Rhabdovirus:

Rhabdovirions are enveloped, with bullet-shaped and bacilliform geometries. These virions are about 75 nm wide and 180 nm long.[[1]](https://en.wikipedia.org/wiki/Rhabdoviridae#cite_note-ViralZone-1) Rhabdoviruses have helical nucleocapsids and their genomes are linear, around 11–15 kb in length.[[1]](https://en.wikipedia.org/wiki/Rhabdoviridae#cite_note-ViralZone-1) Rhabdoviruses carry their genetic material in the form of negative-sense single-stranded [RNA](https://en.wikipedia.org/wiki/RNA). They typically carry genes for five proteins: large protein (L), glycoprotein (G), nucleoprotein (N), phosphoprotein (P), and matrix protein (M). Rhabdoviruses that infect vertebrates (especially mammals and fishes), plants, and insects are usually bullet-shaped.[[*citation needed*](https://en.wikipedia.org/wiki/Wikipedia:Citation_needed)],[[3]](https://en.wikipedia.org/wiki/Rhabdoviridae#cite_note-Nicholas_2007_175–187-3) However, in contrast to paramyxoviruses, rhabdoviruses do not have hemagglutinating and neuraminidase activities.[[3]](https://en.wikipedia.org/wiki/Rhabdoviridae#cite_note-Nicholas_2007_175–187-3)

Filovirus

A virus that fulfills the criteria for being a member of the order [*Mononegavirales*](https://en.wikipedia.org/wiki/Mononegavirales) is a member of the family Filoviridae if:

it causes [viral hemorrhagic fever](https://en.wikipedia.org/wiki/Viral_hemorrhagic_fever) in certain [primates](https://en.wikipedia.org/wiki/Primate)

it infects [primates](https://en.wikipedia.org/wiki/Primate), [pigs](https://en.wikipedia.org/wiki/Pig) or [bats](https://en.wikipedia.org/wiki/Bat) in [nature](https://en.wikipedia.org/wiki/Nature)

it needs to be [adapted](https://en.wikipedia.org/wiki/Adaptation) through [serial passage](https://en.wikipedia.org/wiki/Serial_passage) to cause [disease](https://en.wikipedia.org/wiki/Disease) in [rodents](https://en.wikipedia.org/wiki/Rodent)

it exclusively replicates in the [cytoplasm](https://en.wikipedia.org/wiki/Cytoplasm) of a [host](https://en.wikipedia.org/wiki/Host_(biology)) [cell](https://en.wikipedia.org/wiki/Cell_(biology))

it has a [genome](https://en.wikipedia.org/wiki/Genome) ≈19 [kb](https://en.wikipedia.org/wiki/Base_pair) in length

it has an [RNA](https://en.wikipedia.org/wiki/RNA) genome that constitutes ≈1.1% of the virion mass

its genome has a [molecular weight](https://en.wikipedia.org/wiki/Molecular_mass) of ≈4.2×106

its genome contains one or more [gene overlaps](https://en.wikipedia.org/wiki/Overlapping_gene)

its genome contains seven genes in the order [3'-UTR](https://en.wikipedia.org/wiki/Three_prime_untranslated_region)-NP-VP35-VP40-GP-VP30-VP24-L-[5'-UTR](https://en.wikipedia.org/wiki/Five_prime_untranslated_region)

its VP24 gene is not [homologous](https://en.wikipedia.org/wiki/Homology_(biology)) to genes of other [mononegaviruses](https://en.wikipedia.org/wiki/Mononegavirales)

its genome contains [transcription](https://en.wikipedia.org/wiki/Transcription_(genetics)) initiation and termination signals not found in genomes of other mononegaviruses

it forms nucleocapsids with a [buoyant density](https://en.wikipedia.org/wiki/Buoyancy) in [CsCl](https://en.wikipedia.org/wiki/Caesium_chloride) of ≈1.32 g/cm3

it forms nucleocapsids with a central axial channel (≈10–15 nm in width) surrounded by a dark layer (≈20 nm in width) and an outer helical layer (≈50 nm in width) with a cross striation (periodicity of ≈5 nm)

it expresses a class I fusion [glycoprotein](https://en.wikipedia.org/wiki/Glycoprotein) that is highly N- and O-[glycosylated](https://en.wikipedia.org/wiki/Glycosylation) and [acylated](https://en.wikipedia.org/wiki/Acylation) at its cytoplasmic tail

it expresses a primary [matrix protein](https://en.wikipedia.org/wiki/Viral_matrix_protein) that is not glycosylated

it forms virions that bud from the [plasma membrane](https://en.wikipedia.org/wiki/Cell_membrane)

it forms virions that are predominantly filamentous (U- and 6-shaped) and that are ≈80 nm in width, and several hundred nm and up to 14 μm in length

it forms virions that have surface projections ≈7 nm in length spaced ≈10 nm apart from each other

it forms virions with a [molecular mass](https://en.wikipedia.org/wiki/Molecular_mass) of ≈3.82×108; an [S20W](https://en.wikipedia.org/wiki/Svedberg) of at least 1.40; and a [buoyant density](https://en.wikipedia.org/wiki/Buoyancy) in [potassium tartrate](https://en.wikipedia.org/wiki/Potassium_tartrate) of ≈1.14 g/cm3

it forms virions that are poorly [neutralized](https://en.wikipedia.org/wiki/Neutralisation_(immunology)) [*in vivo*](https://en.wikipedia.org/wiki/In_vivo)

orthomyxovirus

Viruses of this family contain 6 to 8 segments of linear [negative-sense](https://en.wikipedia.org/wiki/Sense_(molecular_biology)) single stranded RNA.[[32]](https://en.wikipedia.org/wiki/Orthomyxoviridae#cite_note-32)

