

Coronavirus at molecular level [16–18]

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This activity looks at the biochemistry of the SARS-CoV-2 coronavirus.

1. a. Below is a description of a single SARS-CoV-2 virion:

Each SARS-CoV-2 virion is a spherical particle with surface projections or spikes. Each has four structural proteins known as the spike (S), envelope (E), membrane (M) and nucleocapsid (N) proteins.

The nucleocapsid protein holds the RNA genome in the centre of the virion. Surrounding the nucleocapsid is a viral envelope. This consists of a lipid bilayer where the membrane, envelope and spike proteins are anchored.

The spike protein is the protein responsible for allowing the virus to attach to and fuse with the membrane host cell.

Use the description to add the following labels to the diagram of a SARS-CoV-2 virion in **Figure 1**.



Figure 1

- b. The shape of proteins is vital to their function.
 - i. Name and describe the four levels of protein structure
 - ii. Describe three types of interaction that result in the three-dimensional structure of proteins.

Explain how each interaction occurs.

2. The SARS-CoV-2 is an RNA virus. It uses single stranded RNA as its genetic material.

Figure 2 shows a single RNA nucleotide.



OH OH

Figure 2

- a. Describe how an RNA nucleotide differs from a nucleotide of DNA.
- RNA nucleotides polymerise to form a polymer chain in a similar way to DNA.
 Circle on Figure 2 the atoms lost during the polymerisation process and explain why this is an example of condensation polymerisation.
- c. RNA stands for ribonucleic acid. Explain why RNA is described as an acid.
- 3. Another RNA virus is influenza or flu. However SARS-CoV-2 is much more contagious.

In a TV interview Dr Hugh Montgomery, an intensive care medicine professor explained how a single person with flu will on average infect 1.3 people, whereas a single person with coronavirus will go on to infect approximately 3 people. He calculated that if each person with flu passes the infection on to 1.3 people this would result in roughly 14 people getting the virus after 10 transmissions. However for coronavirus, after 10 transmissions 59 000 people would be infected.

Show mathematically how he came to these conclusions.

Answers



b. i. **primary structure** = the sequence of amino acids in a polypeptide chain

secondary structure = the local folded structures that form within a polypeptide chain. The most common types of secondary structures are the α helix and the β pleated sheet.

tertiary structure = the three-dimensional folding pattern of a polypeptide chain

quaternary structure = when proteins are made up of more than one polypeptide chain, the arrangement of these polypeptide chains is called a protein's quaternary structure.

ii. **hydrogen bonding** between a lone pair on the oxygen atom of a C=O group and a H atom covalently bonded to N

ionic attraction between charged groups on the <u>side chains</u> of amino acids eg between the $-COO^{-}$ on glutamic acid and $-NH_{3}^{+}$ on lysine

disulfide linkages formed between sulfur containing side chains on cysteines

- 2. a. [1] Thymine is one of the four possible nitrogenous bases in DNA. In RNA is it replaced by uracil.
 - [2] RNA has a hydroxy group (OH) in the 2' position on the pentose ring which isn't present in DNA.
 - b.



where \mathbf{A} = adenine, \mathbf{C} = cytosine, \mathbf{G} = guanine and \mathbf{U} = uracil

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Polymerisation of the nucleotides to form RNA is an example of condensation polymerisation because one molecule of water is eliminated for each nucleotide added.

- c. The phosphate OH group is acidic and readily donates a proton, hence why DNA is acidic.
- 3. Influenza number of people infected after 10 transmissions if each transmission affects approx.
 1.3 people = 1.3¹⁰ = 13.78 or 14 people

Coronavirus– number of people infected after 10 transmissions if each transmission affects approx. 3 people = 3^{10} = **59 049 people**