse transcription complex (RTC). RTC becomes the pre-integration complex upon completion of reverse transcription.

The pre-integration complex (PIC) is a nucleoprotein complex of viral genetic material and associated viral and host proteins which is capable of inserting a viral genome into a host genome. The PIC forms after uncoating of a viral particle following entry through the outer plasma membrane and into the host cell.

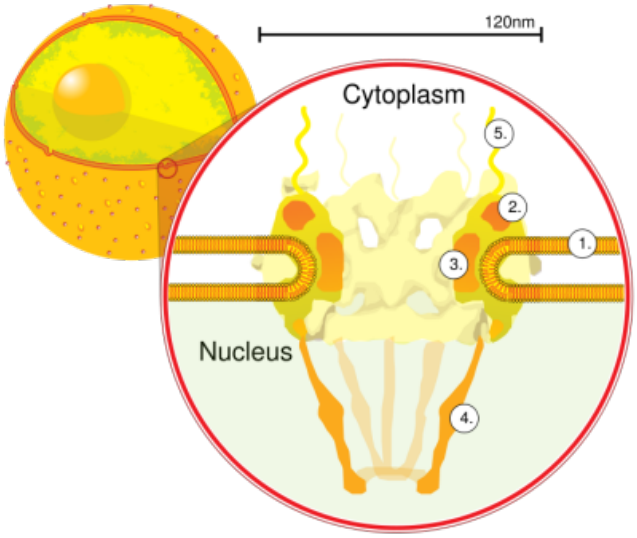
Complementary DNA (cDNA)

The PIC forms after the reverse transcription complex (RTC) has reverse transcribed (copying genetic information) the viral RNA (i.e. SARS-CoV-2 mRNA) into DNA, referred to as complementary DNA (cDNA). cDNA is DNA synthesized from a single-stranded RNA template, such as mRNA or microRNA (miRNA) in a reaction catalyzed by the enzyme reverse transcriptase.

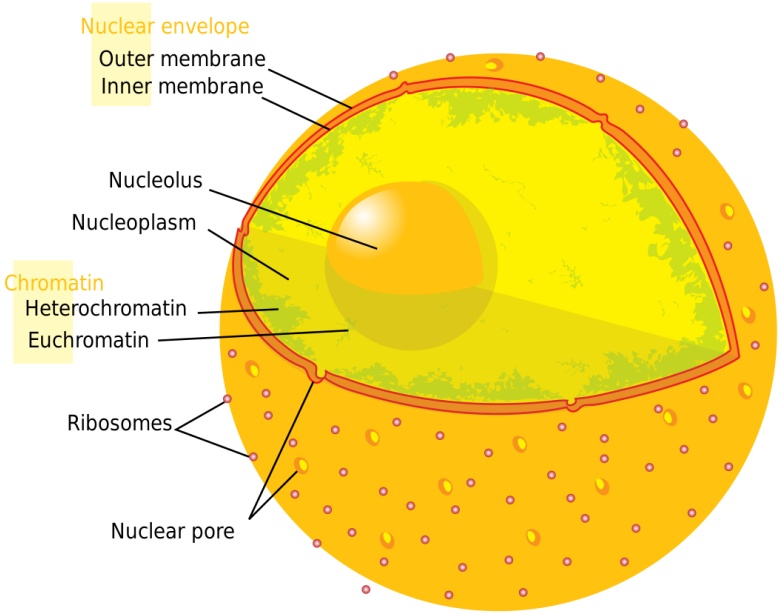


Complementary DNA (cDNA)

Nuclear pore complex (NPC)



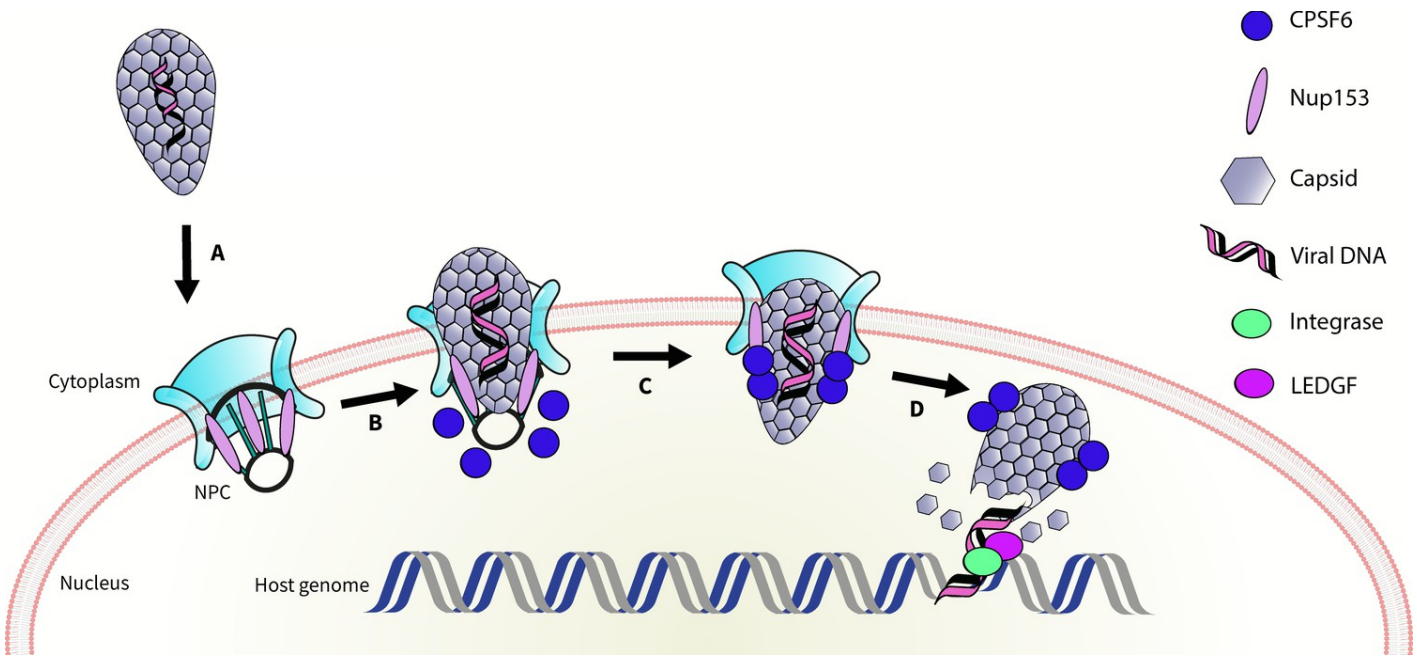
The PIC enters the cellular nucleus through the nuclear pore complex (NPC). A NPC is a part of a large complex of proteins that spans the nuclear envelope, which is the double membrane surrounding the nucleus.



