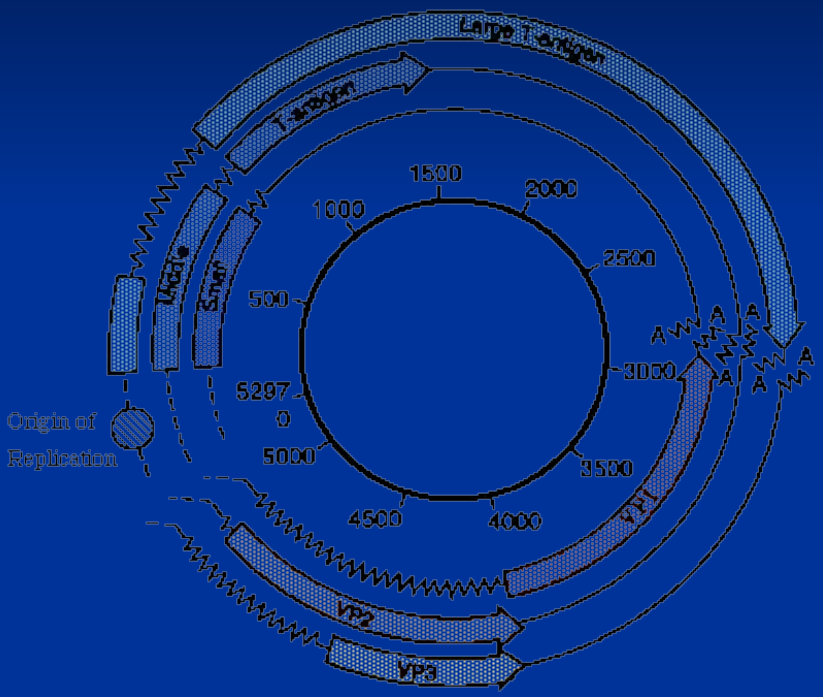
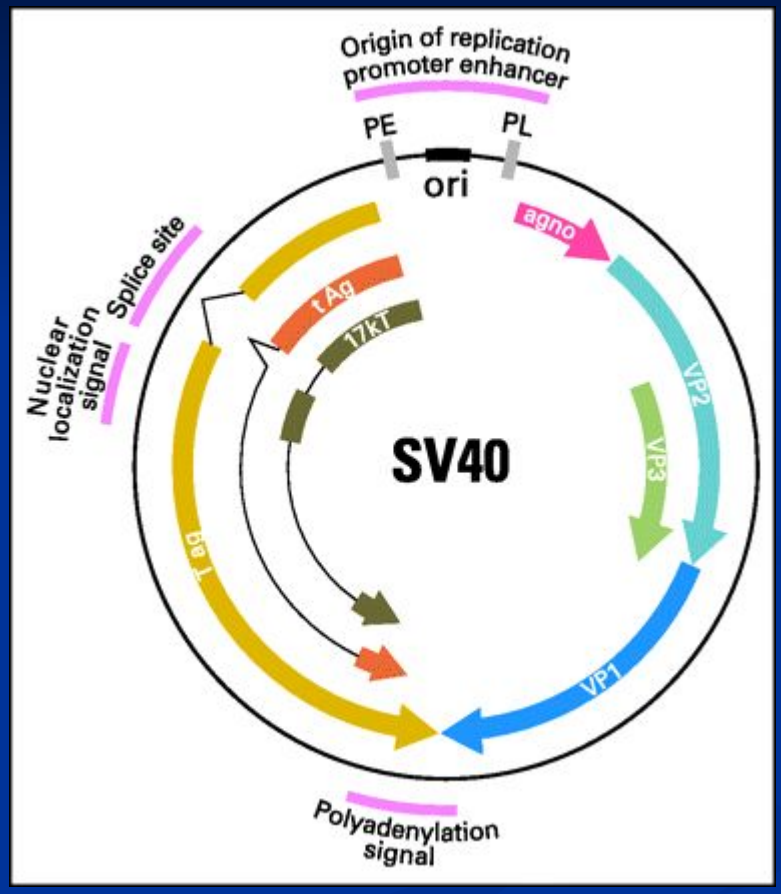
dsDNA

Генетична карта поліомавірусів



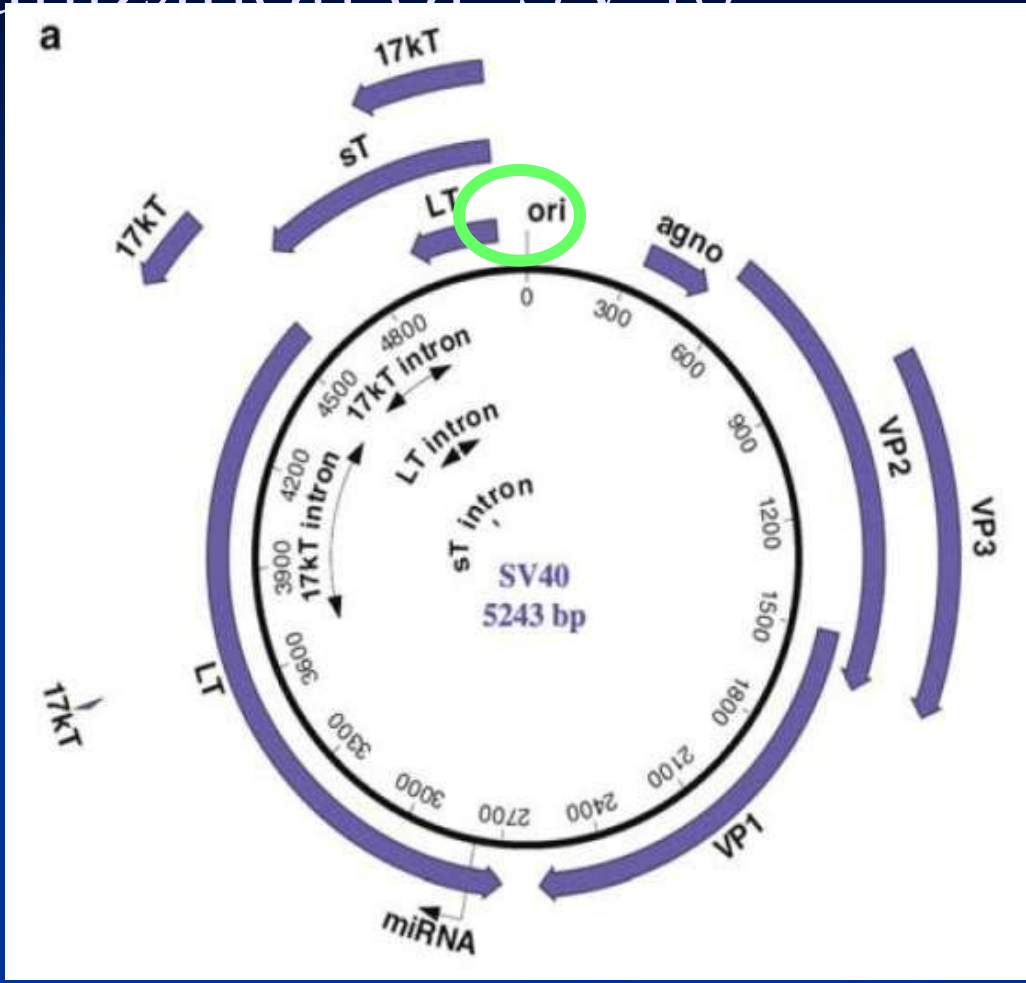
вірусу поліоми



вірусу **SV-40**

Genome Organization of SV40

- Early unit: large T antigen (LT), small t antigen (sT), 17K T antigen (17KT).
- Late unit: VP1, VP2, VP3 ,the agnoprotein (agno) and a pre-microRNA (miRNA).



The regulatory region (ori)

- For the early and late promoter and the origin of replication.

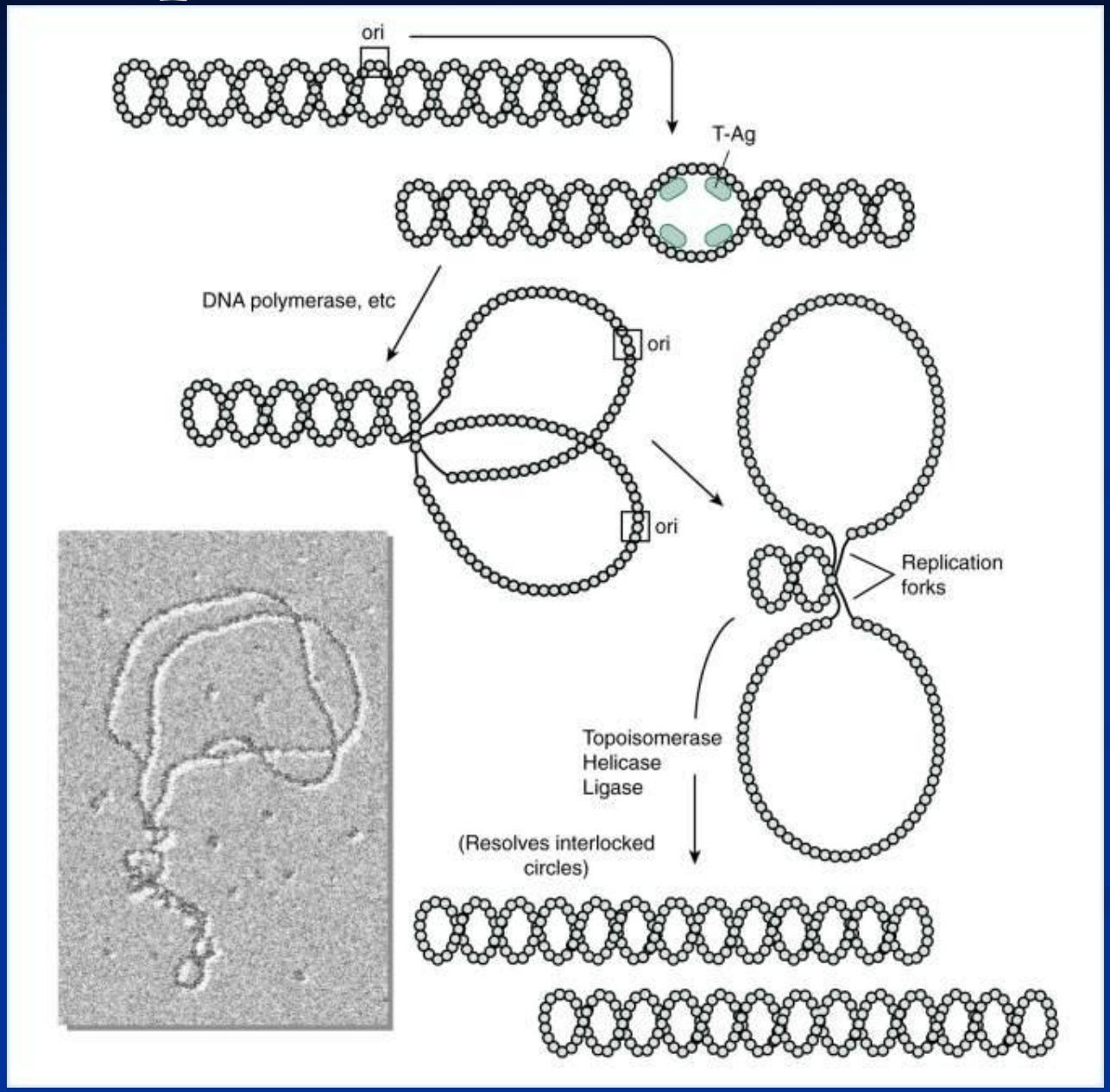
Functional organization of SV40 large T antigen

- 1. Activation of cellular DNA and RNA synthesis
  - binding the cellular Rb and p53
    - causes the infected cell to begin a round of DNA replication.
- 2. Blockage of apoptosis
  - inactivate p53 at inappropiate times in the cell cycle.
- **3. Binding to the SV40 ori to initiate viral DNA replication**
- 4. Shutting off early viral transcription
- 5. Activating late transcription
- 6. Virion assembly

