4

Homogenate Sample Analysis

Nadège Presneau, Abdul Hye, and Nicholas Ashton

Chapter summary

In this chapter we have:

- Introduced a range of techniques that can be used for the identification of nucleic acids and proteins/peptides in homogenate sample preparations.
- Described the different molecular techniques developed around PCR.
- Described microarrays technologies for the high throughput investigation of whole genomes or transcriptomes.
- Provided descriptions of Western blot, ELISA and 2-DGE methods for the identification of proteins.
- Outlined the principles of mass spectrometry and described the various protocols that can be employed.
- Discussed methodological options for the investigation of post-translational modifications.
- Considered ways in which nucleic acids and proteins can be quantified using these methods.
- Provided examples of the application of the technologies in the context of molecular diagnosis and the understanding of disease processes.