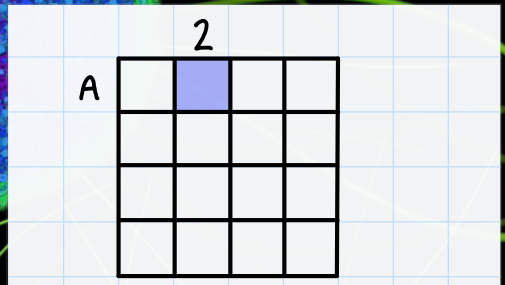
# A2.3 VIRUSES

| Guiding Questions |
| --- |
| How can viruses exist with so few genes? |
| In what ways do viruses vary? |

| Linking Questions |
| --- |
| What mechanisms contribute to convergent evolution? |
| To what extent is the natural history of life characterized by increasing complexity or simplicity? |




Theme: Unity and Diversity

Level of Organization: Cells

Written and drawn by:

Peter Marier

NOTEWORTHY SCIENCE
MARIER

https://pdb101.rcsb.org/sci-art/goodsell-gallery/bacteriophage-t4-infection

# HL LEARNING OUTCOMES

| | | |
|---|---|---|
| A2.3.1 | Structural features common to viruses | Relatively few features are shared by all viruses: small, fixed size; nucleic acid (DNA or RNA) as genetic material; a capsid made of protein; no cytoplasm; and few or no enzymes. |
| A2.3.2 | Diversity of structure in viruses | Students should understand that viruses are highly diverse in their shape and structure. Genetic material may be RNA or DNA, which can be either single- or double-stranded. Some viruses are enveloped in host cell membrane and others are not enveloped. Virus examples include bacteriophage lambda, coronaviruses and HIV. |
| A2.3.3 | Lytic cycle of a virus | Students should appreciate that viruses rely on a host cell for energy supply, nutrition, protein synthesis and other life functions. Use bacteriophage lambda as an example of the phases in a lytic cycle. |
| A2.3.4 | Lysogenic cycle of a virus | Use bacteriophage lambda as an example. |
| A2.3.5 | Evidence for several origins of viruses from other organisms | The diversity of viruses suggests several possible origins. Viruses share an extreme form of obligate parasitism as a mode of existence, so the structural features that they have in common could be regarded as convergent evolution. The genetic code is shared between viruses and living organisms. |
| A2.3.6 | Rapid evolution in viruses | Include reasons for very rapid rates of evolution in some viruses. Use two examples of rapid evolution: evolution of influenza viruses and of HIV. Consider the consequences for treating diseases caused by rapidly evolving viruses. |

HL

# A2.3.1 — Structural features common to viruses
# A2.3.2 — Diversity of structure in viruses

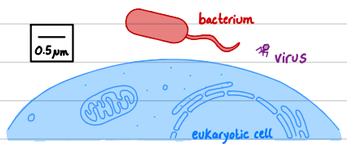
**Virus**: non-cellular infectious agent / parasite which replicates only inside of a living host cell. Viruses infect all life forms (including bacteria, plants and animals), can be species-specific or may 'jump' from species to another

↳ Viruses do not move or grow and rely on their hosts for metabolic processes and replication making them non-self sustaining and <u>not</u> considered alive origin of cells A2.1 Viruses are <u>obligate intracellular parasites</u>

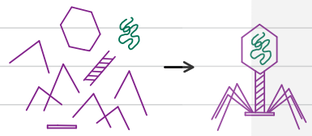
require a host cell for energy, nutrition, metabolism and replication

↳ Viruses display enormous diversity in both form and function, but they all share common structural features:

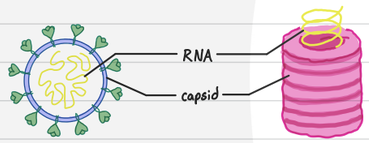
- <u>Small size</u>
  most viruses range from 20nm to 400nm, making them 100 - 1000x smaller than their hosts, allowing easier entry




- <u>fixed size</u>
  viruses do not grow over time. They remain the same size and complexity after being assembled in their host