SV 40 DNA replication

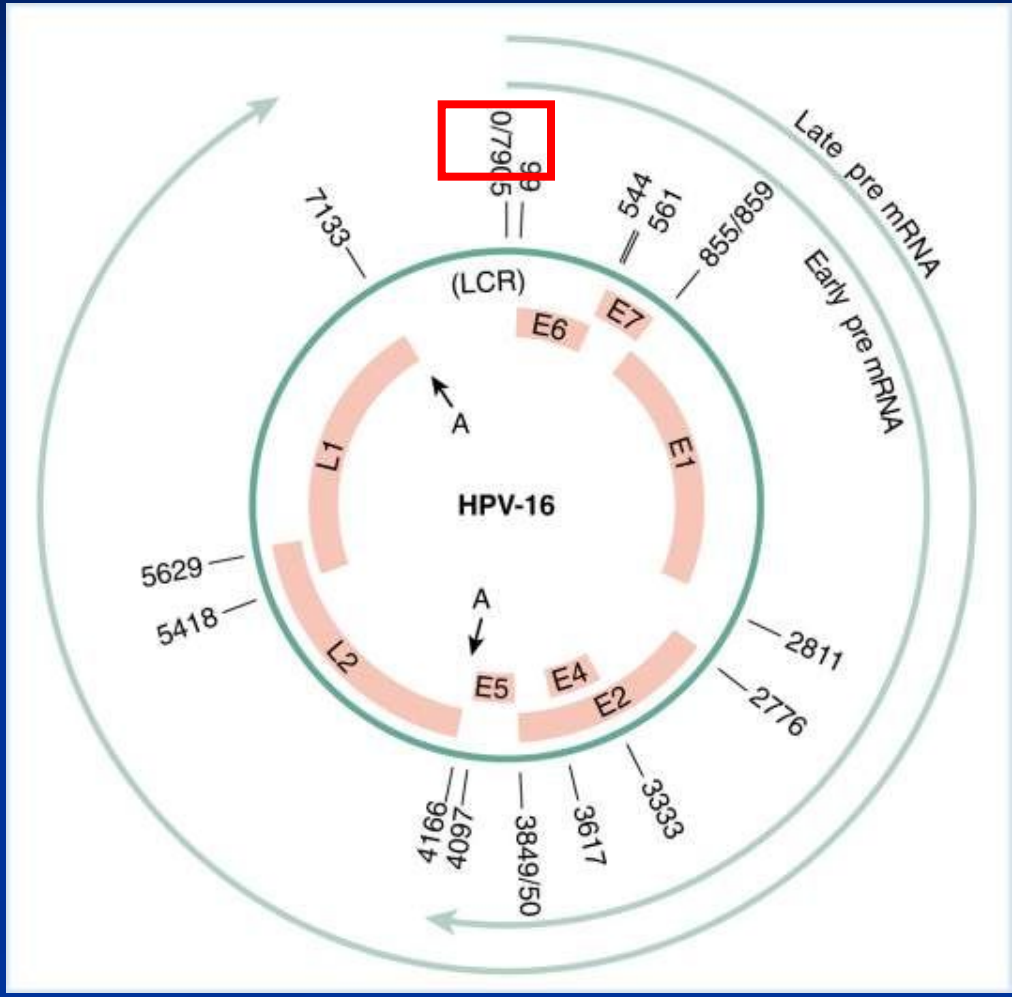
- In the nucleus.
- Large T antigen binds to the SV40 origin
- Using the host cell DNA polymerase,
  - which recognizes the viral origin of replication if the T antigen is present.
- Bi-directional replication
- Host histones complex with the newly made DNA.

The replication of SV40 DNA



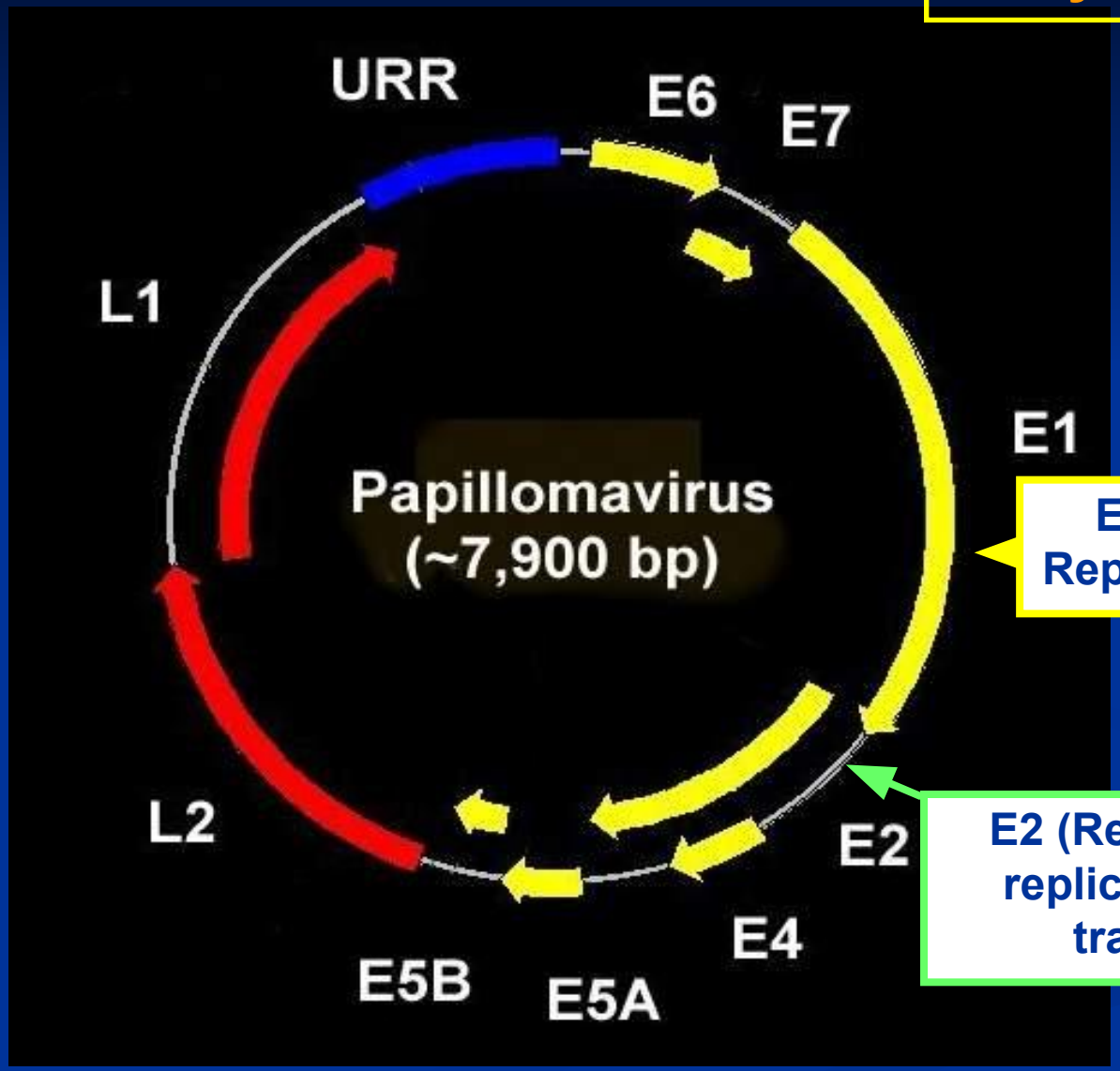
Genomic Organization of Papillomavirus

- Genome
  - 7Kb circular genome
  - Encode all proteins on the same DNA strand
  - RNAs splicing
  - Long control region (LCR) contains transcriptional and replication regulatory elements



Functional Assignments of Viral Early Proteins

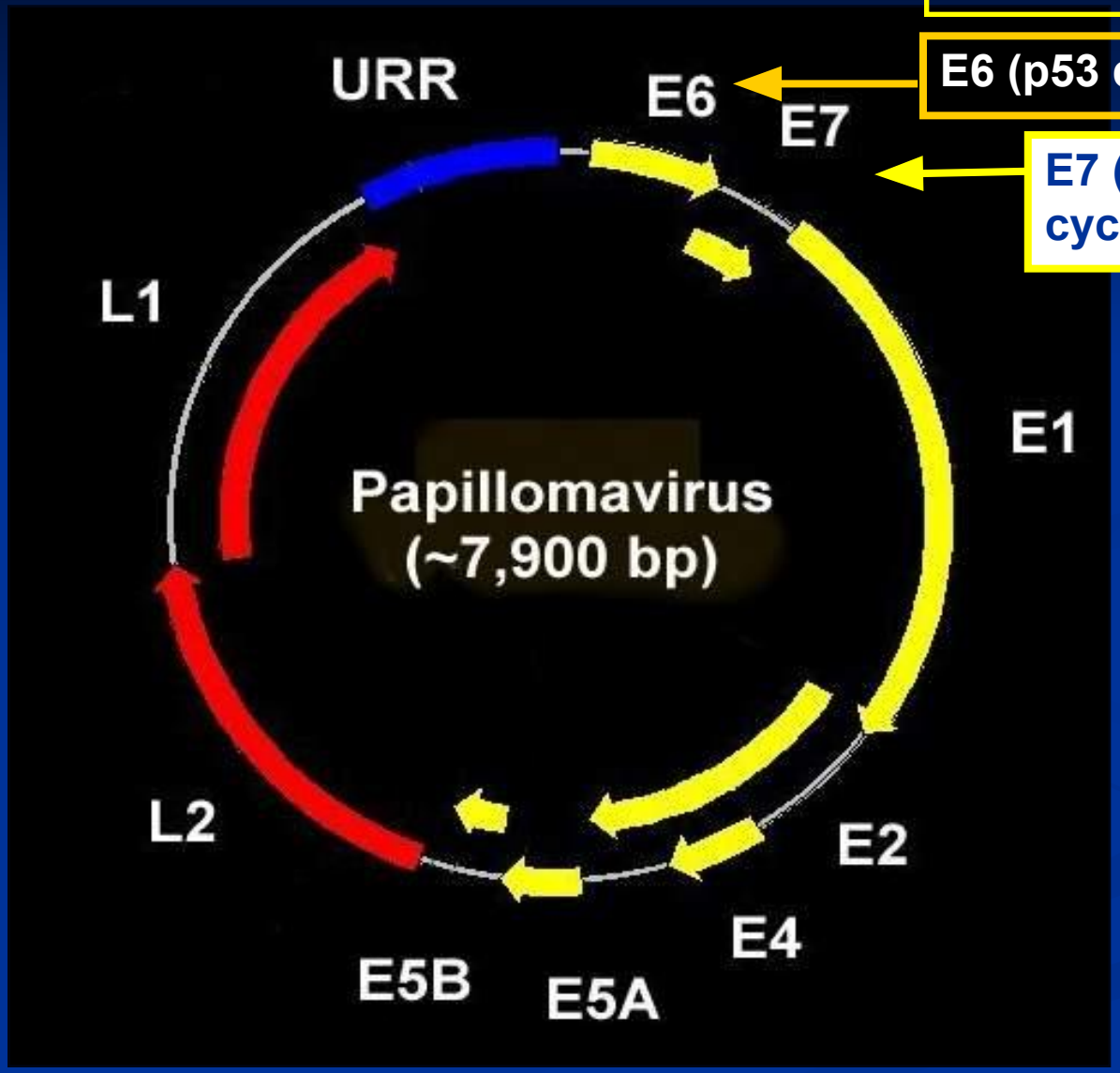
Early Region



E1 (Viral DNA Replication factor)

E2 (Regulator of DNA replication and RNA transcription)