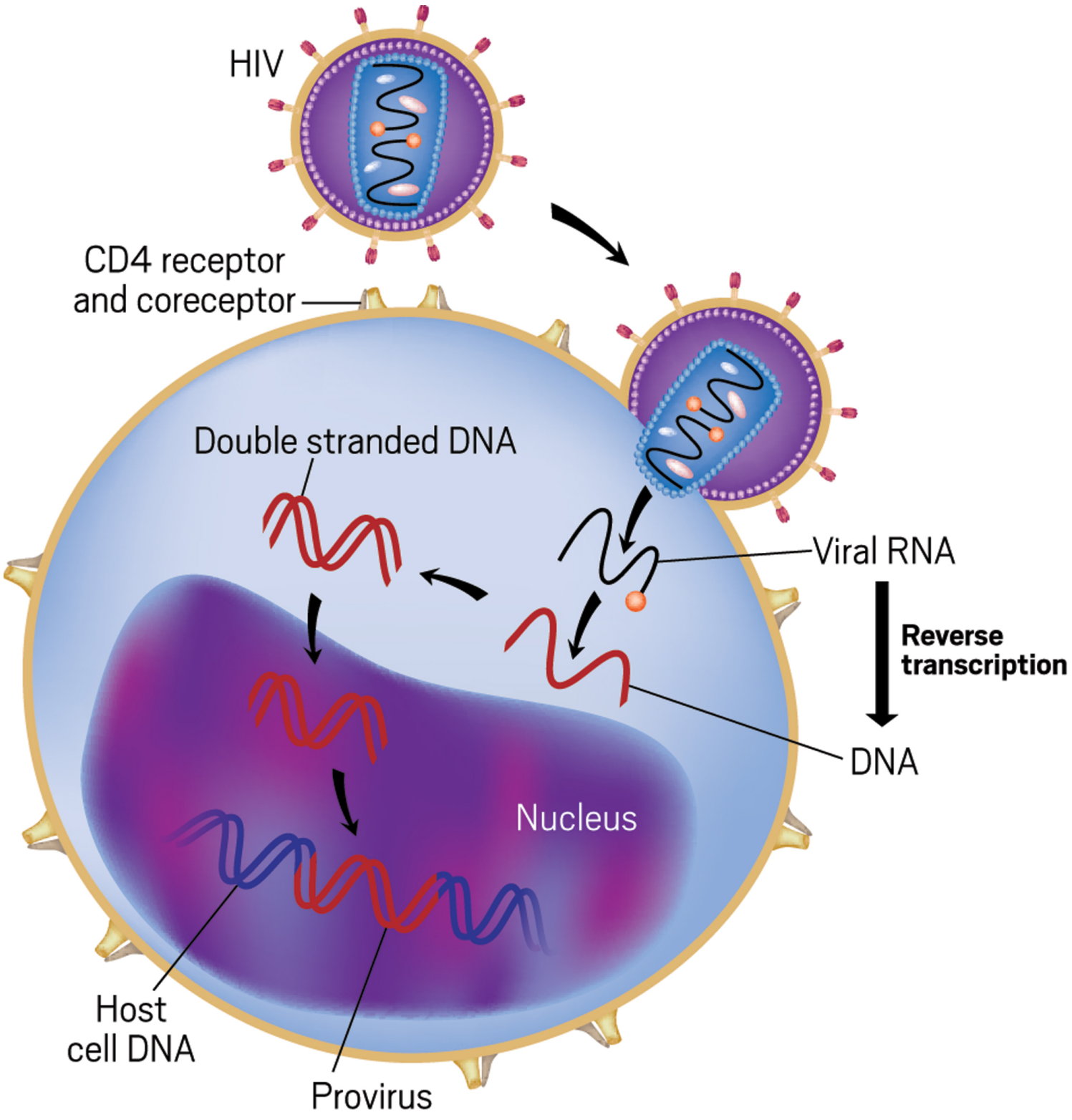
The NPC enters the nucleus without disrupting the nuclear envelope (membrane), thus allowing the lentivirus HIV-1 to replicate in non-dividing cells, as well as those undergoing cell mitosis. Following nuclear entry, the PIC's DNA payload is integrated into the host cell's DNA as a provirus.

Provirus

A provirus is a virus genome that is integrated into the DNA of another healthy host cell. When a retrovirus from outside the body (exogenous) invades a cell, such as the RNA of the Lentivirus HIV-1, it is reverse-transcribed (see later below) into DNA by the enzyme reverse transcriptase.



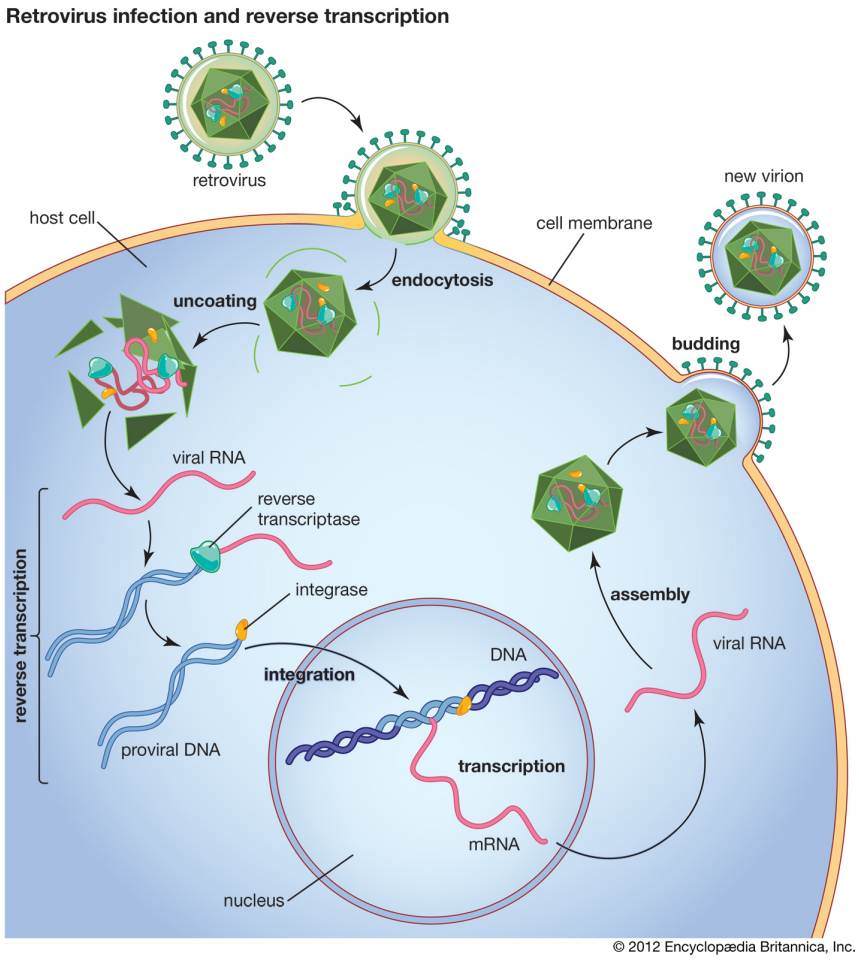
It is then inserted into the host genome by the enzyme integrase. This is the process of transduction by which foreign DNA/RNA is introduced into a cell by a virus or viral vector (a vehicle to artificially carry foreign genetic material into another cell.


HIV
CD4 receptor
and coreceptor
Double stranded DNA
Viral RNA
Reverse
transcription
DNA
Nucleus
Host
cell DNA
Provirus

Provirus

Reverse transcriptase

Reverse transcriptase is an enzyme used to generate complementary DNA (cDNA) from an RNA template, a process termed reverse transcription. Reverse transcriptases are used by HIV-1 to replicate their genomes, by retrotransponson mobile genetic elements to proliferate within the host genome. Retrotransponsons are a type of genetic component that copy and paste themselves into different genomic locations (transponson) by converting RNA back into DNA (cDNA) through the process of reverse transcription using RNA transposition intermediate.

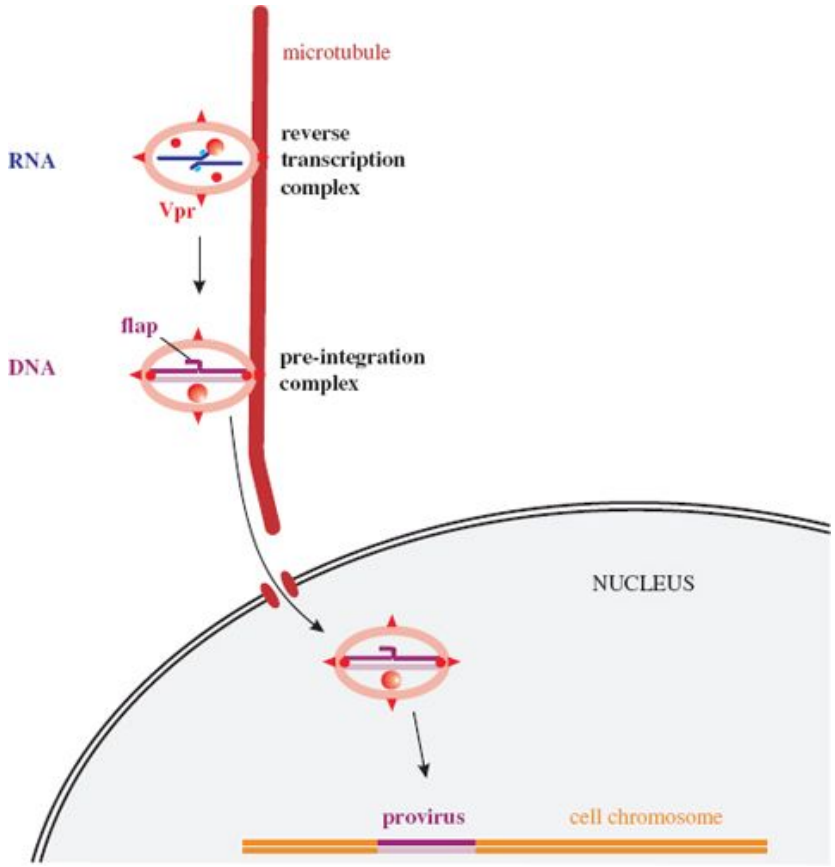


Following retrovirus infection, reverse transcriptase converts viral RNA into proviral DNA, which is then incorporated into the DNA of the host cell in the nucleus.