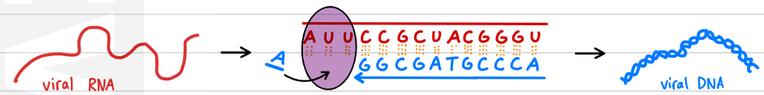
- <u>nucleic acid as genetic material</u>
  all viruses use DNA or RNA as genetic material using the same universal genetic code enabling translation to occur within host




- <u>capsid made of protein</u> (etymology: "box")
  genetic material is enclosed in a capsid (coat made of repeating protein subunits - capsomeres) before being released by host


- <u>no cytoplasm</u>
  all viruses lack a cytoplasm as they do not carry out their own metabolism, rather relying on host's - contributing to their small size

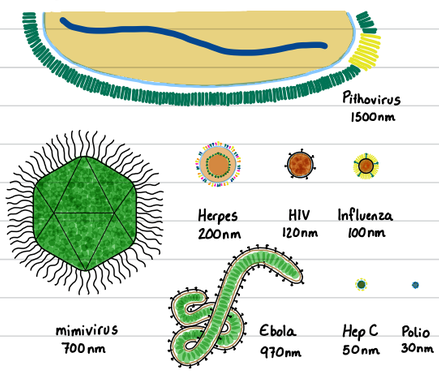
- <u>few or no enzymes</u>
  most enzymes lack their own enzymes, using those in their host instead. Some viruses have a few enzymes that are used to help in infection, lysis of host or replicating their genetic material



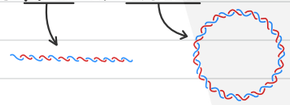

ex: reverse transcriptase in HIV

↳ Viruses are highly diverse in shape and structure:

- <u>vary in size</u>



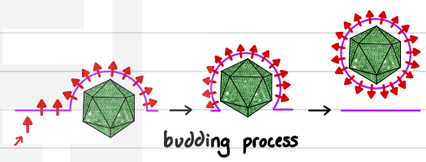

- <u>vary in genetic material</u>
  Viral genetic material can be double-stranded (ds) or single-stranded (ss) which can be negative-sense (-) serving as a template to mRNA or positive-sense (+) and may be translated directly into proteins
  Some also use reverse transcriptase (RT). ※ genetic material can also be <u>linear</u> or <u>circular</u>



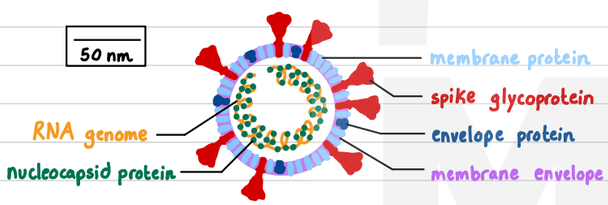
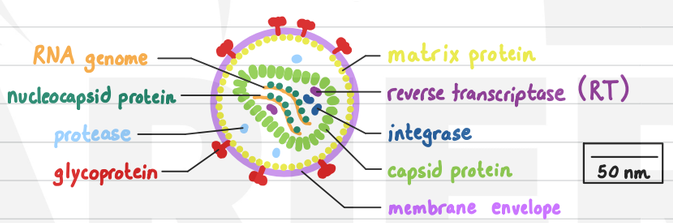
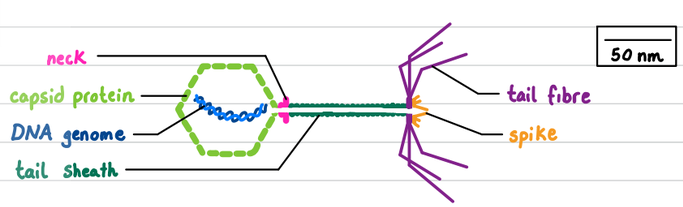
dsDNA → ex: herpes virus
+ssDNA → ex: HPV
dsRNA → ex: rotavirus
+ssRNA → (or via -ssRNA) ex: SARS-CoV-2, Polio virus
-ssRNA → ex: Ebola virus, influenza virus, rabies virus
+ssRNA-RT (RT) → ex: HIV
dsDNA-RT (RT) → ex: Hep-B virus

