

# Cell Atlas

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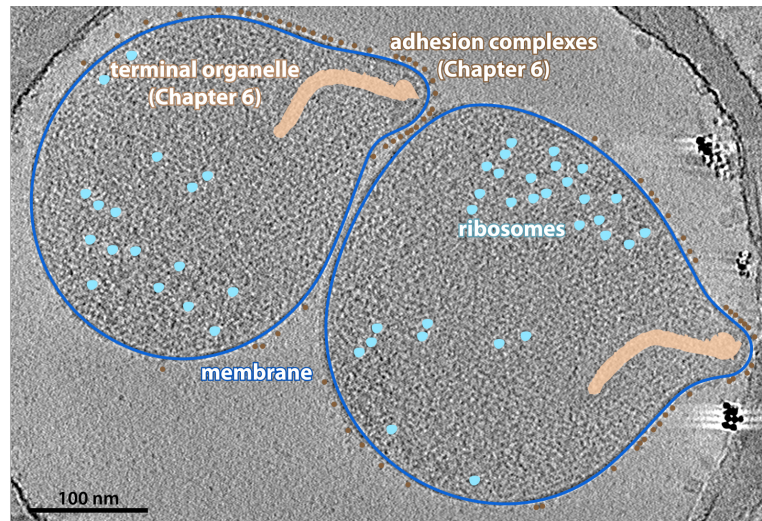
# Chapter 1

## Introduction

The fundamental unit of life is the cell – a contained self-replicating assembly. For many species, including all bacteria and archaea, the organism consists of a single cell. And for nearly all species, no matter how many cells an organism eventually contains (probably around 10 trillion in your case), it started life as a single cell. As you’ll see, the details of these cells vary, but every cell on Earth is the same at heart – a DNA-based replicator machine built from four macromolecules: nucleic acids, proteins, lipids and carbohydrates.

Imagine that you’re a structural engineer tasked with building one of these cells. What’s the first step? Let’s start with the container. No matter what the first self-replicating molecules were (likely RNA), they didn’t constitute a cell until they became packaged in a container. You’d probably want a flexible container that allowed you to sort a subset of molecules from the environment. Evolution agrees. All cells are enclosed by a selectively permeable membrane, made of lipids and proteins Schematic – Lipid bilayer, that allows them to differentiate their contents from the environment. This selectivity is a critical feature for the life of the cell Schematic – ATP synthase. The compartment enclosed by a cell’s membrane is called the cytoplasm (“cell mold,” the membrane being the container for the mold).

Almost all archaea and many bacteria, like these *Mycoplasma genitalium* cells, are monoderms (“single skin”). This means that their cytoplasm is enclosed by a single membrane. At the resolution of this image, the membrane looks like a single dark line, but remember that it’s really a bilayer, as you’ll see in some later images.



Video goes above.

## Chapter 2

# Schematic – Lipid bilayer

You can label chapter and section titles using `{#label}` after them, e.g., we can reference Chapter 2. If you do not manually label them, there will be automatic labels anyway, e.g., Chapter 4.

Figures and tables with captions will be placed in `figure` and `table` environments, respectively.

```
par(mar = c(4, 4, .1, .1))
plot(pressure, type = 'b', pch = 19)
```

Reference a figure by its code chunk label with the `fig:` prefix, e.g., see Figure 2.1. Similarly, you can reference tables generated from `knitr::kable()`, e.g., see Table 2.1.

```
knitr::kable(
  head(iris, 20), caption = 'Here is a nice table!',
  booktabs = TRUE
)
```

You can write citations, too. For example, we are using the **bookdown** package (Xie, 2019) in this sample book, which was built on top of R Markdown and **knitr** (Xie, 2015).



Figure 2.1: Here is a nice figure!

Table 2.1: Here is a nice table!

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
5.1	3.5	1.4	0.2	setosa
4.9	3.0	1.4	0.2	setosa
4.7	3.2	1.3	0.2	setosa
4.6	3.1	1.5	0.2	setosa
5.0	3.6	1.4	0.2	setosa
5.4	3.9	1.7	0.4	setosa
4.6	3.4	1.4	0.3	setosa
5.0	3.4	1.5	0.2	setosa
4.4	2.9	1.4	0.2	setosa
4.9	3.1	1.5	0.1	setosa
5.4	3.7	1.5	0.2	setosa
4.8	3.4	1.6	0.2	setosa
4.8	3.0	1.4	0.1	setosa
4.3	3.0	1.1	0.1	setosa
5.8	4.0	1.2	0.2	setosa
5.7	4.4	1.5	0.4	setosa
5.4	3.9	1.3	0.4	setosa
5.1	3.5	1.4	0.3	setosa
5.7	3.8	1.7	0.3	setosa
5.1	3.8	1.5	0.3	setosa



## Chapter 3

# Schematic - ATP synthase

Here is a review of existing methods.



## Chapter 4

# Methods

We describe our methods in this chapter.



## Chapter 5

# Applications

Some *significant* applications are demonstrated in this chapter.

### 5.1 Example one

### 5.2 Example two



## Chapter 6

# Final Words

We have finished a nice book.





# Bibliography

Xie, Y. (2015). *Dynamic Documents with R and knitr*. Chapman and Hall/CRC, Boca Raton, Florida, 2nd edition. ISBN 978-1498716963.

Xie, Y. (2019). *bookdown: Authoring Books and Technical Documents with R Markdown*. R package version 0.14.