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1.4.3.3 Regulation of transcription elongation in eukaryotes1.4.3.4 Conclusions; 1.4.4 Differential/alternative pre-mRNA splicing; 1.4.5 Trans-RNA splicing; 1.4.6 Regulation of mRNA transport; 1.4.7 Directed intracellular mRNA localisation; 1.4.8 Regulation of mRNA polyadenylation; 1.4.9 Antisense RNA; 1.4.10 RNA editing; 1.4.11 Summary and conclusions; 1.5 Post-translational modification of proteins; 1.5.1 Introduction; 1.5.2 Proteolytic cleavage of proteins; 1.5.3 Acylation; 1.5.4 Prenylation; 1.5.5 Methylation; 1.5.6 Sulphation; 1.5.7 Phosphorylation; 1.5.8 Ubiquitination
1.5.9 Glycosylation1.5.10 Conclusions; 1.6 Correlation of mRNA and protein expression; 1.6.1 Introduction; 1.6.2 Levels of mRNA and protein expression: correlations and discrepancies; 1.6.3 Conclusions; 1.7 Housekeeping genes, internal and external standards; 1.7.1 What are housekeeping genes?; 1.7.2 Survey of the most important housekeeping genes; 1.7.2.1 Glyceraldehyde-3-phosphate dehydrogenase; 1.7.2.2 -Actin; 1.7.3 Other commonly used housekeeping genes; 1.7.3.1 Ribosomal RNA (rRNA); 1.7.4 New identified 'maintenance genes'; 1.7.5 Methods of quantification
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2.2.3 Surface affinity chromatography

Sommario/riassunto

This book combines the experience of 225 experts on 900 pages. Scientists worldwide are currently overwhelmed by the ever-increasing number and diversity of genome projects. This handbook is your guide through the jungle of new methods and techniques available to analyse gene expression - the first to provide such a broad view of the measurement of mRNA and protein expression in vitro, in situ and even in vivo. Despite this broad approach, detail is sufficient for you to grasp the principles behind each method. In each case, the authors weigh up the advantages and disadvantages, paying parti