- <u>vary in shape</u>
  viruses vary in their capsid structure and overall shape:

ex: icosahedral, helical, complex



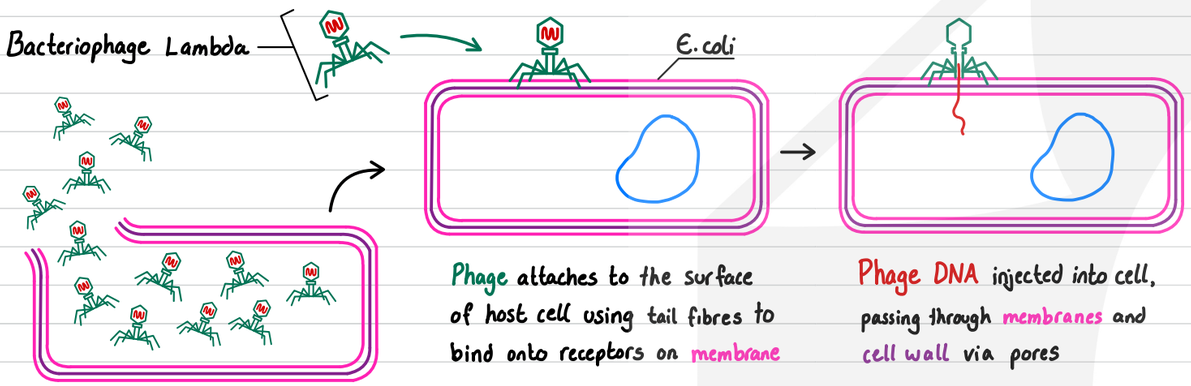

viruses may also be enveloped in their host's cell membrane during exocytosis (along with viral surface glycoproteins) allowing more protection and easier cell infection via binding

| | SARS-CoV-2 (Severe Acute Respiratory Syndrome Corona Virus 2) ("crown") | HIV (Human Immunodeficiency Virus) | Bacteriophage lambda (λ) |
|---|---|---|---|
| Genetic material | 1 copy of linear +ssRNA genome of ~30000 base pairs | 2 copies of linear +ssRNA genome of ~9700 base pairs | linear dsDNA genome of ~48000 base pairs with ss sticky ends |
| Structural features |   |   |   |
| Envelopment | Enveloped | Enveloped | Non-Enveloped |
| Host | Mammalian (human) epithelium cells in respiratory system | human white blood cells (helper T, macrophages, dendritic cells) | E. coli (gram-negative bacterium) |
| Associated disease | COVID-19 (COrona VIrus Disease of 2019) | AIDS (Acquired ImmunoDeficiency Syndrome) | |

HL

# A2.3.3—Lytic cycle of a virus. A.2.3.4—Lysogenic cycle of a virus A2.3.5—Evidence for several origins of viruses from other organisms. A2.3.6—Rapid evolution in viruses

**Lytic cycle** ("lysis"): virus reproduces within the host cell and the many new copies burst out, killing the host and spreading new viruses. Viruses in lytic cycle are <u>virulent</u> as they cause disease




**Lysogenic cycle**: virus integrates its genetic material into the host bacterium's genome Each time host replicates its DNA it will also replicate viral DNA, thus passing it onto daughter cells. Viruses in lysogenic cycle are temperate - not active/harmful to host, but stress could switch it to lytic cycle

※ viruses are extremely diverse in structure, complexity, and genome suggesting different potential origins:

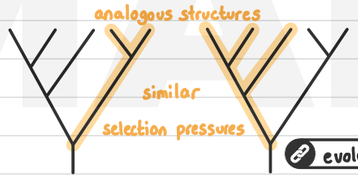
**Virus-first hypothesis**: viruses evolved from proteins and nucleic acid (RNA), which gave rise to first cells
- RNA is enzymatic, allowing it to self-replicate.
- ✕ viruses require a cellular host to replicate
- ✕ viruses share more protein structures in common with cells than each other