The total genome length is 12000–15000 [nucleotides](https://en.wikipedia.org/wiki/Nucleotide) (nt). The size of each segment is as follows:

|  |  |  |  |
| --- | --- | --- | --- |
| **segment** | **protein** | **size (nt)** | **protein size (aa)** |
| PB1 | polymerase | 2300–2500 | 757+87 (F2) |
| PB2 | polymerase | 2300–2500 | 759 |
| PA | polymerase | 2200–2300 | 716 |
| HA | Hemagglutinin | 1700–1800 | 550 |
| NP | nucleoprotein | 1500–1600 | 498 |
| NA | Neuraminidase | 1400–1500 | 454 |
| M | Membrane protein(s) | 1000–1100 | 252+97 |
| NS | non-structural protein(s) | 800–900 | 230+121 |

The Genome sequence has terminal repeated sequences; repeated at both ends. Terminal repeats at the 5'-end 12–13 nucleotides long. Nucleotide sequences of 3'-terminus identical; the same in genera of same family; most on RNA (segments), or on all RNA species. Terminal repeats at the 3'-end 9–11 nucleotides long. Encapsidated nucleic acid is solely genomic. Each virion may contain defective interfering copies. In Influenza A (H1N1) **PB1-F2** is produced from an alternative reading frame in PB1. The **M** and **NS** genes produce 2 different genes via [alternative splicing](https://en.wikipedia.org/wiki/Alternative_splicing).[[33]](https://en.wikipedia.org/wiki/Orthomyxoviridae#cite_note-33)

The following applies for [Influenza A viruses](https://en.wikipedia.org/wiki/Influenza_A_virus), although other influenza strains are very similar in structure:[[34]](https://en.wikipedia.org/wiki/Orthomyxoviridae#cite_note-34)

The influenza A virus particle or *virion* is 80–120 nm in diameter and usually roughly spherical, although filamentous forms can occur.[[35]](https://en.wikipedia.org/wiki/Orthomyxoviridae#cite_note-35) Unusually for a virus, the influenza A [genome](https://en.wikipedia.org/wiki/Genome) is not a single piece of nucleic acid; instead, it contains eight pieces of segmented negative-sense [RNA](https://en.wikipedia.org/wiki/RNA) (13.5 kilobases total), which encode 11 proteins (HA, NA, NP, M1, M2, NS1, NEP, PA, PB1, PB1-F2, PB2).[[36]](https://en.wikipedia.org/wiki/Orthomyxoviridae#cite_note-Ghedin-36) The best-characterised of these viral proteins are [hemagglutinin](https://en.wikipedia.org/wiki/Hemagglutinin) and [neuraminidase](https://en.wikipedia.org/wiki/Neuraminidase), two large [glycoproteins](https://en.wikipedia.org/wiki/Glycoprotein) found on the outside of the viral particles. Neuraminidase is an [enzyme](https://en.wikipedia.org/wiki/Enzyme) involved in the release of [progeny](https://en.wikipedia.org/wiki/Offspring) virus from infected cells, by cleaving sugars that bind the mature viral particles. By contrast, hemagglutinin is a [lectin](https://en.wikipedia.org/wiki/Lectin) that mediates binding of the virus to target cells and entry of the viral genome into the target cell.[[37]](https://en.wikipedia.org/wiki/Orthomyxoviridae#cite_note-37) The hemagglutinin (H) and neuraminidase (N) [proteins](https://en.wikipedia.org/wiki/Protein) are targets for antiviral drugs.[[38]](https://en.wikipedia.org/wiki/Orthomyxoviridae#cite_note-38) These proteins are also recognised by [antibodies](https://en.wikipedia.org/wiki/Antibody), i.e. they are [antigens](https://en.wikipedia.org/wiki/Antigen).[[15]](https://en.wikipedia.org/wiki/Orthomyxoviridae#cite_note-Hilleman-15) The responses of antibodies to these proteins are used to classify the different [serotypes](https://en.wikipedia.org/wiki/Serotype) of influenza A viruses, hence the *H* and *N* in *H5N1*

Paramyxovirus

Virions are enveloped and can be spherical, filamentous or pleomorphic. The diameter is around 150 nm. Genomes are linear, around 15kb in length.[[2]](https://en.wikipedia.org/wiki/Paramyxoviridae#cite_note-ViralZone-2) Fusion proteins and attachment proteins appear as spikes on the virion surface. Matrix proteins inside the envelope stabilise virus structure. The nucleocapsid core is composed of the genomic RNA, nucleocapsid proteins, phosphoproteins and polymerase proteins.