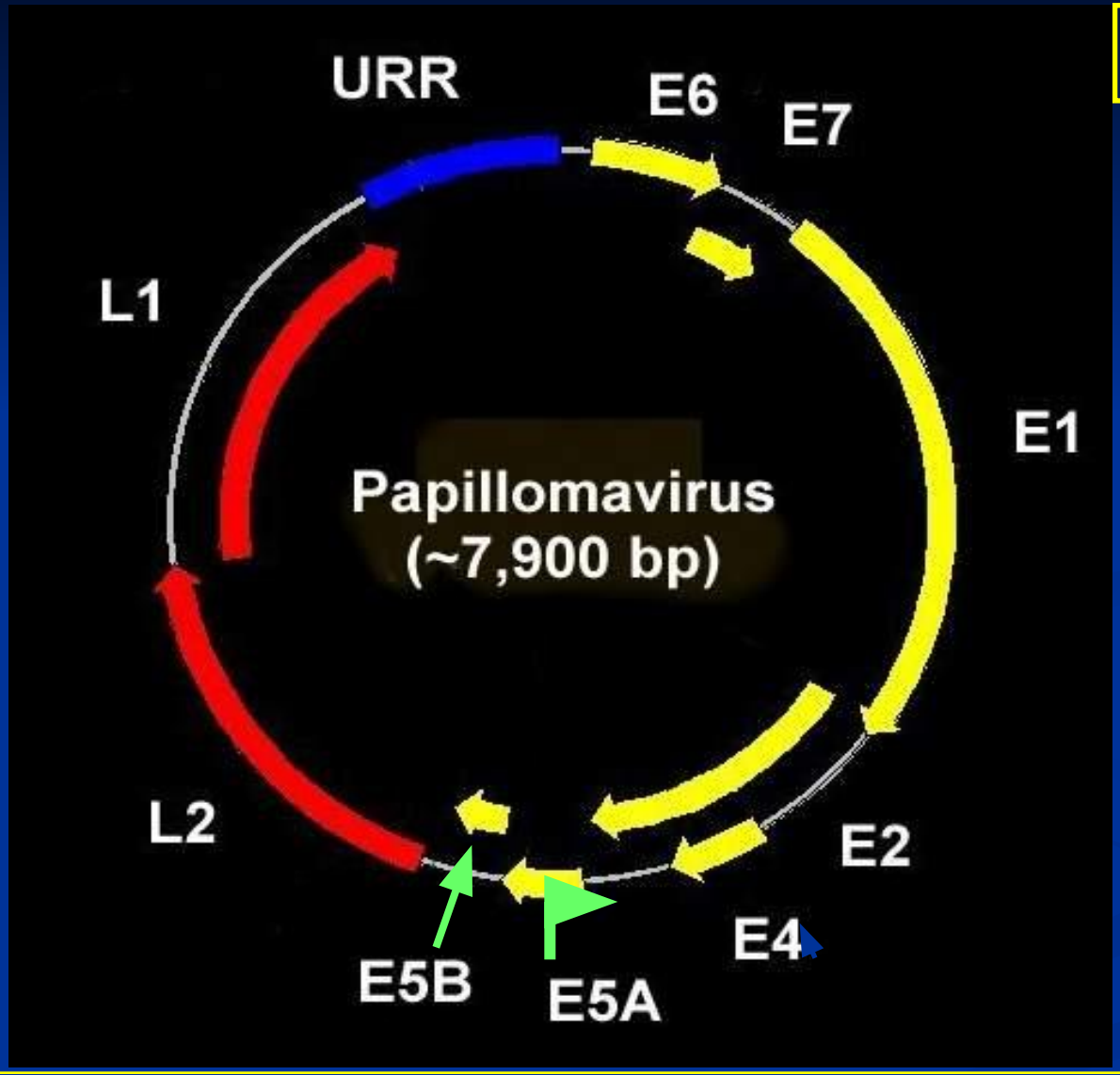
Functional Assignments of Viral Early Proteins



Early Region

- E6 (p53 degradation)
- E7 (disrupts cell cycle)