*least likely

**Progressive hypothesis**: viruses developed from genetic components (DNA, RNA) which 'escaped' from genes of a cell
- Retroviruses like HIV convert RNA to DNA using reverse transcriptase which then integrates within host genome. Retrotransposons within eukaryotes also transcribe into RNA and then DNA and integrate into new location in genome
- ✕ viruses have unique, complex structures not present in cells such as capsids

**Regressive hypothesis**: viruses developed from parasitic cells in a progressive loss of cellular components, becoming obligate
- Viruses such as Mimivirus are very large with a complex structure and large genome, similar to parasitic bacteria
- ✕ even very small cellular parasites do not resemble viruses

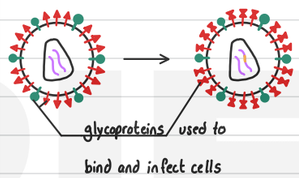
※ Since all viruses share an extreme form of obligate parasitism, their common structural features (analogous structures) may have arisen independently from convergent evolution: when species occupying a similar niche are subject to similar selection pressures and adapt similarly




evolution A4.1

Viruses undergo very rapid rates of **evolution**: change in heritable characteristics of a population evolution A4.1
- ↳ viruses reproduce very quickly resulting in short generation times - allows more selection over shorter timespan
- ↳ genetic variation (new alleles) arises from mutations. RNA Viruses have high mutation rates as their enzymes do not proofread during replication, resulting in many errors and new base sequences allowing potential adaptation
- ↳ natural selection acts on variation in populations resulting in adaptive advantageous features being more successful and selected, driving evolution. As viruses are parasites, hosts actively seek to destroy them leading to a constant, strong selection pressure and rapid evolutionary change natural selection D4.1

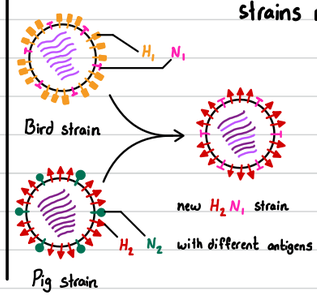
**Antigenic Drift**: genetic variation from accumulation of mutations resulting in new strain




ex: HIV and influenza virus
1. during viral RNA replication many errors are made, leading to mutations
2. some mutations may lead to new glycoproteins and strains

defence against disease C3.2

**Antigenic Shift**: recombination of different viral strains resulting in abrupt change



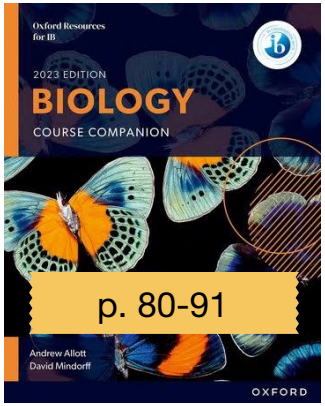

ex: Influenza virus
1. Avian and swine flu infect pig cells
2. RNA from each mix, forming new strain
3. new strain infects humans

※ As HIV and influenza's structure keep changing it poses a challenge for the immune system and treatments with drugs

