- **Q1:** What percentage of structures in the PDB are solved by X-Ray and Electron Microscopy.

  92.5%

- **Q2:** What proportion of structures in the PDB are protein?

  97.8%

- **Q3:** Type HIV in the PDB website search box on the home page and determine how many HIV-1 protease structures are in the current PDB?

  4486

- **Q4**: Water molecules normally have 3 atoms. Why do we see just one atom per water molecule in this structure?

  We only see one atom because the other two atoms are bonded

- **Q5**: There is a conserved water molecule in the binding site. Can you identify this water molecule? What residue number does this water molecule have (see note below)?

  ASP25:CG

- Q7: How many amino acid residues are there in this pdb object?

  198

- Q8: Name one of the two non-protein residues?

  HOH and MK1

- Q9: How many protein chains are in this structure?

  2

- Q10. Which of the packages above is found only on BioConductor and not CRAN?

  Biocmanager

- Q11. Which of the above packages is not found on BioConductor or CRAN?:

  devtools

- Q12. True or False? Functions from the devtools package can be used to install packages from GitHub and BitBucket?

  TRUE

- Q13. How many amino acids are in this sequence, i.e. how long is this sequence?

  214