Functional Assignments of Viral Early Proteins

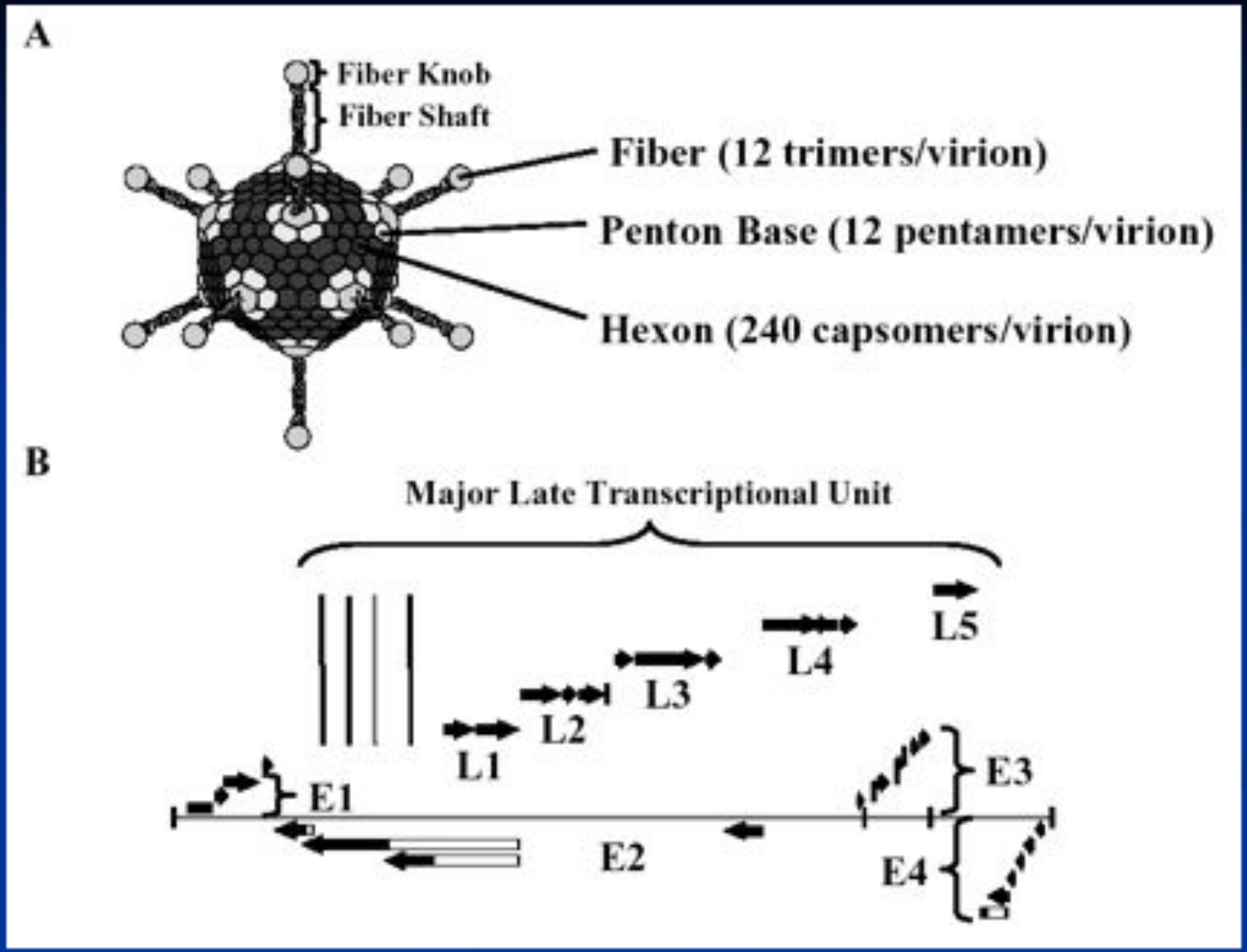


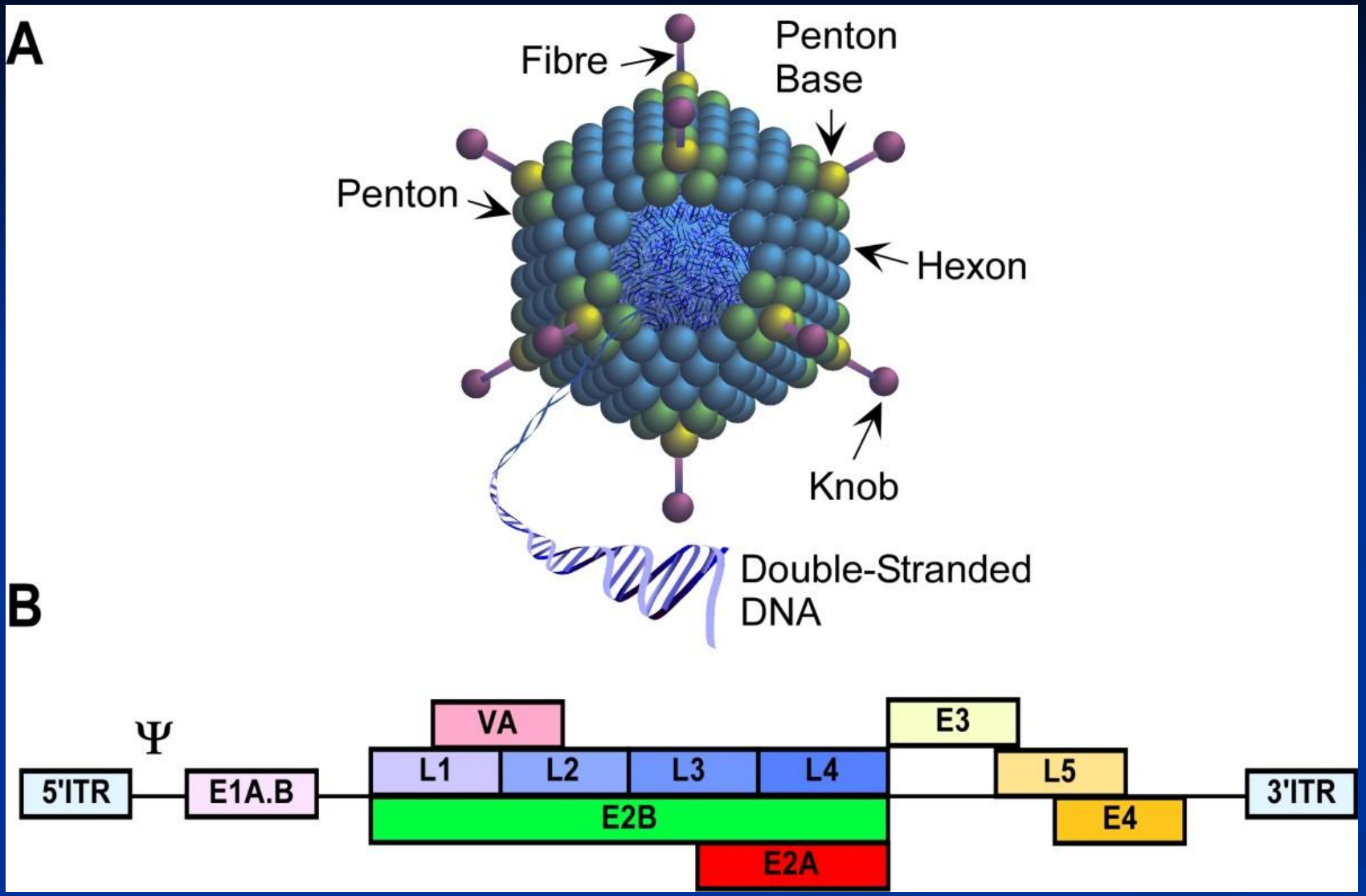
Early Region

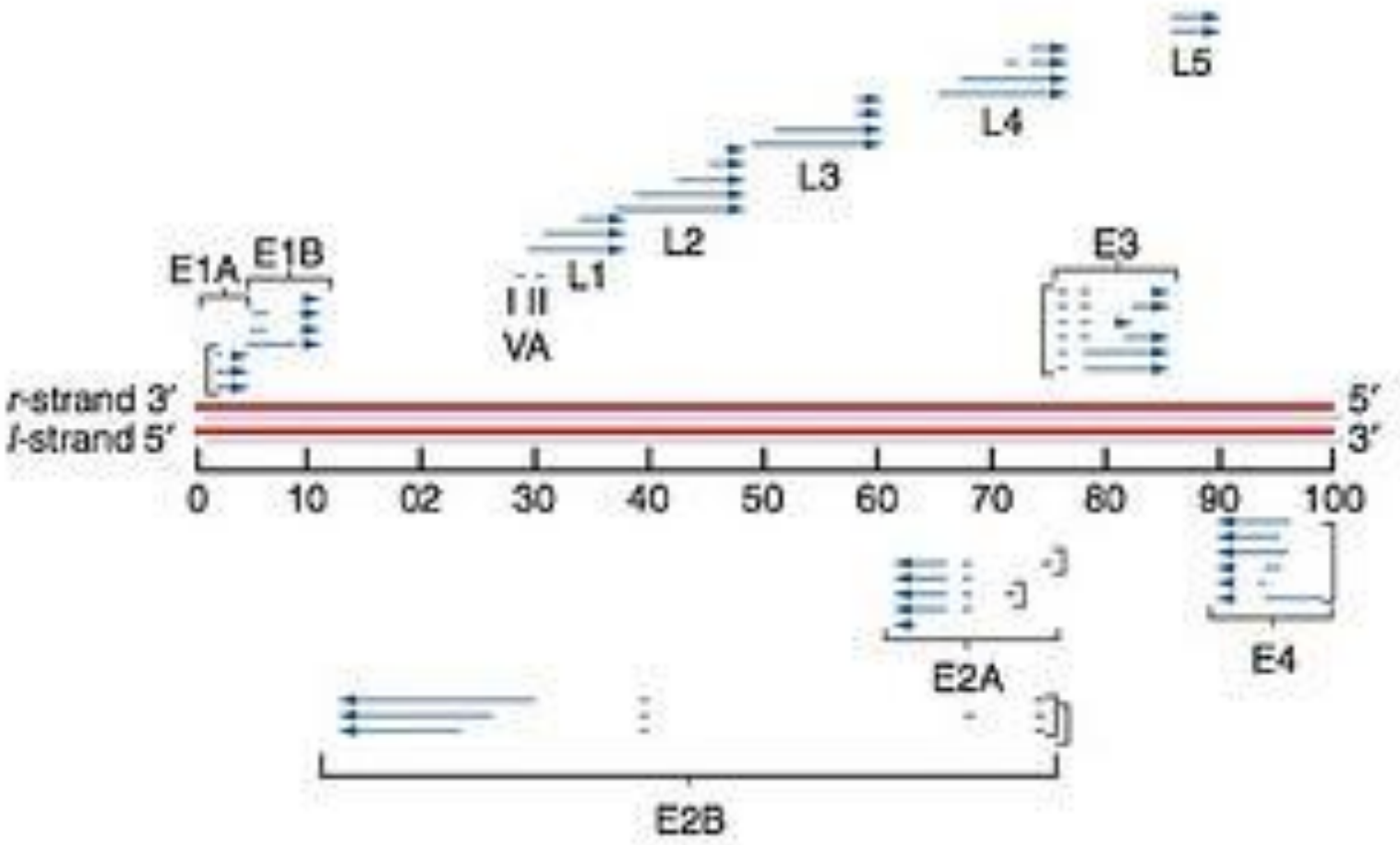
Modulation of growth regulatory mechanisms

Adenoviruses Adenoviridae

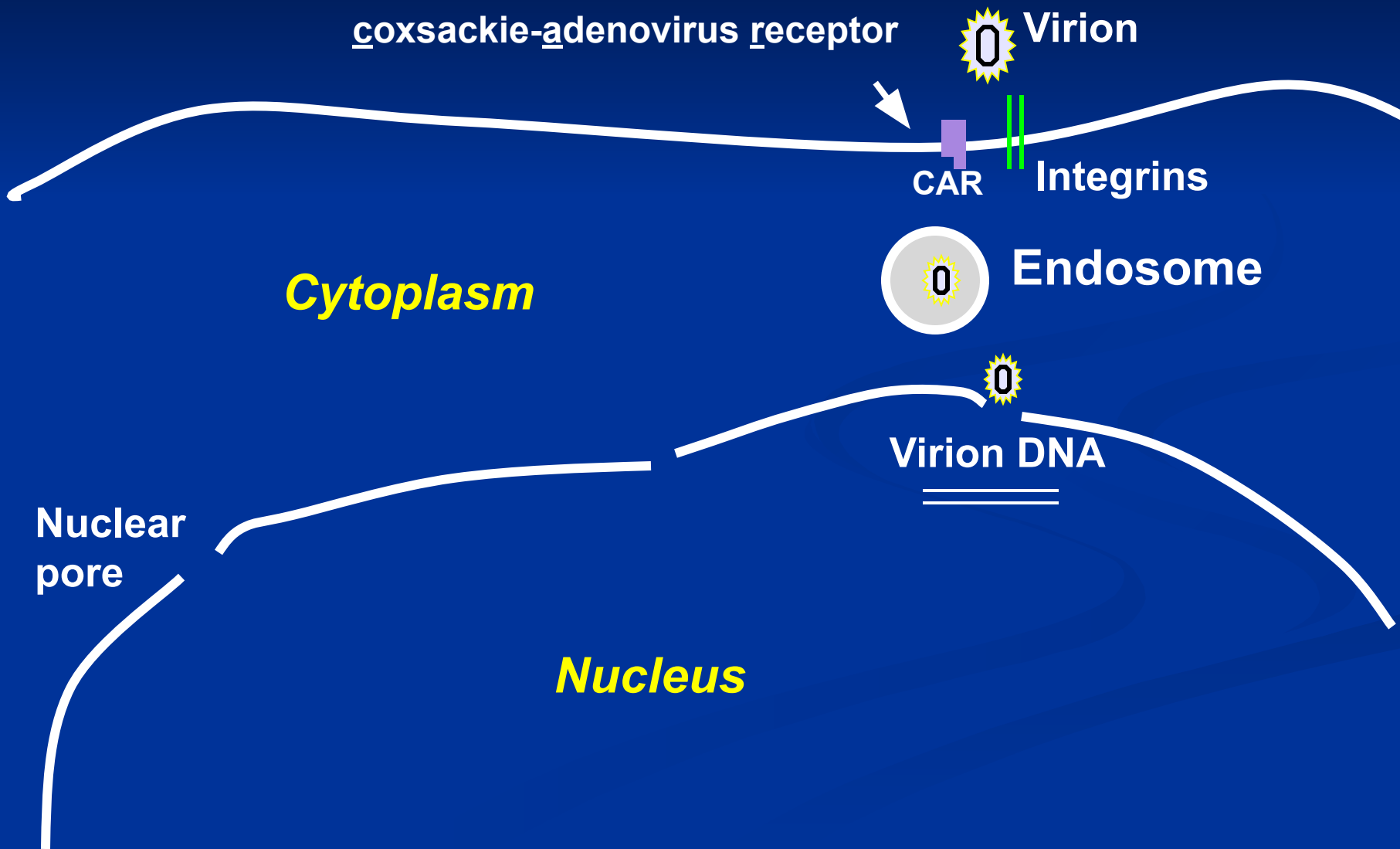
- Characteristics
  - double stranded DNA viruses; linear molecular
  - non-enveloped, icosa hedral particles 70 - 90 nm
  - vertices exhibit viral attachment protein(VAP) as fibers or spikes
    - possess hemagglutinin, and type-specific viral antigen
    - capsid proteins are toxic to host cell and may inhibit cellular synthesis
  - viral genome encodes many viral proteins
    - early proteins promote the growth the infected cell
      - E1A/E1B viral proteins bind and inactivate cellular p53 and RB(p1050 genes, thus stimulating cells growth
    - virus also provides its own DNA dependent DNA polymerase
    - some viral proteins suppress the host immune response including inflammation
    - late proteins provide structural proteins and those carried in mature virion
  - viral cycle takes 32 - 36 hours and produces 10, 000 virions
    - virus enters the cell by endocytosis, lyses the endosomal vesicle, and capsid is removed as it delivers the DNA to the nucleus
  - 51 human adenoviruses in groups A - F
    - based upon DNA homology, disease tropism, and fiber antigens


A
Fiber Knob
Fiber Shaft
Fiber (12 trimers/virion)
Penton Base (12 pentamers/virion)
Hexon (240 capsomers/virion)
B
Major Late Transcriptional Unit
L5
L4
L3
L2
L1
E1
E3
E2
E4

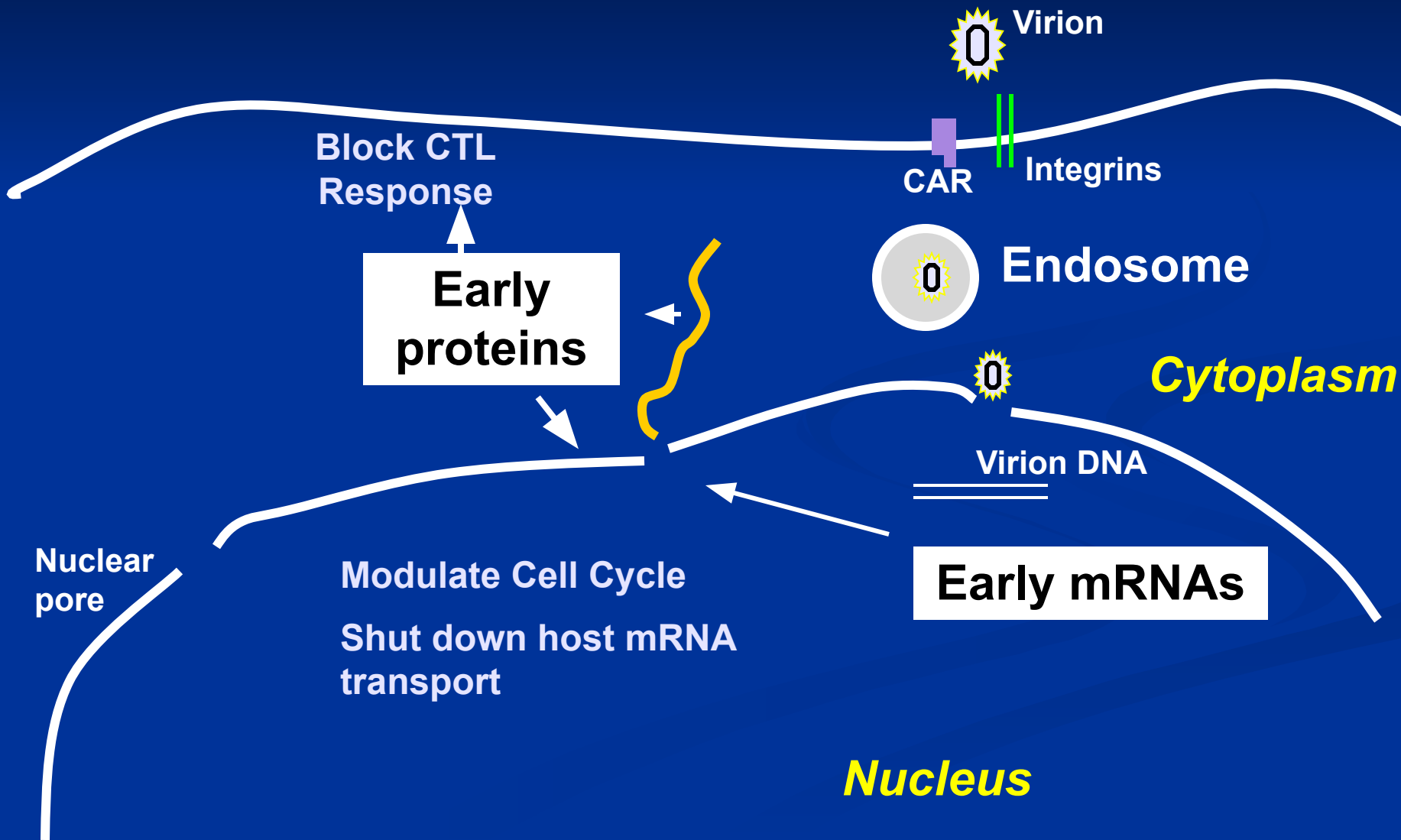

A
Fibre
Penton Base
Penton
Hexon
Knob
Double-Stranded DNA
B
Ψ
5'ITR
E1A.B
VA
L1
L2
L3
L4
E2B
E2A
E3
L5
E4
3'ITR