| **Genus** | **Structure** | **Symmetry** | **Capsid** | **Genomic arrangement** | **Genomic segmentation** |
| --- | --- | --- | --- | --- | --- |
| *Avulavirus* | Spherical |  | Enveloped | Linear | Monopartite |
| *Morbillivirus* | Spherical |  | Enveloped | Linear | Monopartite |
| *Aquaparamyxovirus* | Spherical |  | Enveloped | Linear | Monopartite |
| *Henipavirus* | Spherical |  | Enveloped | Linear | Monopartite |
| *Respirovirus* | Spherical |  | Enveloped | Linear | Monopartite |
| *Rubulavirus* | Spherical, Filamentous |  | Enveloped | Linear | Monopartite |
| *Ferlavirus* | Spherical |  | Enveloped | Linear | Monopartite |

**Genome structure[**[**edit**](https://en.wikipedia.org/w/index.php?title=Paramyxoviridae&action=edit&section=5)**]**

The [genome](https://en.wikipedia.org/wiki/Genome) is non-segmented negative-sense RNA, 15–19 kilobases in length and contains 6–10 genes. Extracistronic (non-coding) regions include:

A 3’ leader sequence, 50 [nucleotides](https://en.wikipedia.org/wiki/Nucleotides) in length, which acts as a [transcriptional](https://en.wikipedia.org/wiki/Transcription_(genetics)) promoter.

A 5’ trailer sequence, 50–161 nucleotides long

Intergenomic regions between each [gene](https://en.wikipedia.org/wiki/Gene), which are three nucleotides long for morbilliviruses, respiroviruses and henipaviruses, and variable length (1-56 nucleotides) for rubulaviruses.

Each gene contains transcription start/stop signals at the beginning and end, which are transcribed as part of the gene.

Gene sequence within the genome is conserved across the family due to a phenomenon known as transcriptional polarity (see [*Mononegavirales*](https://en.wikipedia.org/wiki/Mononegavirales)) in which genes closest to the 3’ end of the genome are transcribed in greater abundance than those towards the 5’ end. This is a result of structure of the genome. After each gene is transcribed, the RNA-Dependent RNA polymerase pauses to release the new mRNA when it encounters an intergenic sequence. When the RNA polymerase is paused, there is a chance that it will dissociate from the RNA genome. If it dissociates, it must reenter the genome at the leader sequence, rather than continuing to transcribe the length of the genome. The result is that the further downstream genes are from the leader sequence, the less they will be transcribed by RNA polymerase.

Evidence for a single promoter model was verified when viruses were exposed to UV light. UV radiation can cause dimerization of RNA, which prevents transcription by RNA polymerase. If the viral genome follows a multiple promoter model, the level inhibition of transcription should correlate with the length of the RNA gene. However, the genome was best described by a single promoter model. When paramyxovirus genome was exposed to UV light, the level of inhibition of transcription was proportional to the distance from the leader sequence. That is, the further the gene is from the leader sequence, the greater the chance of RNA dimerization inhibiting RNA polymerase.

The virus takes advantage of the single promoter model by having its genes arranged in relative order of protein needed for successful infection. For example, nucleocapsid protein, N, is needed in greater amounts than RNA polymerase, L.

Viruses in the *Paramyxoviridae* family are also antigenically stable, meaning that the glycoproteins on the viruses are consistent between different strains of the same type. There are two reasons for this phenomenon. The first is that the genome is non-segmented and thus cannot undergo [genetic reassortment](https://en.wikipedia.org/wiki/Reassortment). In order for this process to occur, segments are needed as reassortment happens when segments from different strains are mixed together to create a new strain. With no segments, nothing can be mixed with one another and so there is no [antigenic shift](https://en.wikipedia.org/wiki/Antigenic_shift). The second reason relates to the idea of [antigenic drift](https://en.wikipedia.org/wiki/Antigenic_drift). Since RNA dependent RNA polymerase does not have an error checking function, many mutations are made when the RNA is processed. These mutations build up and eventually new strains are created. Due to this concept, one would expect that paramyxoviruses should not be antigenically stable; however, the opposite is seen to be true. The main hypothesis behind why the viruses are antigenically stable is that each protein and amino acid has an important function. Thus, any mutation would lead to a decrease or total loss of function, which would in turn cause the new virus to be less efficient. These viruses would not be able to survive as long compared to the more virulent strains, and so would die out.

Many paramyxovirus genomes follow the ["rule of six"](https://en.wikipedia.org/wiki/Rule_of_six_(viruses)). The total length of the genome is almost always a multiple of six. This is probably due to the advantage of having all RNA bound by N protein (since N binds hexamers of RNA). If RNA is left exposed, the virus does not replicate efficiently. Members of the sub-family Pneumovirinae do not follow this rule

The gene sequence is:

Nucleocapsid – Phosphoprotein – Matrix – Fusion – Attachment – Large (polymerase)