Encyclopædia Britannica, Inc.

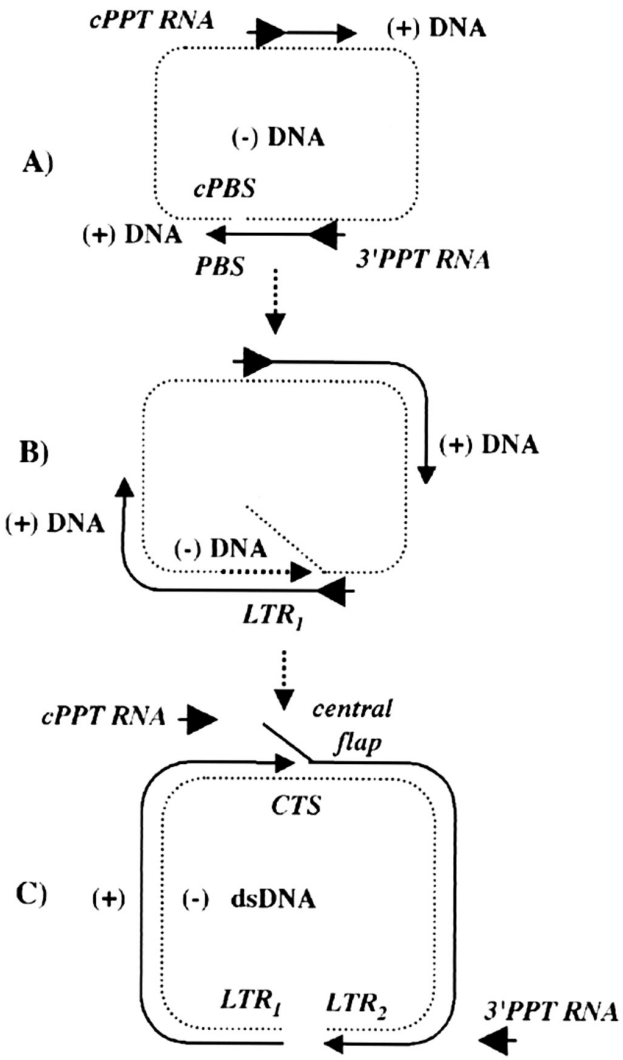
The final product: Central DNA flap

The final product of HIV-1 reverse transcription is a linear DNA molecule bearing in its center a stable 99 nucleotide-long plus strand overlap, here referred to as the central DNA flap. The distinctive features of Lentiviral reverse transcription account for the unique capacity of Lentiviruses, among retroviruses, to replicate in nondividing cells.

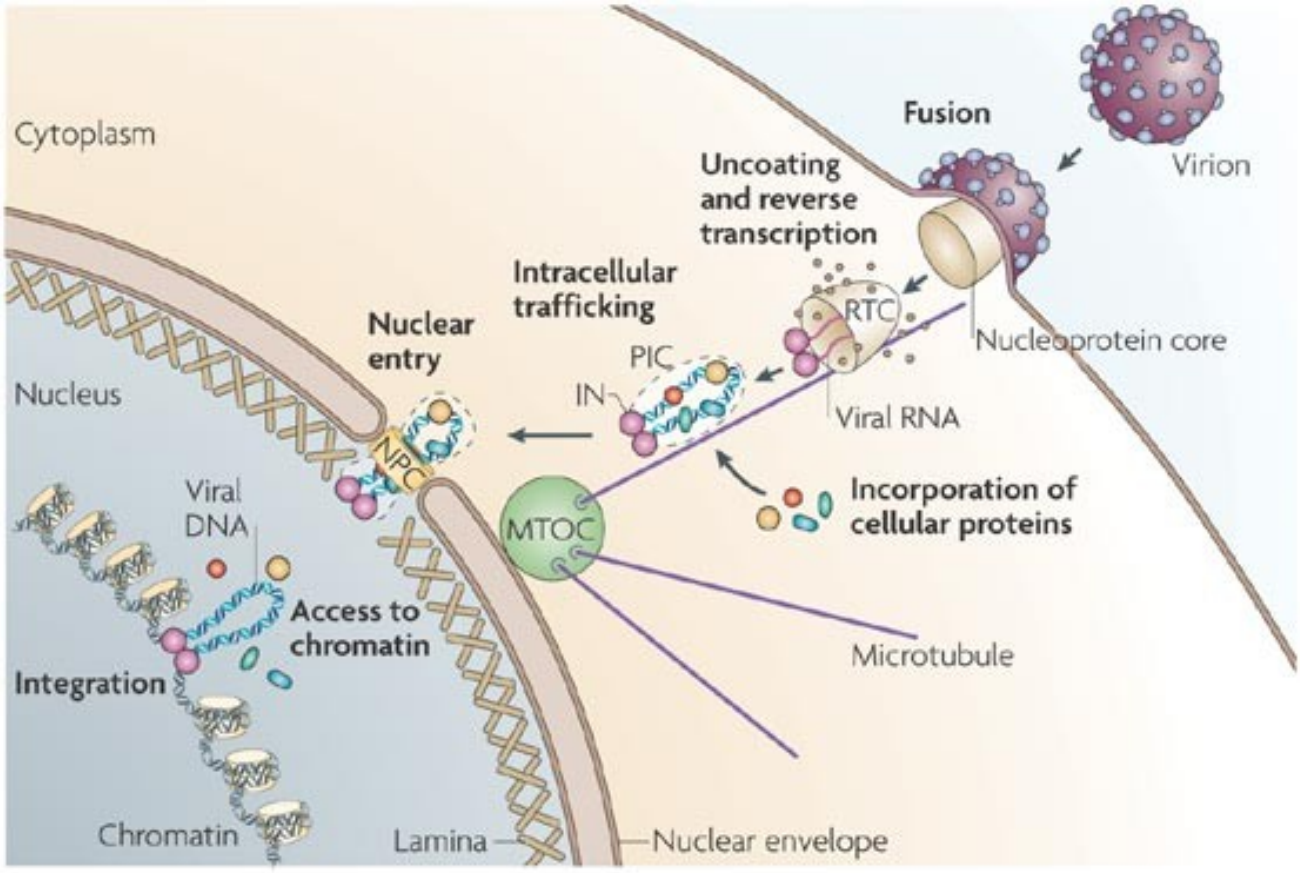


HIV-1 reverse transcription and integration of the provirus.A DNA flap is formed during reverse transcription. There is evidence that the pre-integration complex is transported toward the nucleus via the microtubule network.