L5
L4
L3
L2
L1
E1A
E1B
I II
VA
E3
r-strand 3′
l-strand 5′
5′
3′
0
10
02
30
40
50
60
70
80
90
100
E2A
E4
E2B

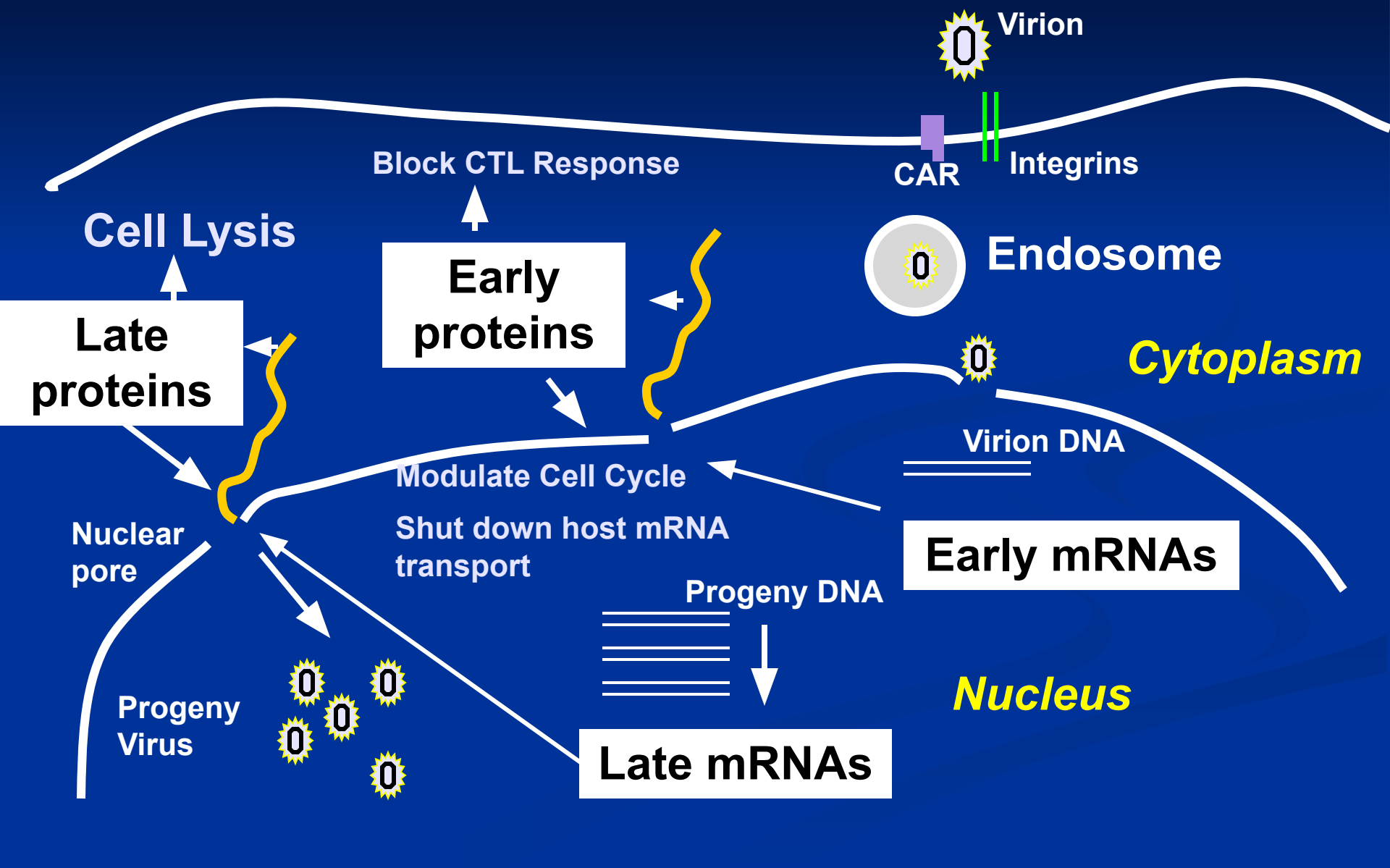
Adenovirus Replication



Adenovirus Replication

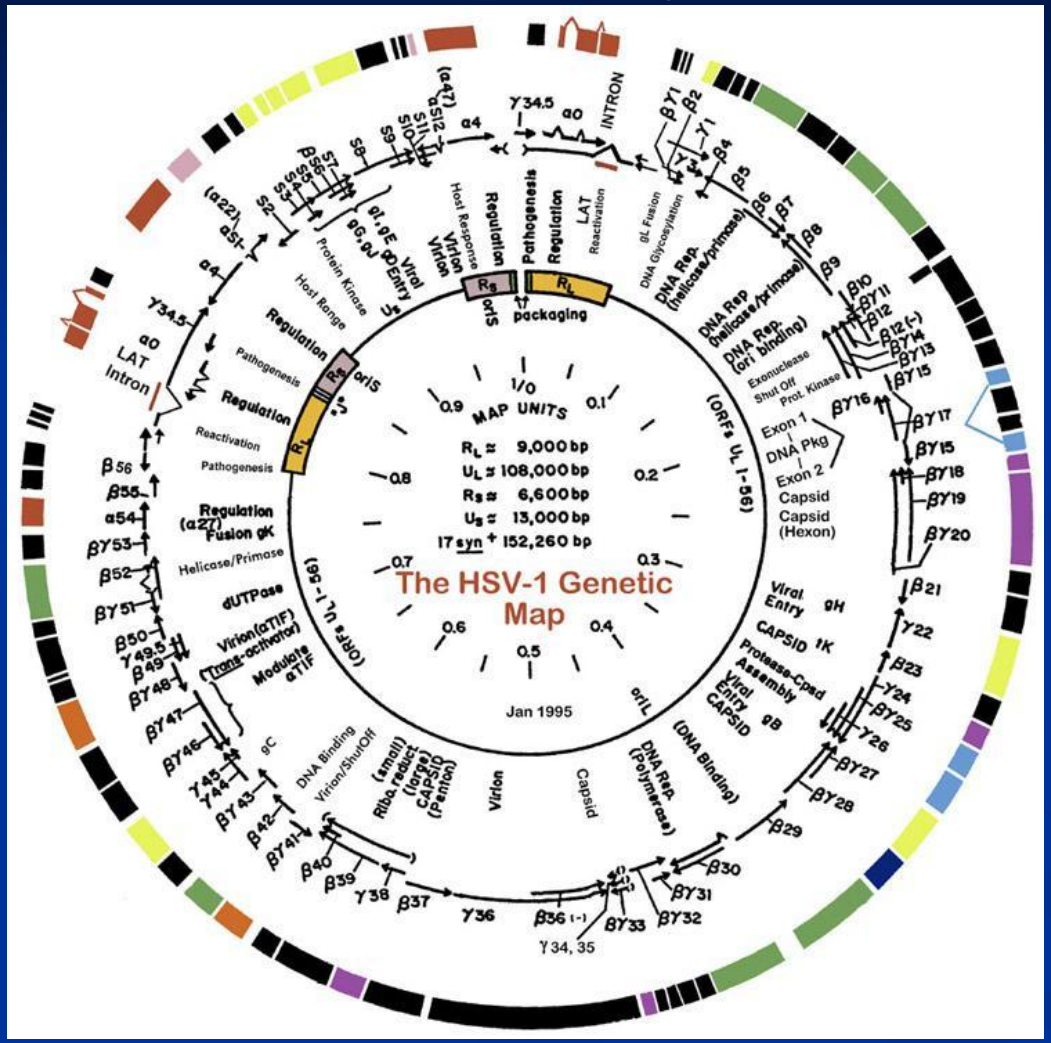


Adenovirus Replication



- The early protein include:
  - For transcription
    - EIA is referred to as an 'immediate early' gene)
  - For adenovirus DNA synthesis
    - viral DNA polymerase)
  - Alter expression of host cell genes
    - Against the host anti-viral response and/or interfere with cell cycle regulation