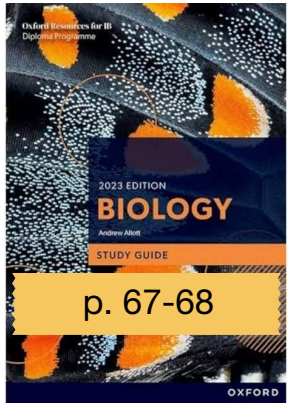
# Resource Links

each resource is hyperlinked

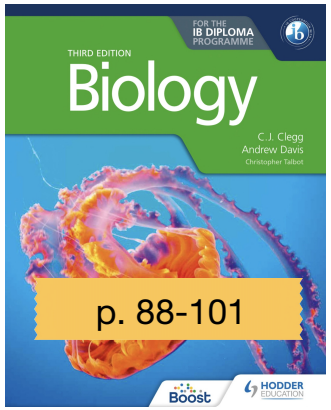
## Textbooks



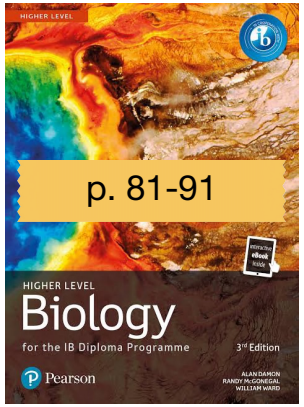
p. 80-91



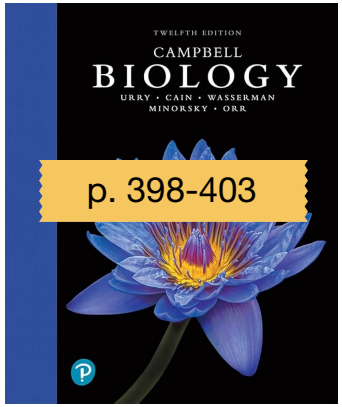
p. 67-68



p. 88-101



p. 81-91

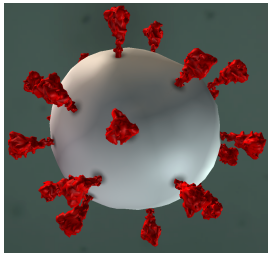


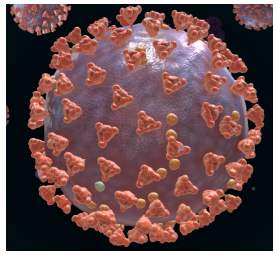
p. 398-403

## 3D models


HIV


T7 phage


SARS-CoV-2


SARS-CoV-2

## Articles


Carrat, F., & Flahault, A. (2007). Influenza vaccine: the challenge of antigenic drift. Vaccine, 25(39-40), 6852–6862. https://doi.org/10.1016/j.vaccine.2007.07.027

Koonin, E. V., Krupovic, M., & Agol, V. I. (2021). The Baltimore classification of viruses 50 years later: How does it stand in the light of virus evolution? Microbiology and Molecular Biology Reviews, 85(3). https://doi.org/10.1128/mmbr.00053-21

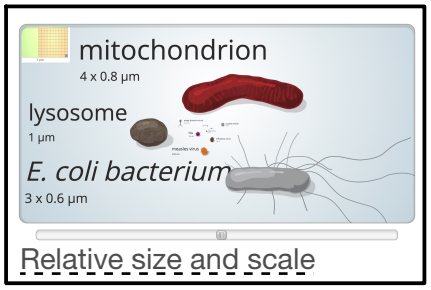
Li, F., Hou, C. D., Lokareddy, R. K., Yang, R., Forti, F., Briani, F., & Cingolani, G. (2023). High-resolution cryo-EM structure of the Pseudomonas bacteriophage E217. Nature Communications, 14(1). https://doi.org/10.1038/s41467-023-39756-z

Nasir, A., Kim, K. M., & Caetano-Anollés, G. (2012). Viral evolution. Mobile Genetic Elements, 2(5), 247–252. https://doi.org/10.4161/mge.22797

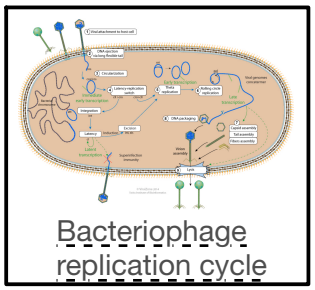
Origin of Viruses | Learn Science at Scitable. (n.d.). https://www.nature.com/scitable/topicpage/the-origins-of-viruses-14398218/#

Petrova, V. N., & Russell, C. A. (2017b). The evolution of seasonal influenza viruses. Nature Reviews Microbiology, 16(1), 47–60. https://doi.org/10.1038/nrmicro.2017.118


## Simulators / Interactives



Relative size and scale


Bacteriophage replication cycle