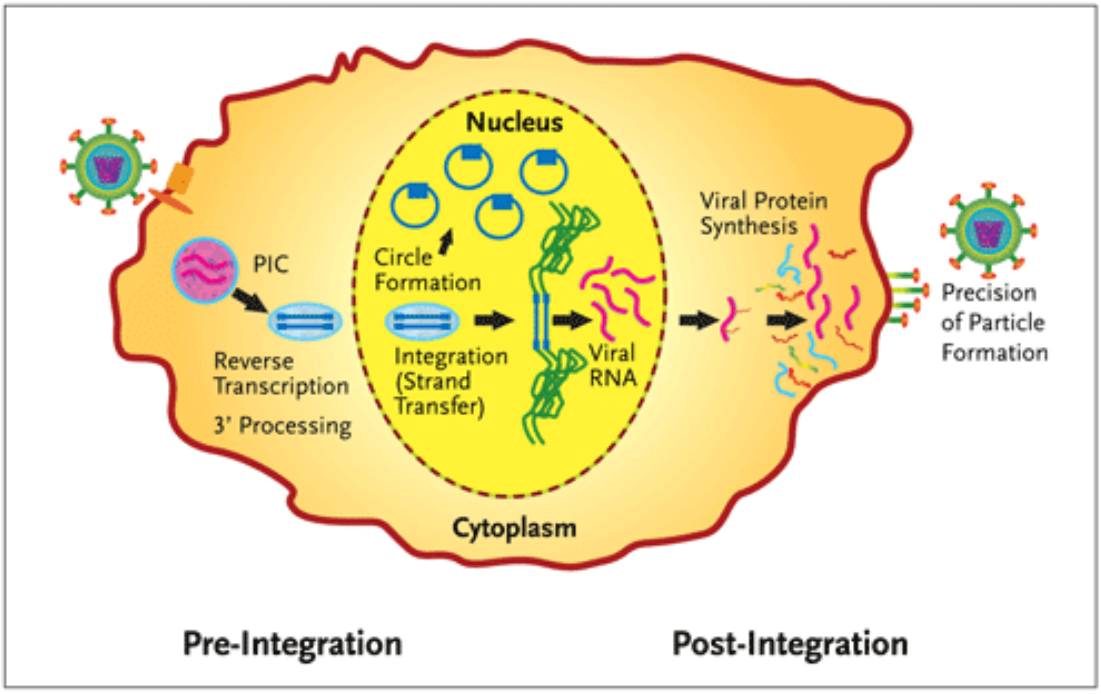
Whereas the proviruses of most retroviruses are entirely double strand DNA (dsDNA), those of HIV and other lentiviruses have a short triple-stranded sequence known as a central DNA flap. This comes about because there are two initiation sites for (+) DNA synthesis; as well as the polypurine tract (PPT) toward the 3' end of the virus genome, there is also a central PPT within the *pol* region. Synthesis of the (+) DNA initiated at the 3' PPT stops soon after reaching the (+) DNA initiated at the central PPT, resulting in a short overlapping DNA sequence. This DNA flap plays a vital role in the early stages of infection.

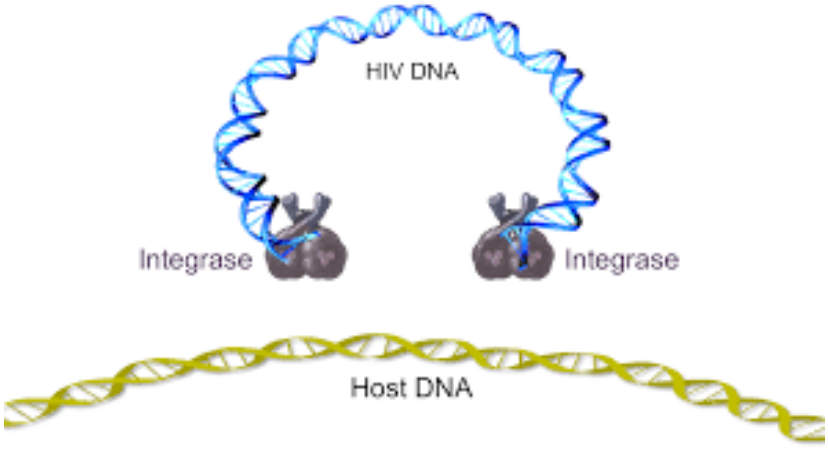


After reverse transcription has been completed, the pre-integration complex (PIC) which contains host proteins as well as virus proteins, is transported into the nucleus. There is evidence that transport toward the nucleus takes place on the microtubule network. Most retroviruses can productively infect only if there is breakdown of the nuclear membranes. The pre-integration complex of HIV, however, can enter an intact nucleus, such as that of a resting T cell or a macrophage, and is transported through a nuclear pore complex (NPC).

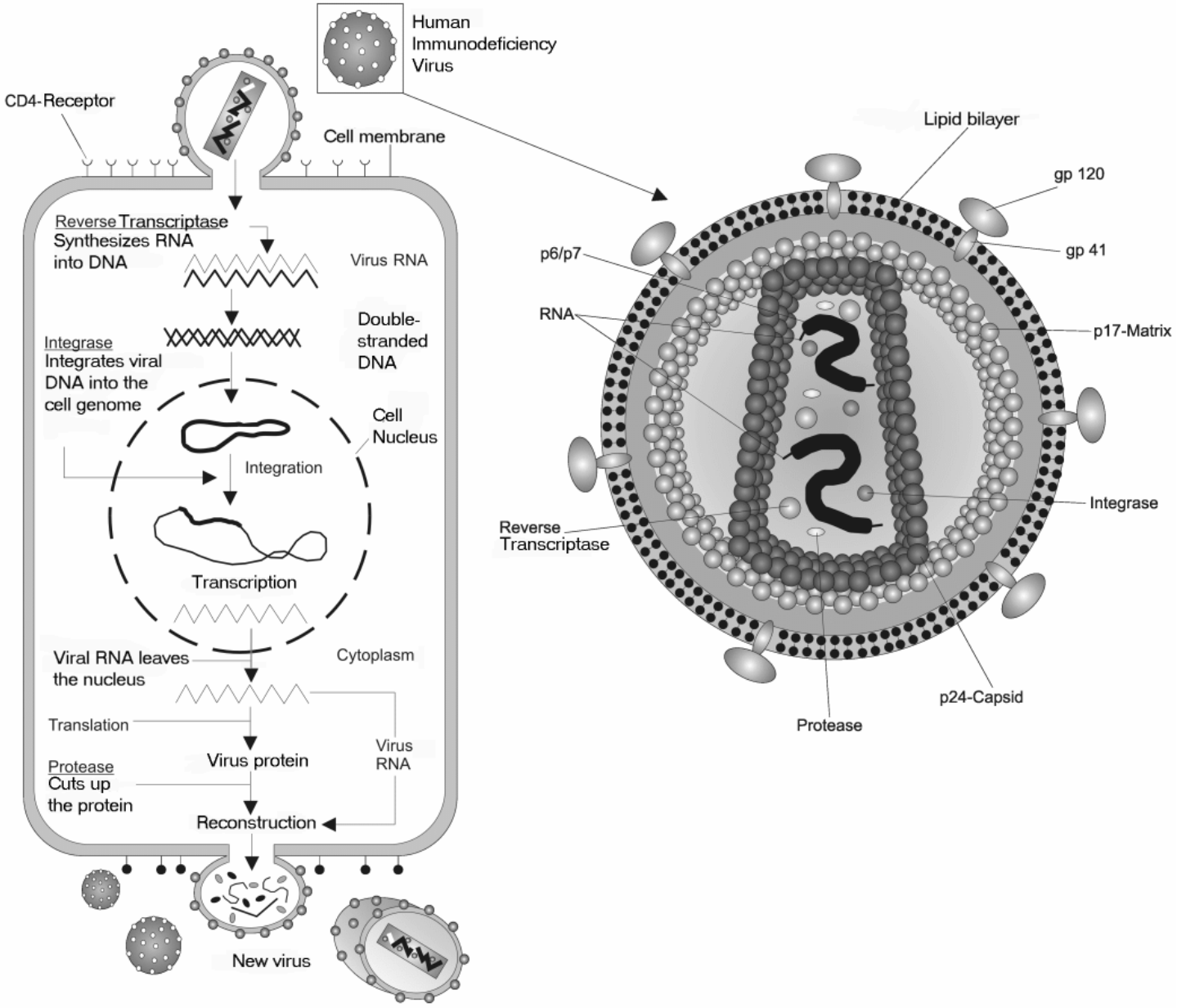


The viral integrase and cell enzymes are involved in the integration of the provirus into a cell chromosome; cell enzymes remove the DNA flap and repair the gap. There is evidence that integration of the provirus in a resting memory CD4 T cell may result in a latent infection. Latently infected cells can provide a reservoir of infection that is significant for the survival of the virus in individuals receiving anti-retroviral drug therapy. In many cells, though, provirus integration is the prelude to a productive infection in which two phases of gene expression can be distinguished.