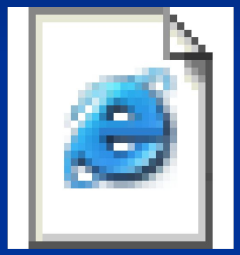
Генетична карта вірусу простого герпесу



Транскрипція вірусу простого герпесу

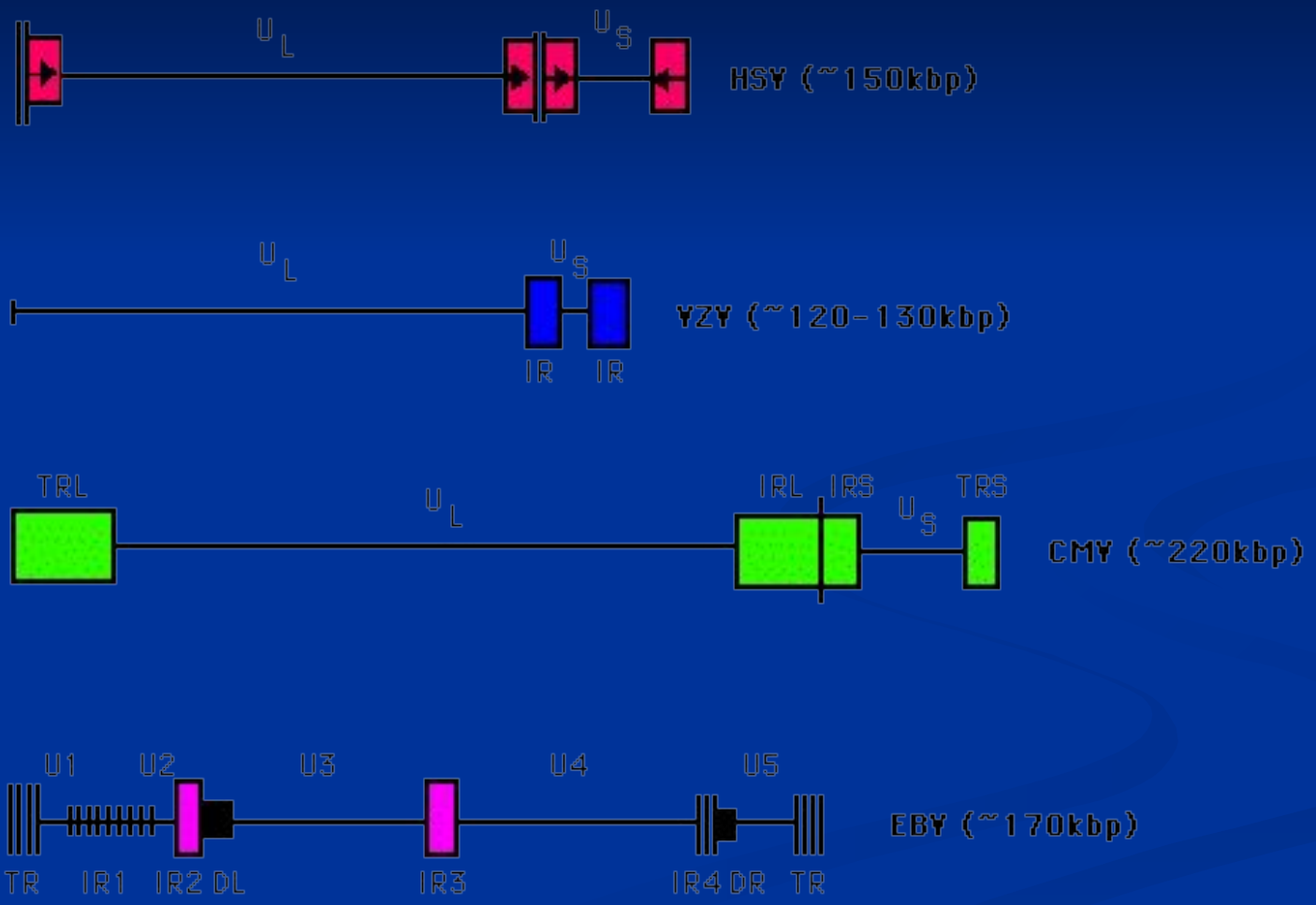
Hsvrna.swf

Реплікація ДНК вірусу простого герпесу



Dnarep.swf

Блочний запис генетичної інформації у герпесвірусів



Генетична карта бактеріофагу T4

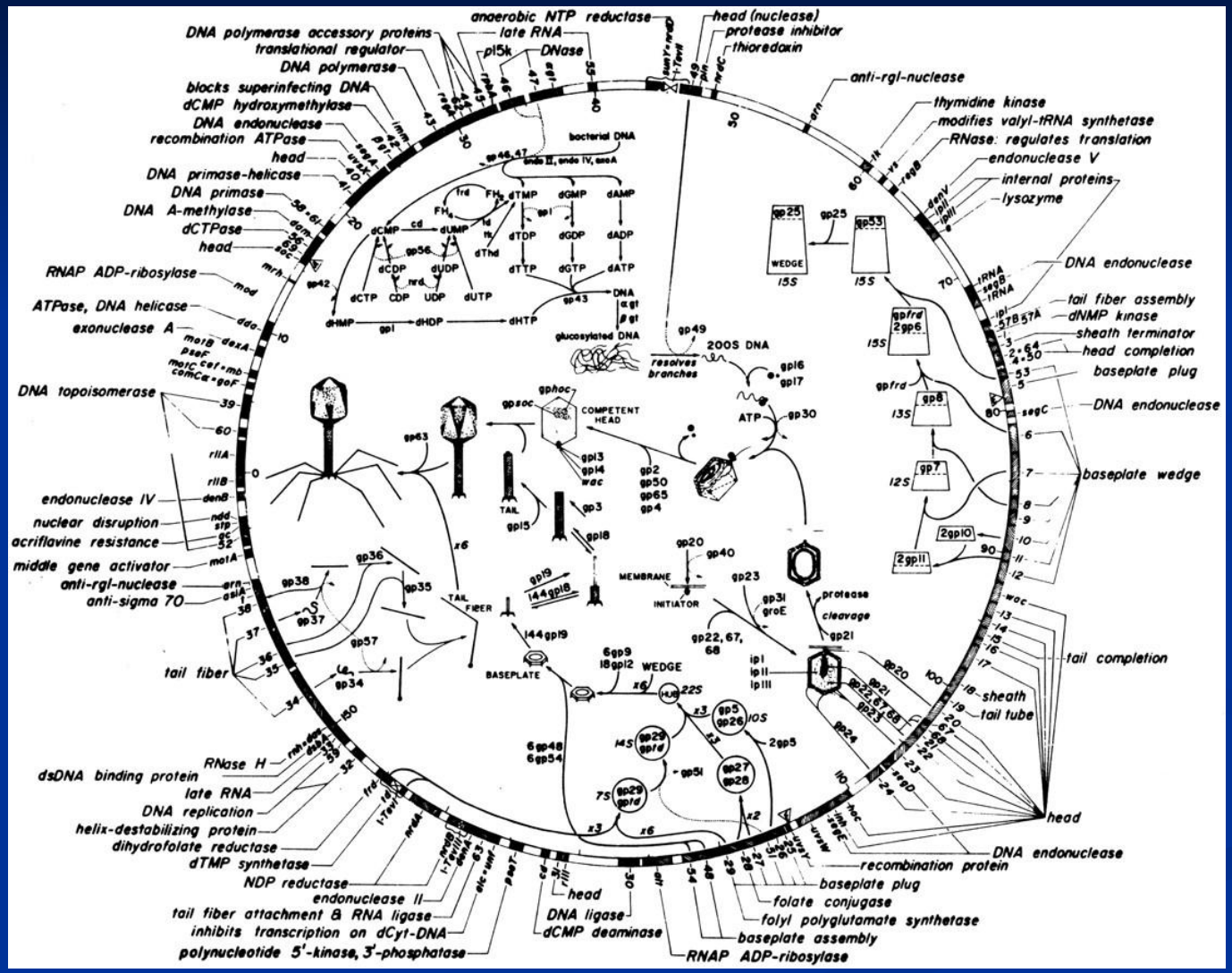


Схема розрізання конкатемеру фага Т4

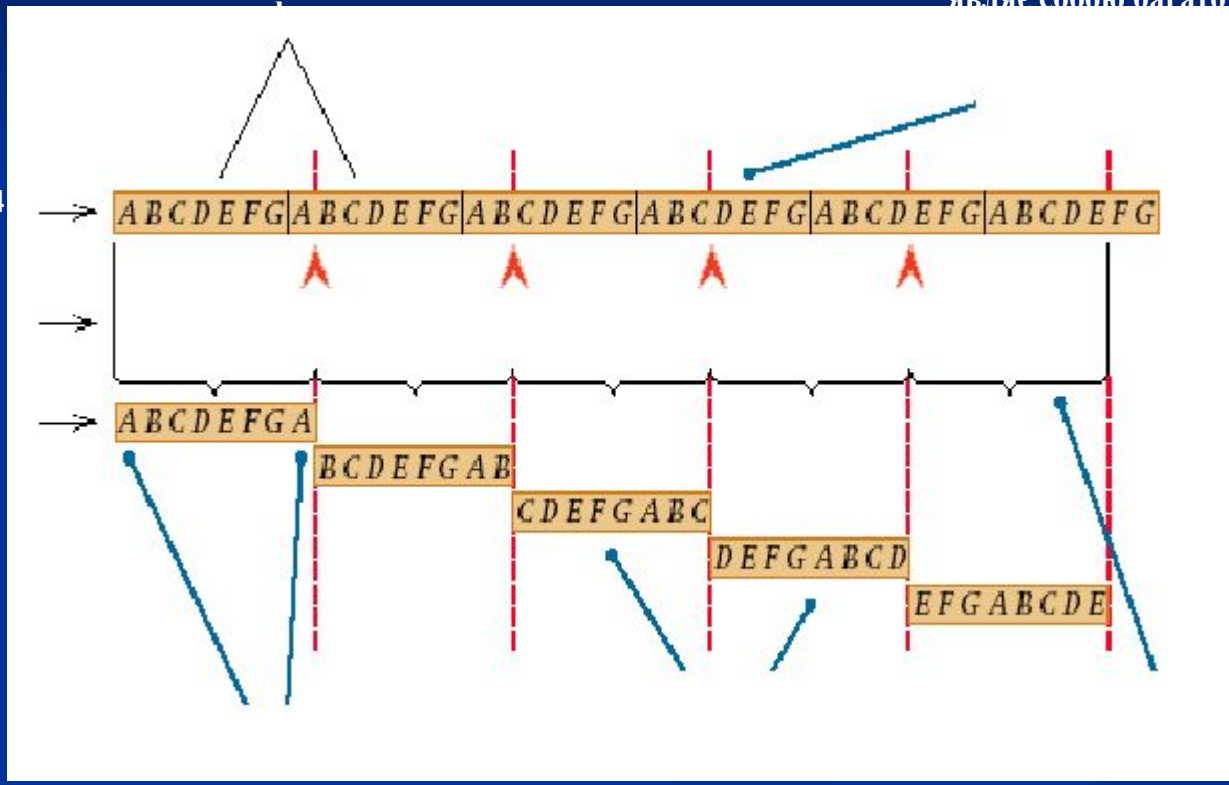
Мінімальний

Фагова прегеномна ДНК
являє собою багато копій
нанних

Конкатемер ДНК фагу Т4

Розрізання

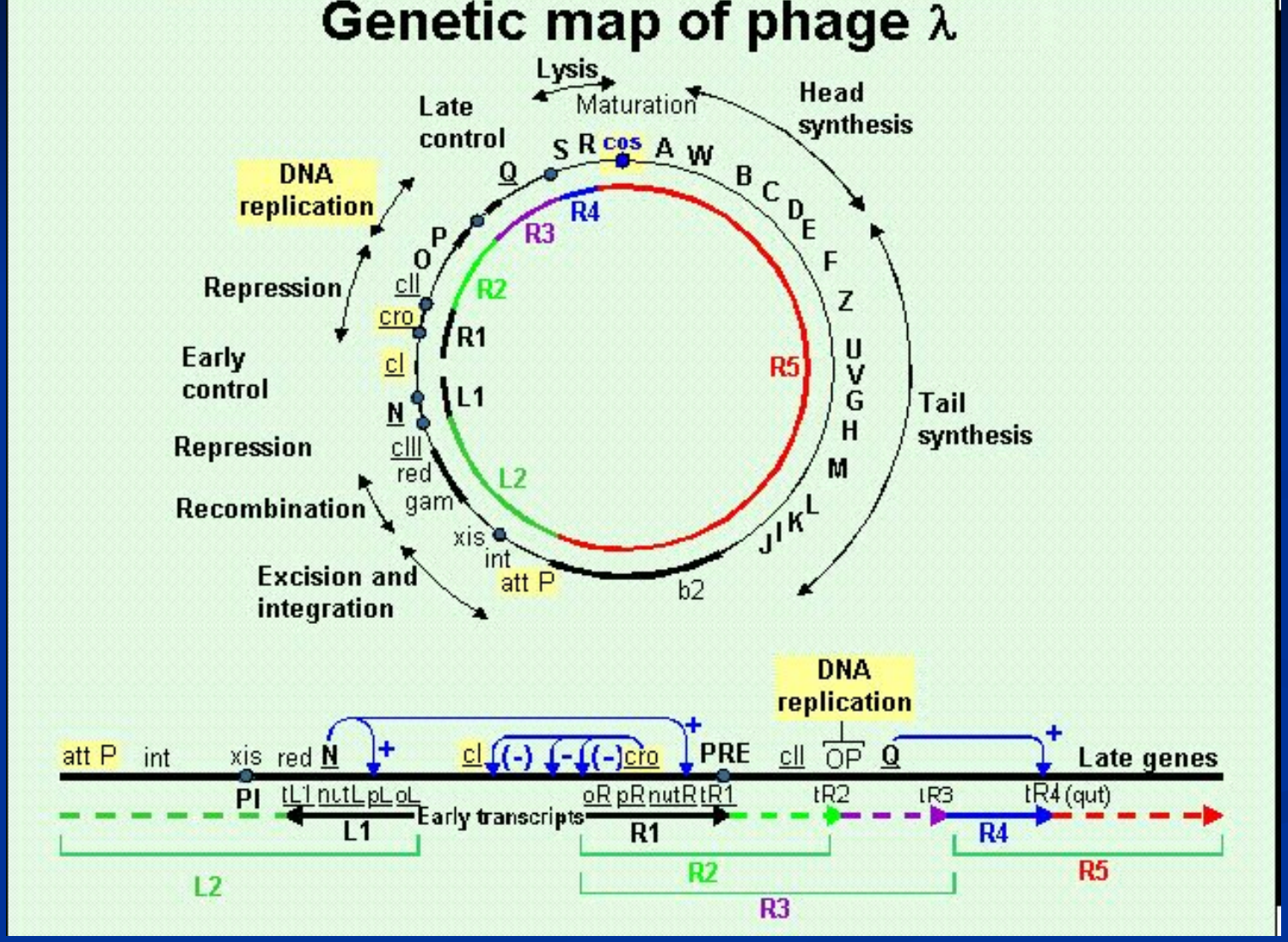
Геном фагу, що пакується
в головку



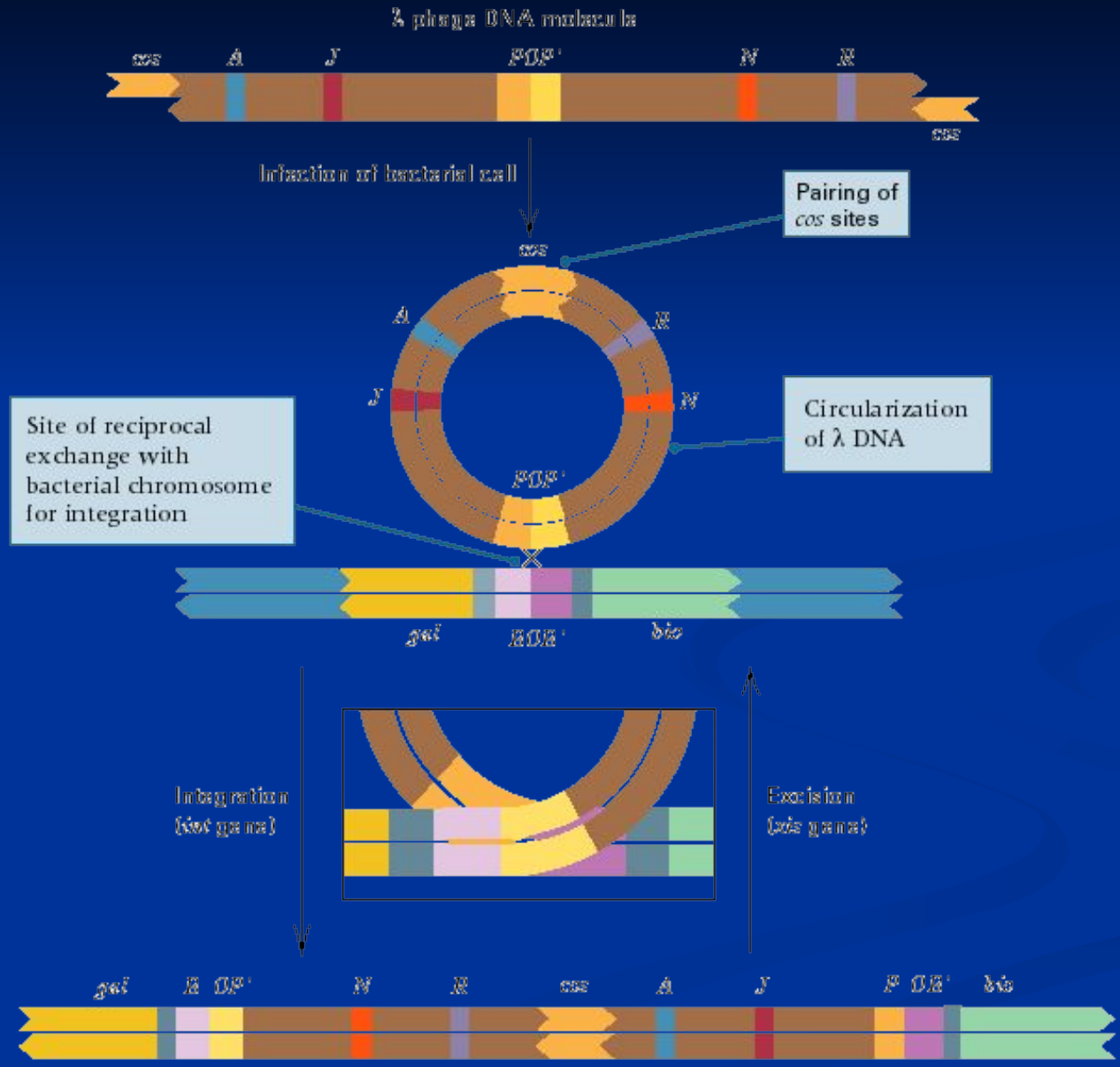
фагу
ормації,
ий геном

генетичній карті

Генетична карта бактеріофагу лямбда



Інтеграція геному фагу лямбда



