

1. Which statement about bile is correct?

- ☐ It is a protease
- ☐ It emulsifies lipids
- ☐ It breaks every nutrient into monomers

2. Why blot all samples before the final weighing?

- ☐ To remove surface solution consistently
- ☐ To stop all molecular movement
- ☐ To make every final mass equal

3. Which change can leave the amino-acid sequence unchanged?

- ☐ A substitution producing a synonymous codon
- ☐ Every deletion of one base
- ☐ Every insertion of one base

4. Which comparison of two cell images is reliable?

- ☐ Compare screen lengths only
- ☐ Convert both lengths using their own scale bars
- ☐ Assume both images have the same zoom

5. What does a 25% probability in $Aa \times Aa$ mean?

- ☐ Exactly one of every four siblings must be aa
- ☐ Each fertilization has probability one quarter of aa under this model
- ☐ The fourth child must be aa

6. A fixed endpoint takes 50 s. Calculate the rate proxy $1/\text{time}$.

_____ $1/\text{s}$

7. A 40 cm reading has an absolute uncertainty of 1 cm. Find percentage uncertainty.

_____ %

8. 9.0 cubic centimetres of gas are collected in 3.0 minutes. Find the rate.

_____ cm^3/min

10. A value rises from 4.0 to 5.0. Calculate the percentage increase.

_____ %

1. It emulsifies lipids

Bile is made in the liver and emulsifies lipids: it breaks large fat droplets into smaller ones, increasing the surface area for lipase. Bile is not an enzyme, so it is not a protease, and it digests nothing itself, so it cannot break nutrients into monomers.

2. To remove surface solution consistently

Blotting removes solution clinging to the surface, which is not water that entered the tissue. Doing it the same way for every cylinder keeps the comparison fair; blotting cannot stop molecular movement and is not meant to equalise masses.

3. A substitution producing a synonymous codon

The genetic code is degenerate: several codons can specify the same amino acid, so a substitution that produces a synonymous codon leaves the sequence unchanged. Deleting or inserting one base shifts the reading frame and changes every downstream codon.

4. Convert both lengths using their own scale bars

Reliable comparison needs a shared real scale. Converting each image length with its own scale bar gives real sizes that can be compared; screen lengths alone depend on zoom, which differs between the images.

5. Each fertilization has probability one quarter of aa under this model

The 25% is a probability for each fertilization under the model: each child of Aa x Aa parents has a one-quarter chance of aa. Chance has no memory, so no fixed number of aa children is guaranteed in any family of four.

6. 0.02 1/s

The result is 0.02 1/s. Known: the endpoint is reached in 50 s. Use rate proxy = 1/time. Rate proxy = 1/50 = 0.02 per second. This proxy is comparable with the 40 s worked case (0.025 per second) only because the same endpoint definition is used.

7. 2.5 %

The result is 2.5 %. Known: reading 40 cm; absolute uncertainty 1 cm. Use percentage uncertainty = absolute uncertainty / value x 100. Percentage uncertainty = 1/40 x 100 = 2.5%. Smaller measured values carry larger percentage uncertainties for the same absolute uncertainty.

8. 3 cm³/min

The result is 3 cm³/min. Known: 9.0 cubic centimetres of gas collected in 3.0 minutes. Use rate = volume / time. Rate = 9.0/3.0 = 3.0 cubic centimetres per minute. This is an average rate over the collection interval.

9. 20

The result is 20 . Known: 12 cases among 600 people. Use rate per 1,000 = cases / population x 1,000. Rate = 12/600 x 1,000 = 20 cases per 1,000 people. Rates per equal population size allow a fair comparison between groups of different size.

The result is 25 %. Known: the value rises from 4.0 to 5.0 units. Increase = final - initial = 5.0 - 4.0 = 1.0 unit. Use percentage increase = increase / initial x 100. Percentage increase = 1.0/4.0 x 100 = 25%. The change is evidence of a disturbance, not a diagnosis by itself.