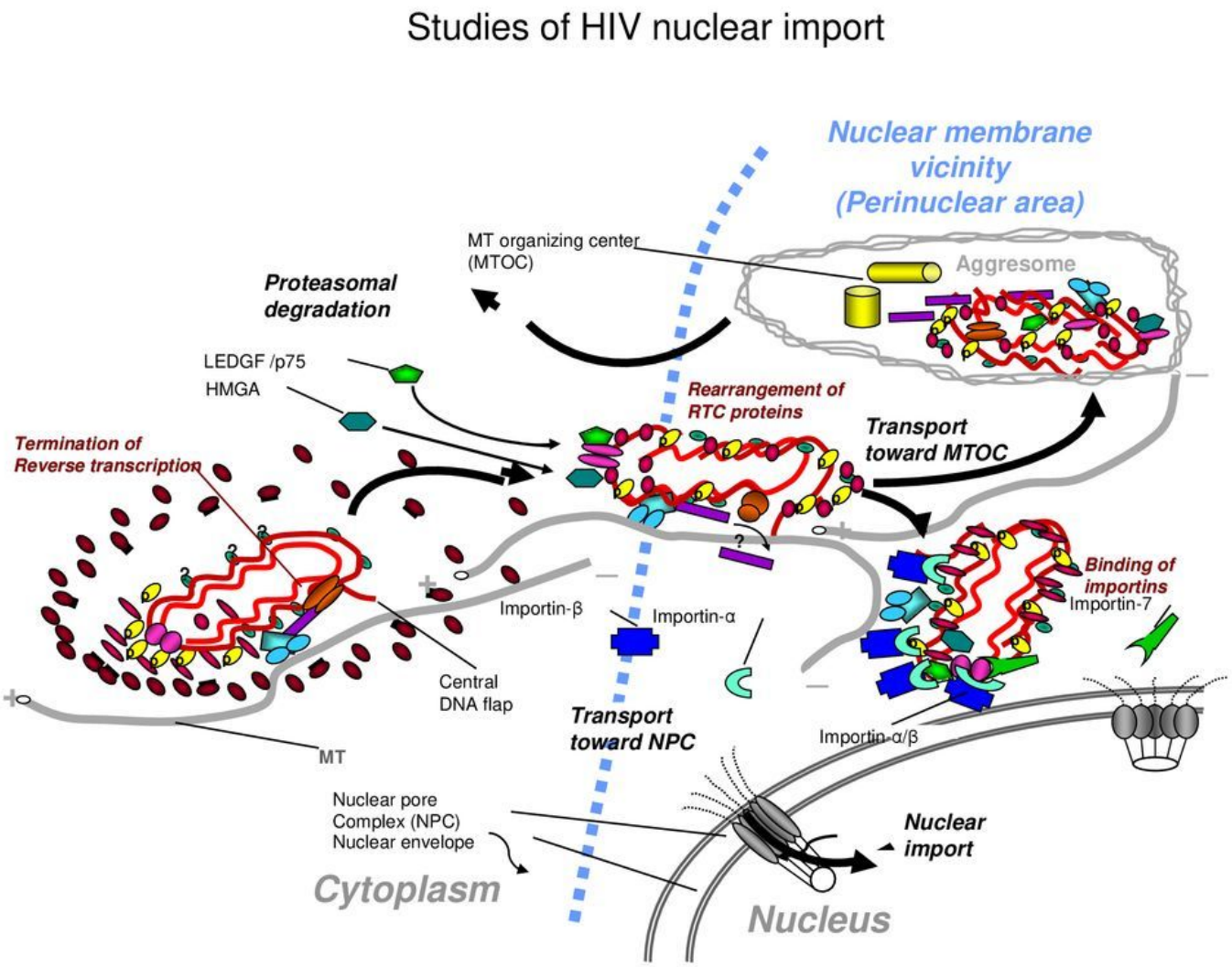




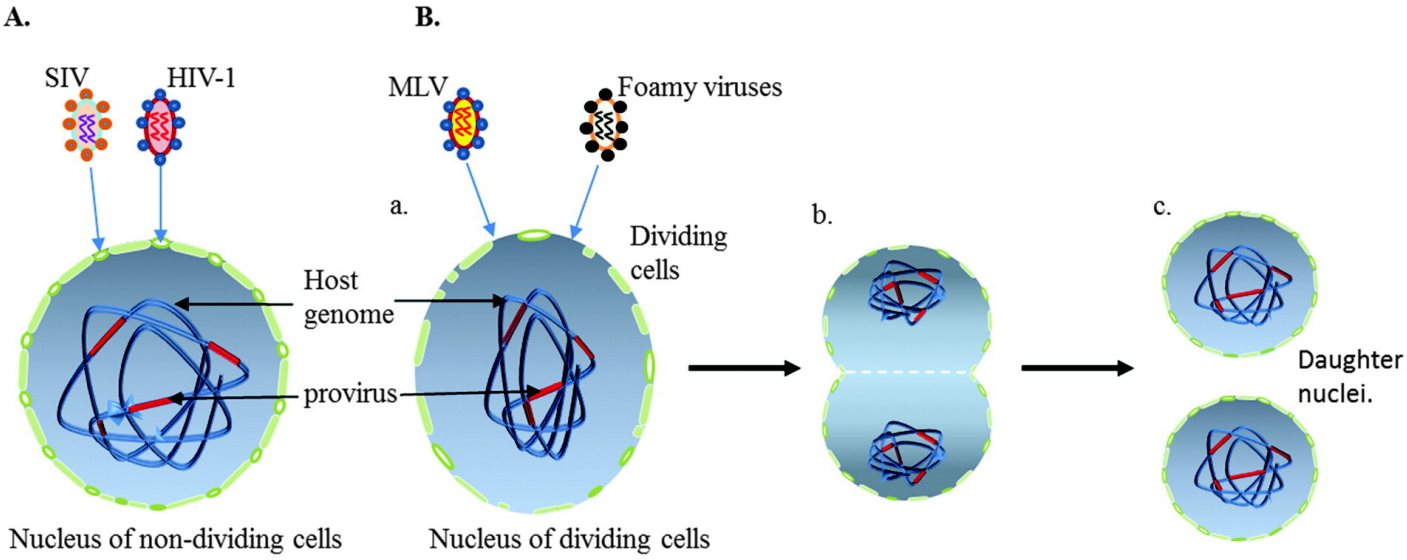
Laboratory results establish that the central initiation by the central DNA flap of reverse transcription is necessary for HIV-1 replication in nondividing as well as proliferating cells. The central DNA flap of HIV-1, created by central initiation and termination steps during reverse transcription, is necessary for HIV-1 pre-integration complexes (PICs) to enter the host cell nucleus.



In the absence of this central DNA flap, viral DNA nuclear import is severely impaired at a stage immediately preceding or during the translocation of HIV-1 DNA through the nuclear pore. Thus, without the third strand DNA flap, all of the HIV-1 DNA is unable to enter the nucleus. It is the key determinant for nuclear import of the HIV-1 genome.