POXVIRIDAE

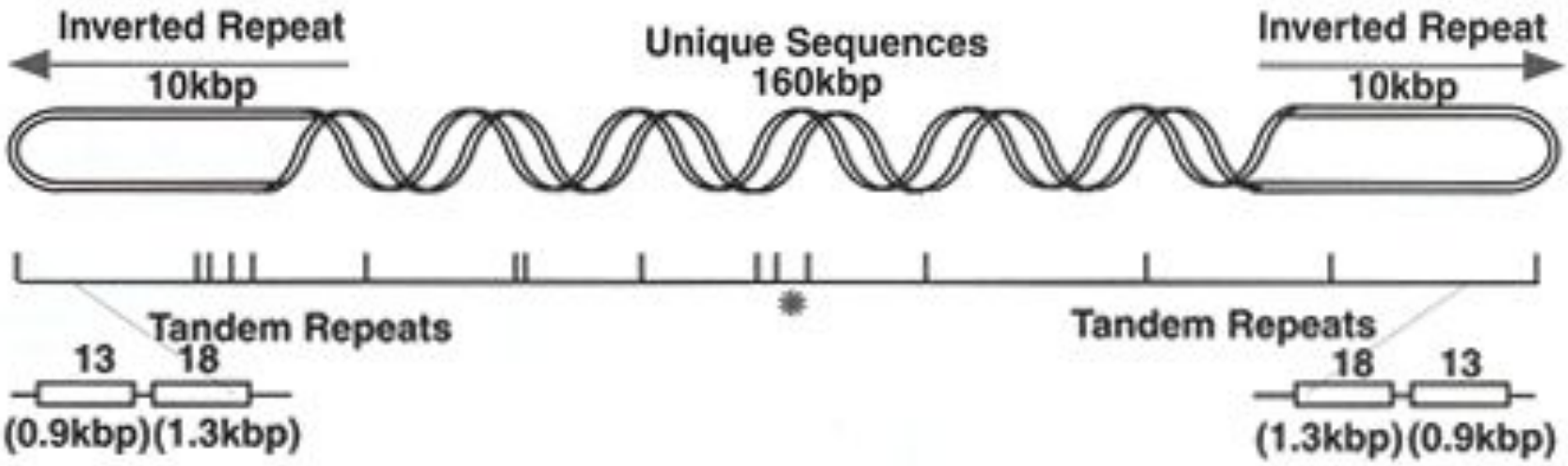


Figure 2 Schematic representation of the DNA of *Vaccinia virus* (VACV) (WR strain): (Top) Linear double-stranded molecule with terminal hairpins and inverted repeats (not to scale). The denatured DNA forms a single-stranded circular molecule. (Bottom) *Hind* III cleavage sites of the *Vaccinia virus* (WR strain) genome, the asterisk indicates the fragment that contains the thymidine kinase gene used in construction of phylogenetic trees. Each 10-kbp terminal portion includes two groups of tandem repeats of short sequences rich in AT. (Redrawn from Fenner, Wittek, and Dumbell, 1989, with permission.)

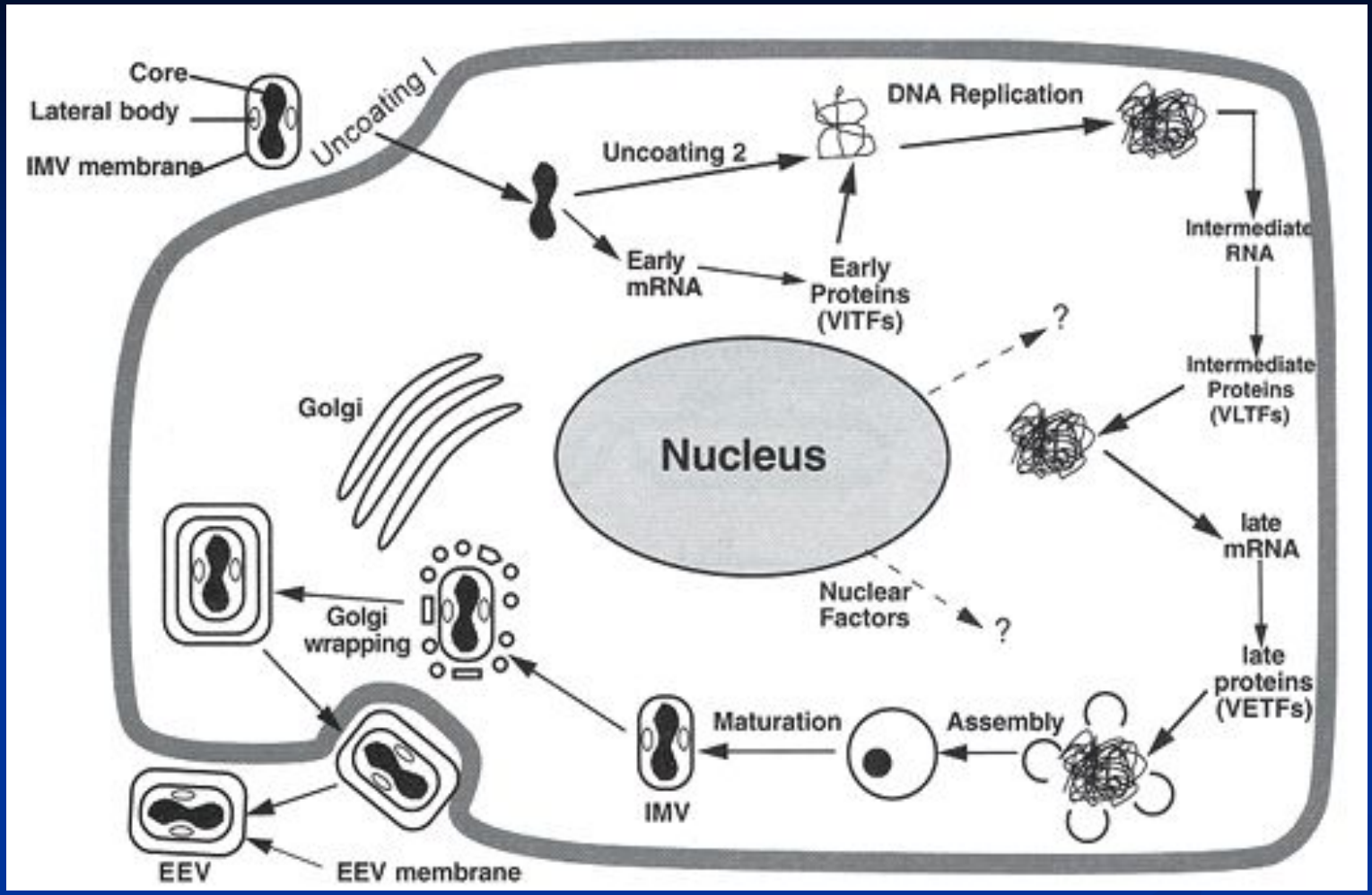
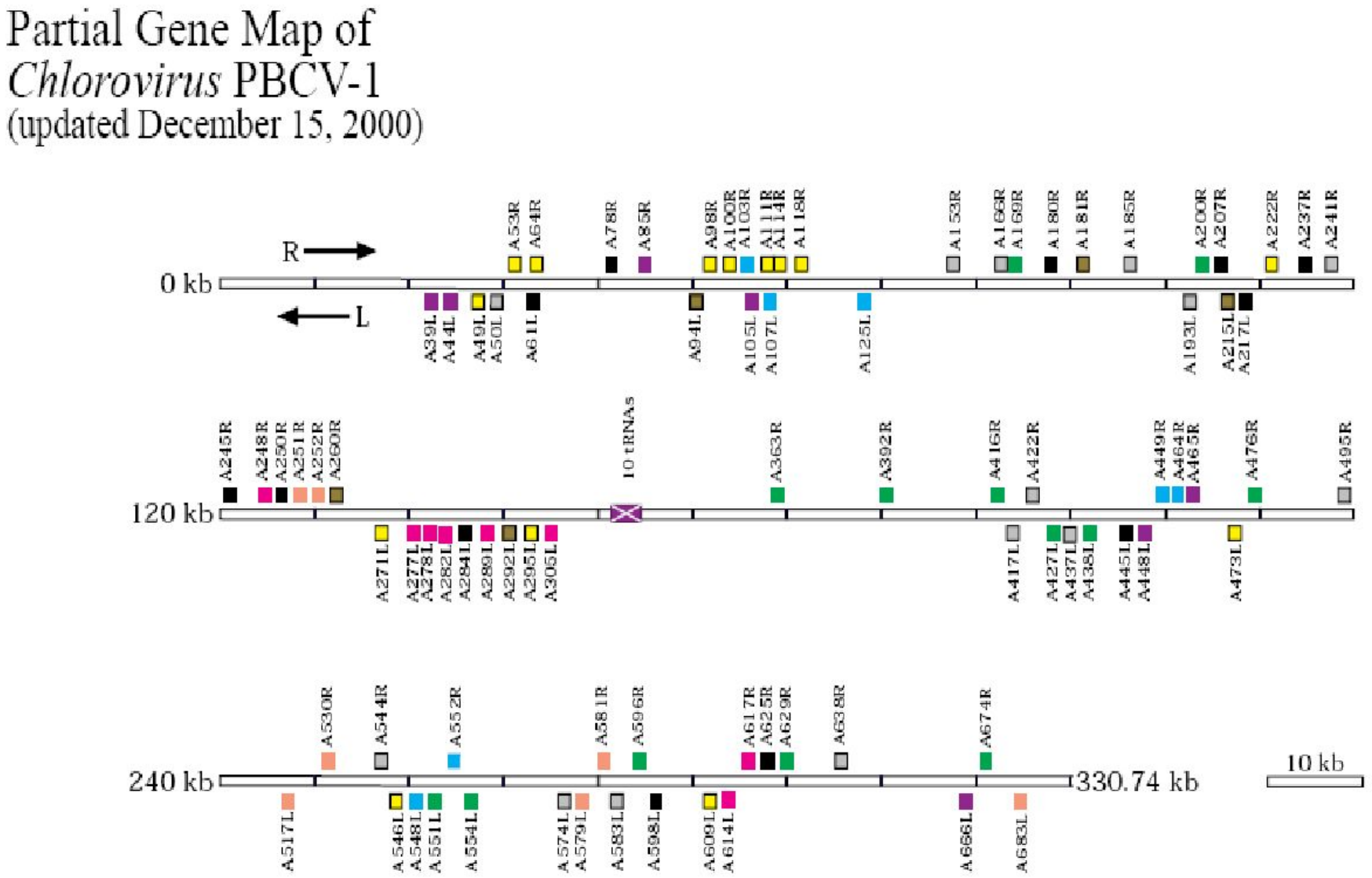


Figure 3 The infectious cycle of *Vaccinia virus* (VACV): IMV, intracellular mature virus; EEV, extracellular enveloped virus; VITF, vaccinia intermediate transcription factor; VLTF, vaccinia late transcription factor; VETF, vaccinia early transcription factor.

- The poxvirus genome comprises a linear molecule of dsDNA with covalently closed termini; terminal hairpins constitute two isomeric, imperfectly paired, “flip-flop” DNA forms consisting of inverted complementary sequences. Variably sized, tandem repeat sequence arrays may or may not be present near the ends (Fig. 2The poxvirus genome comprises a linear molecule of dsDNA with covalently closed termini; terminal hairpins constitute two isomeric, imperfectly paired, “flip-flop” DNA forms consisting of inverted complementary sequences. Variably sized, tandem repeat sequence arrays may or may not be present near the ends (Fig. 2). Replication takes place predominately if not exclusively within the cytoplasm (Fig. 3). Entry into cells of intracellular virus (IMV) and extracellular enveloped virus (EEV) is suggested to be *via* different pathways. After virion adsorption, IMV entry into the host cell is by fusion between the plasma membrane after which cores are released into the cytoplasm and uncoated further. EEV entry, unlike IMV, may necessitate fusion with endosomal membranes to release the core.
- Polyadenylated, capped primary mRNA transcripts, representing about 50% of the genome, are initially synthesized from both DNA strands by enzymes within the core, including a virus-encoded multisubunit RNA polymerase; transcripts are extruded from the core for translation by host ribosomes. During synthesis of early proteins, host macromolecular synthesis is inhibited. Virus reproduction ensues in the host cell cytoplasm, producing basophilic (B-type) inclusions termed “viroplasms” or “virus factories”. The genome contains closely spaced ORFs, lacking introns, some of which may partially overlap preceded by virus-specific promoters that temporally regulate transcription of three classes of genes. One class, the early genes, are expressed from partially uncoated virions prior to DNA replication (these encode many non-structural proteins, including enzymes involved in replicating the genome and modifying DNA, RNA, and proteins designed to neutralize the host response). Early genes also encode intermediate transcription factors. Intermediate genes (which encode late transcription factors), are expressed during the period of DNA replication and are required for subsequent late gene transcription. Finally, late genes are expressed during the post-replicative phase (these mainly encode virion structural proteins but also early transcription factors). Despite a cytoplasmic site of replication, there is mounting evidence for the requirement of host nuclear proteins in post-replicative transcription. The mRNAs are capped, polyadenylated at the 3 termini, but not spliced. Many intermediate, late and some early mRNAs have 5 -poly(A) tracts, which precede the encoded mRNA. Early protein synthesis is generally decreased during the transition to late gene expression, but some genes are expressed from promoters with both early and late activity. Certain proteins are modified post-translationally (e.g., by proteolytic cleavage, phosphorylation, glycosylation, ribosylation, sulfation, acylation, palmitylation and myristylation). Proteolytic cleavage of late proteins is required for virion morphogenesis.
- The replication of the DNA genome appears to be mainly through the action of viral enzymes. DNA replication appears to involve a self-priming, unidirectional, strand displacement mechanism in which concatemeric replicative intermediates are generated and subsequently resolved via specific cleavages into unit length DNAs that are ultimately covalently closed. Genetic recombination within genera has been shown, and may occur between daughter molecules during replication. Non-genetic genome reactivation generating infectious virus has been shown within and between genera of the *Chordopoxvirinae*.
- Virus morphogenesis begins following DNA replication and expression of early, intermediate and late genes. Particle assembly is initiated with the formation of crescent-shaped membrane structures. Replicated, concatameric DNA is resolved into unit genomes and packaged into immature virion particles, which further mature to form intracellular mature virions (IMVs) which are fully infectious if liberated from cells. A portion of the IMVs are further enveloped by modified Golgi membranes, transported to the periphery of the cell where fusion of the wrapped virions with the plasma membrane ultimately results in release of extracellular enveloped virions (EEVs) by an as yet incompletely understood process. Enveloped virions thereby acquire host cell lipids and additional virus-specific proteins, including the virus hemagglutinin protein. The envelope is closely positioned to the surface membrane. While both IMVs and EEVs are infectious, the external antigens on the two virus forms are different and upon infection, the two forms of virus bind to different cellular receptors and are likely uncoated by different mechanisms. Virus DNA and several proteins are organized as a nucleoprotein complex within the core of all infectious virions. The IMVs contain an encompassing surface membrane, lateral bodies, and the nucleoprotein core complex (see Fig. 1). For *Vaccinia virus*, the core has a 9 nm thick membrane with a regular subunit structure. Within the vaccinia virion, negative stain indicates that the core assumes a biconcave shape (Fig. 1) apparently due to the large lateral bodies, although some evidence suggests the shape may represent an artifact of sample preparation. The lipoprotein surface membrane surrounding the *Vaccinia virus* core and lateral bodies is about 12 nm thick and contains irregularly shaped surface tubules composed of small globular subunits. During natural infections, the virus is likely spread by that population of virus released from the cells (EEV). Although the internal structure of *Vaccinia virus* is revealed in thin sections, the detailed internal structure of parapoxvirus particles is less evident (Fig. 1). In negatively stained preparations of parapoxviruses, superimposition of dorsal and ventral views of the surface filament sometimes produces a distinctive “criss-cross” surface appearance.

Генетична карта вірусу PBCV-1



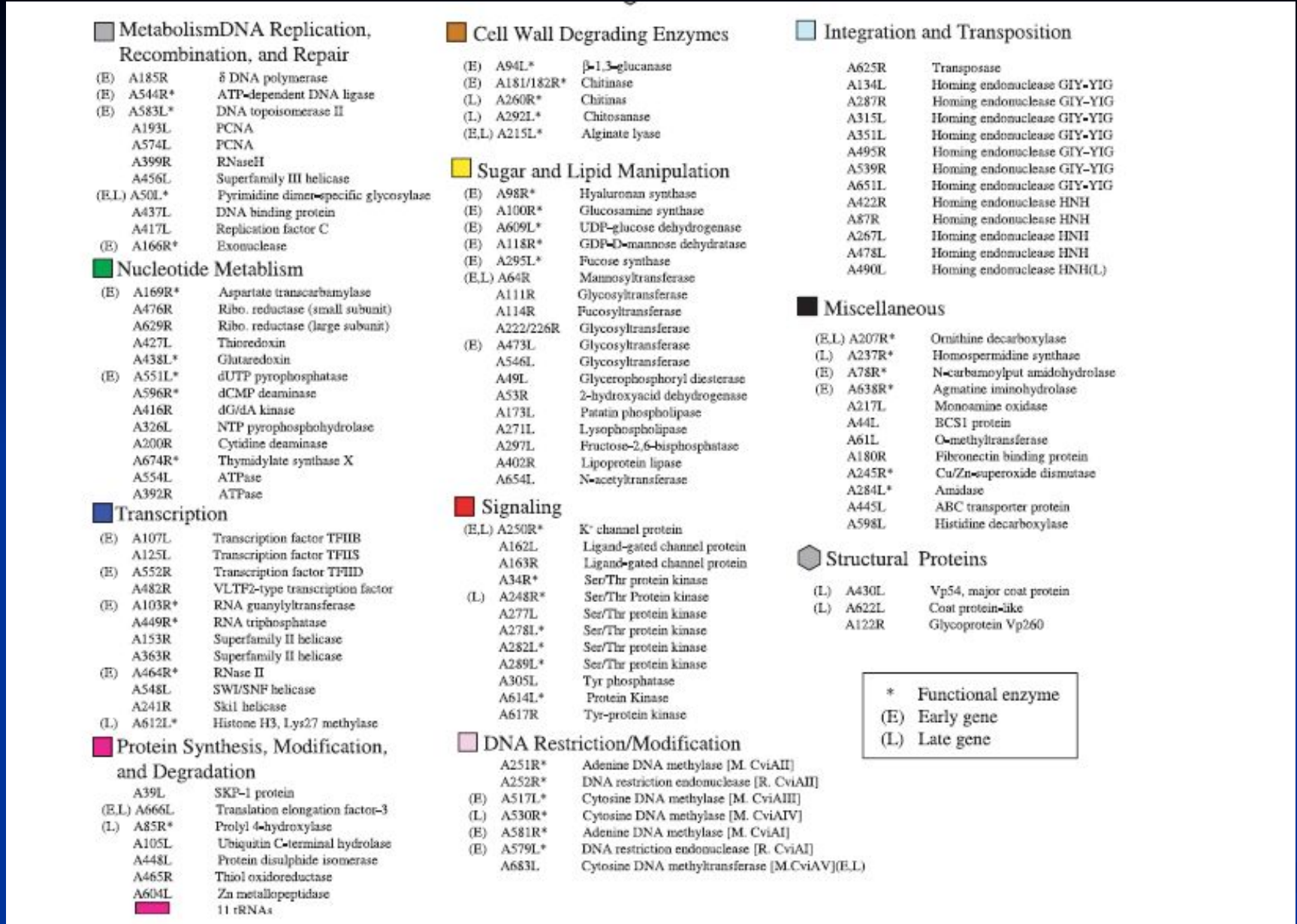


Fig. 2 Partial gene map of the PBCV-1 genome. Genes listed above the genome are transcribed from left to right (R, →), and genes listed below the genome are transcribed from right to left (L, ←). The genes that have similar or related function are assigned into the same group and are labelled by a code in the same colour. *Genes characterized and known to encode functional enzymes. (E) Genes transcribed early; (L) genes transcribed late. For many genes both the transcription patterns and the functions of gene products are unknown.