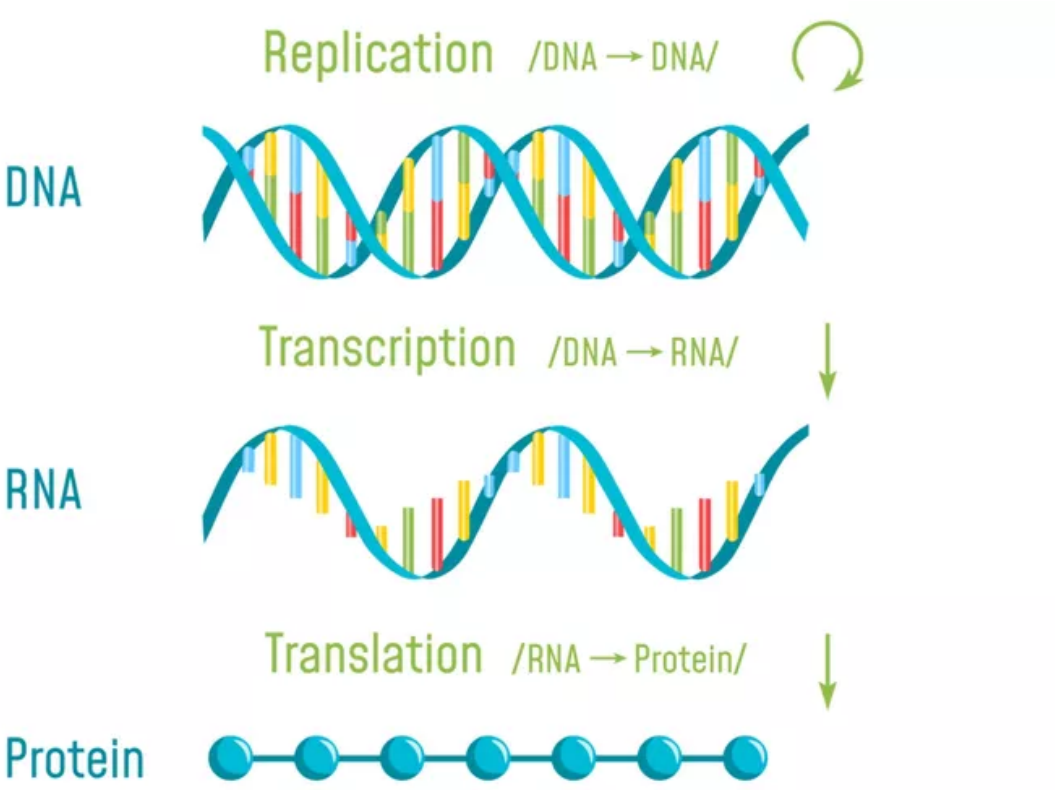


The original mechanism of HIV-1 nuclear import is the crucial role of this three-stranded DNA structure, the central DNA flap, in this process. HIV-1 possesses a complex reverse transcription strategy, creating a DNA flap at the center of a single strand of HIV-1 DNA molecules. It is the determinant of the nuclear import of the HIV-1 genome, and its capacity to infect nondividing target cells. The lack of the DNA flap leads to a virus that is almost noninfectious in dividing and nondividing cells.



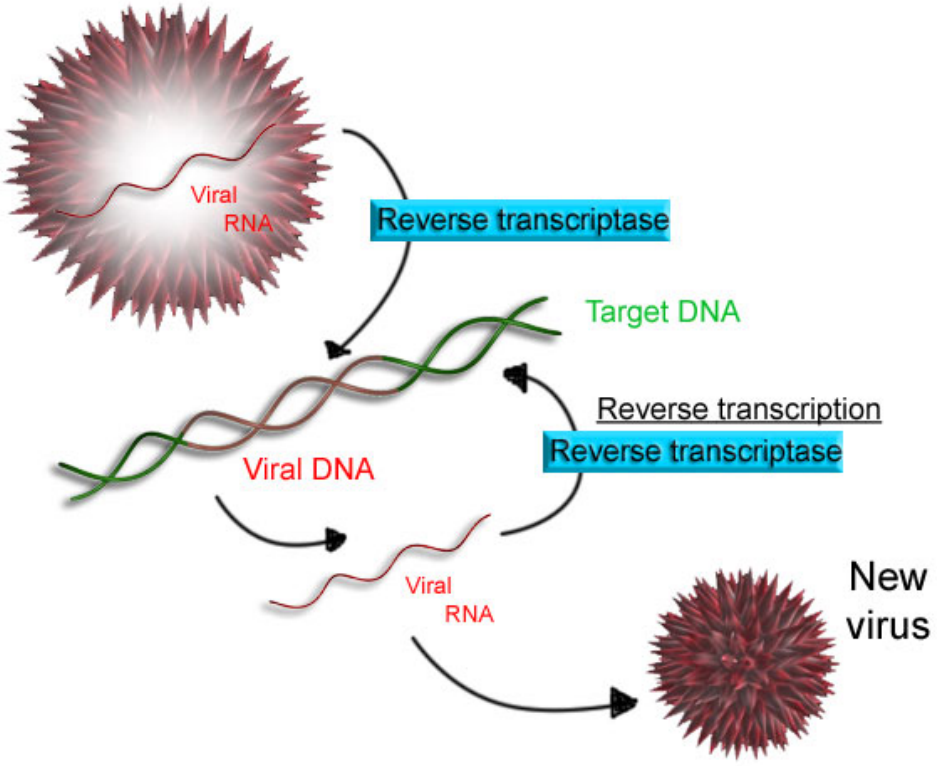
The presence of a DNA flap at the center of the genome is found in all lentiviruses. The entire process of complementary DNA (cDNA) synthesis from messenger RNA (mRNA) is completed prior to translocation of the HIV pre-integration complex (PIC) through the nuclear pore complex (NPC), and into the nucleus for integration through covalent linking with the host DNA.

The single-stranded mRNA of SARS-CoV-2 contains 16 genomic fragments of HIV-1. These code for specific gain of function purposes. In this case, ensuring the entry of the SARS-CoV-2 virus into the host DNA by utilizing the inherent central third-stranded DNA flap of HIV-1.



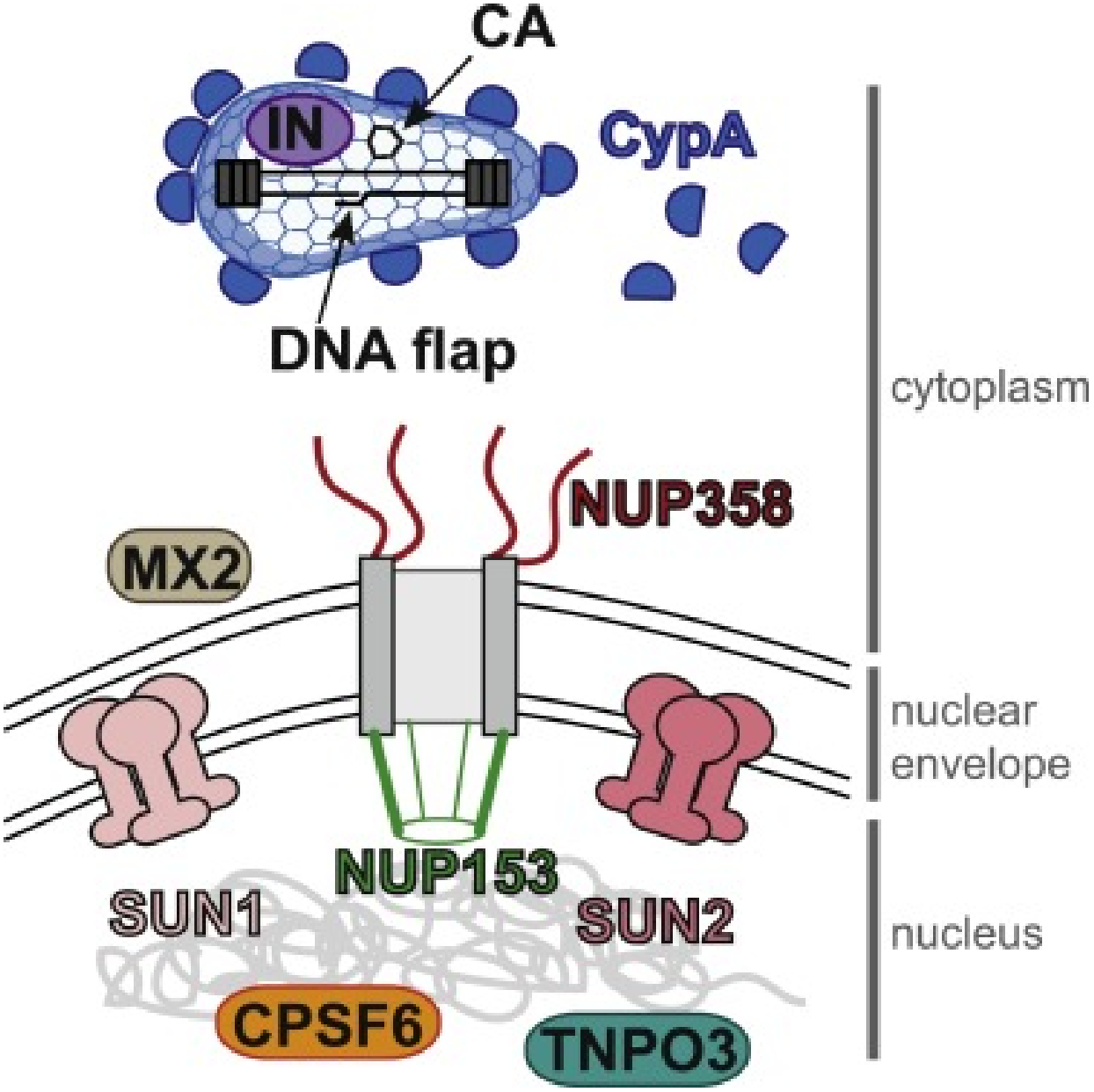
Although this appears counter-intuitive, it must be kept in mind with respect to SARS-CoV-2 and its mRNA-based vaccines, the natural process has been reversed given the production of DNA (cDNA) from mRNA. The natural process involves DNA first transcribing to RNA, with RNA secondarily translating proteins.

The mRNA based vacccines reverse transcribe to cDNA in the cytosol within the surrounding outer plasma membrane of the cell. Consequently, outside the membrane of the nucleus. The central DNA flap (third strand of DNA) is part of this cDNA.



Given this flap is only 99 nucleotides in length, and not a complete linear strand, it is labeled as a flap, Hence, cDNA is still considered as two complete linear strands of the original mRNA delivered by the vaccines, having transcribed them through employment of the enzyme reverse transcriptase.

What is not appreciated is the presence and function of this central DNA flap within the mRNA based vaccines. As stated before, what is unique about lentiviruses, specifically HIV-1, is this central DNA flap. Its normal biological function is to mediate the folding of the two linear strands of cDNA, while incorporating the enzyme integrase.



This, for the translocation of the SARS-CoV-2 viral genomes through the nuclear pore complex (NPC) to covalently bond with the host DNA. The central DNA flap ensures the two strands of cDNA are compact enough to fit through one of the 1,000 pores of the double-layered nuclear membrane.

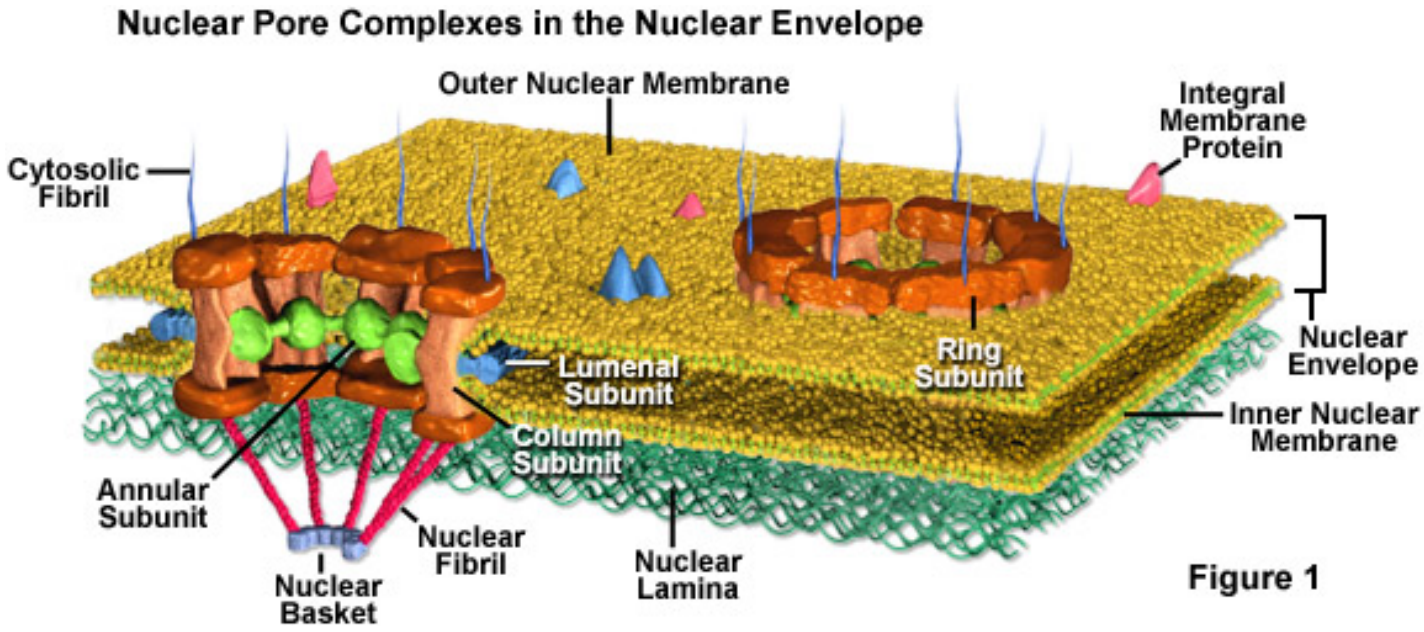
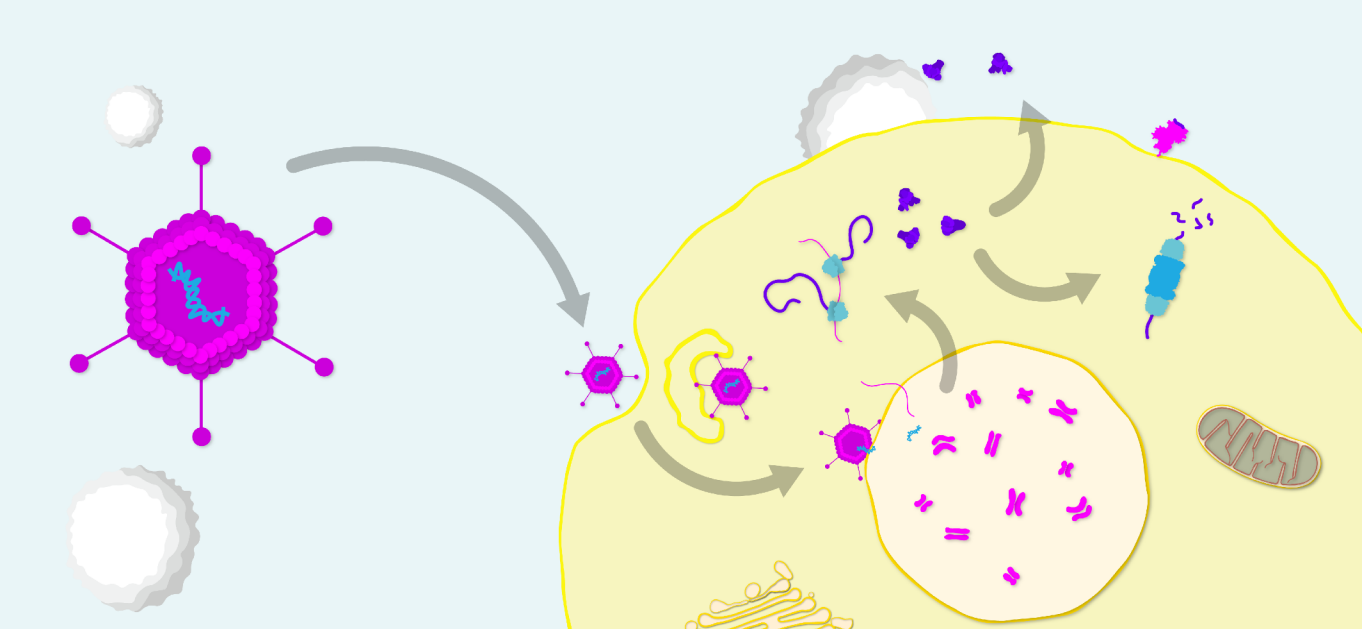


Figure 1

The DNA based vaccines transcribe to mRNA. Therefore, the entirety of the processes outlined above apply to them as well. The only difference is the order of occurance. In this, these vaccines follow the natural biological sequence of DNA transcribing to RNA.

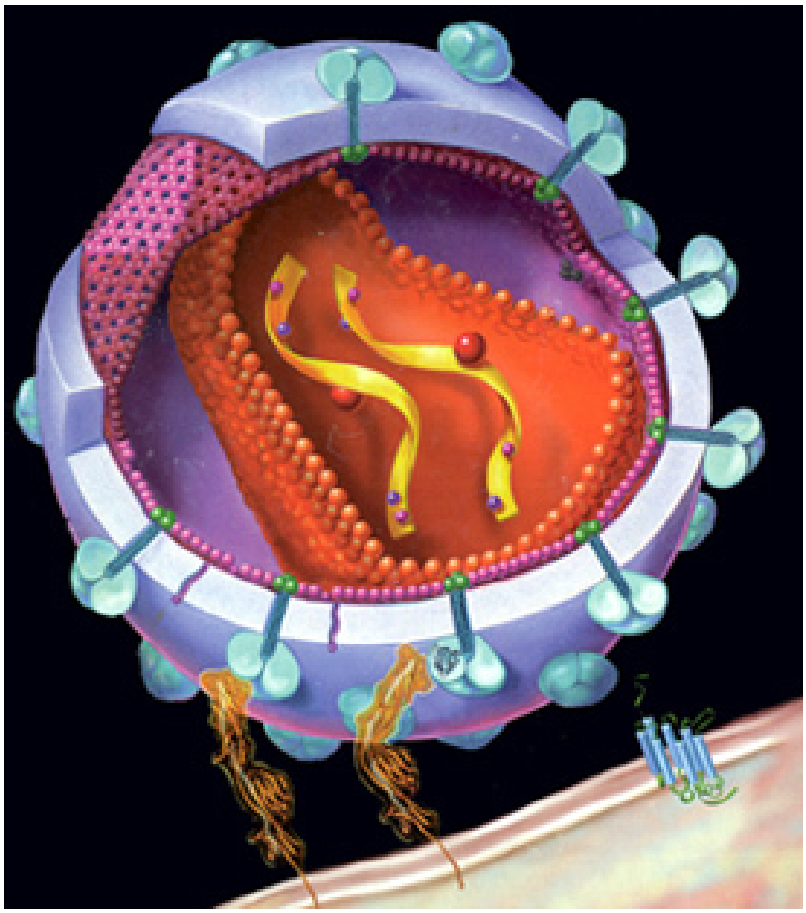
In keeping with the aforementioned reversal of normal biological orders, is the subject of vectors. In this instance, the use of a vector. A tool commonly used by molecular biologists to deliver genetic materials into cells. A transport vehicle.

There are two orders to consider here, incorporating mid-stream, a role reversal. Firstly, SARS-CoV-2 the virus, acting as a vector for 16 genomic fragments of HIV-1. Secondly, the reversal, 16 HIV-1 fragments acting as a vector for the SARS-CoV-2 virus itself.



SARS-CoV-2 the virus, acting as a vector for 16 genomic fragments of HIV-1 is necessitated by the lack of a fully intact viral genomic sequence for HIV-1. The partial genetic information of HIV-1 is incorporated within the overall genomic sequence of SARS-CoV-2 itself. Thus, wherever the virus goes, so too the 16 genomic fragments of HIV-1. Where these move, the virus SARS-CoV-2 moves.

Because this is an intact sequence of mRNA, both in the form of the virus itself, and as a vaccine (both mRNA and DNA-based), it moves as a unit. Whether entering through the outer plasma cell membrane, or through the cytosol within, and through the double membrane of the nucleus, the genetic materials remain together. In fact, they replicate together, employing the enzyme reverse transcriptase, to express cDNA.

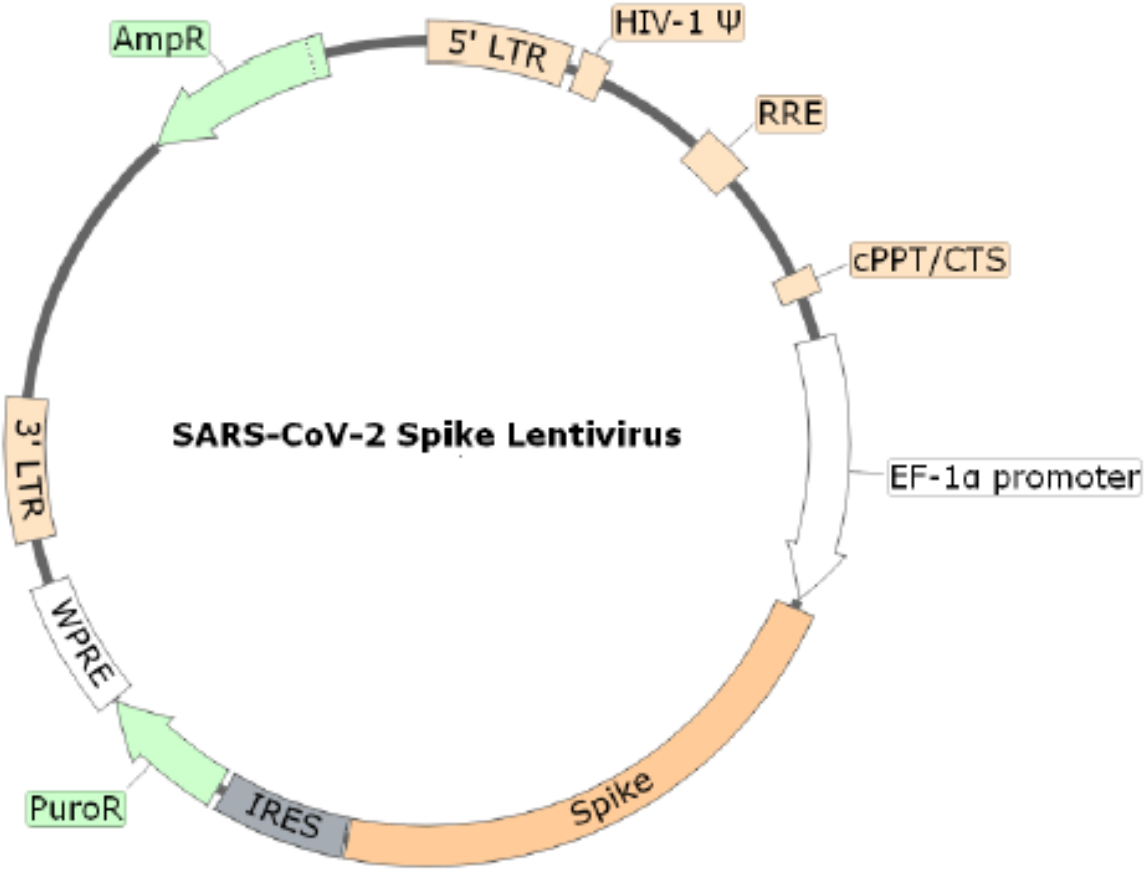


The copies, known as complementary, are of the entire mRNA genomic sequence of SARS-CoV-2. Again, this sequence contains each of the 16 genomic fragments of HIV-1. Their presence is for gain of function purposes. Specifically, to ensure integration with the host DNA of the viral genetic material of SARS-CoV-2. It accomplishes this fucntion as a natural lentiviral action of HIV-1.

The individual genomic fragments of HIV-1 were selectively chosen for their specific function of enabling the translocation through the nuclear pore complexes (NPCs) of the remaining genetic materials comprising SARS-CoV-2. The so-called "gain of function" for the virus.

Editor's Note: It should be emphasized, the contracting of SARS-CoV-2 does not indicate a concurrent contracting of HIV-1. The mRNA sequence of SARS-CoV-2 contains only portions of the entire HIV-1 virus itself.

The sequences responsible for formation of the DNA flap are found at the center of all lentiviral genomes. This central position has developed due to the formation of the pre-integration complexes (PICs). The left and right arms of the linear cDNA (reverse transcribed from the mRNA of SARS-CoV-2) molecule fold around this central flap. This is necessary for efficient translocation of this cDNA through the nuclear pore complexes (NPCs).



The presence of this central DNA flap within all lentiviruses, explains the purpose for the inclusion of 16 genomic fragments of HIV-1 within the overall genomic mRNA sequence of SARS-CoV-2. The intent is for the permanent alteration of the host DNA the virus thus infects. The same holds true for any and all vaccines for SARS-CoV-2 and its mutations. This is the function of molecular biology.

Over the last five years, there has been an enormous increase in the amount of research into RNA modifications, a field called epitranscriptomics.

Epitranscriptomics includes all the biochemical modifications of RNA (the transcriptome) within a cell. This involves all functionally relevant changes to the transcriptome that do not involve a change in the ribonucleotide sequence. Thus, the epitranscriptome can be defined as the ensemble of such functionally relevant changes. The transcriptome is the set of all RNA transcripts, including coding and non-coding, in an individual or a population of cells.

In the case of SARS-CoV-2, the 16 genomic fragments of HIV-1 found within its mRNA genomic sequence, are representative as an ensemble of functionally relevant changes to the virus. These, again, are referred to in the literature as "gain of function" changes.

Additional specific research on the integration of the SARS-CoV-2 RNA into the human genome can be found here:

SARS-CoV-2 RNA reverse-transcribed and integrated into the human genome

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