1.	Record Nr.	UNINA990007909590403321
	Autore	Bernardus Claraevallensis <1091-20 aug. 1153>
	Titolo	Trattati / san Bernardo
	Pubbl/distr/stampa	Milano : Scriptorium Claravallense-Fondazione di studi cistercensi, 1984
	ISBN	88-311-9180-2
	Descrizione fisica	LXIV, 954 p. ; 24 cm
	Disciplina	240
	Locazione	DFD FLFBC
	Collocazione	XI CL S 17(1) 230.2 BER 1 (1)
	Lingua di pubblicazione	Italiano Latino
	Formato	Materiale a stampa
	Livello bibliografico	Monografia

2. Record Nr.	UNINA9910146242103321
Titolo	Analysing gene expression [[electronic resource]] : a handbook of methods: possibilities and pitfalls / / edited by Stefan Lorkowski and Paul Cullen
Pubbl/distr/stampa	Weinheim ; ; New York, : Wiley-VCH, c2003
ISBN	1-280-52042-6 9786610520428 3-527-60533-9 3-527-60149-X
Descrizione fisica	1 online resource (984 p.)
Altri autori (Persone)	LorkowskiStefan CullenPaul, Dr.
Disciplina	572.8/65 572.865
Soggetti	Gene expression Electronic books.
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Analysing Gene Expression A Handbook of Methods Possibilities and Pitfalls; Foreword; Preface; Contents; List of Contributors; Volume 1; 1 Basic concepts of gene expression; 1.1 Introduction; 1.2 Basics of transcription and translation in the cell; 1.2.1 Introduction; 1.2.2 Transcription; 1.2.3 Translation; 1.2.4 Summary; 1.3 Regulation of transcription; 1.3.1 Introduction; 1.3.2 mRNA expression profiles - the transcriptome; 1.3.3 Protein expression profiles - the proteome; 1.3.4 Interaction between genes and proteins - the interactome; 1.3.5 The transcription machinery and core promoters 1.3.6 Regulatory promoters1.3.7 Enhancers; 1.3.8 Locus control regions; 1.3.9 Matrix attachment regions; 1.3.10 Insulators; 1.3.11 RIDGEs - Regions of increased gene expression; 1.3.12 Enhanceosomes; 1.3.13 Chromatin; 1.3.14 Silencer elements; 1.3.15 Transcription factors, repressors and co-repressors; 1.3.16 Epigenetics; 1.3.17 Summary and conclusions; 1.4 Post-transcriptional regulation; 1.4.1 Introduction; 1.4.2 Regulation of RNA stability and

degradation; 1.4.3 Regulation of transcription elongation; 1.4.3.1 Introduction; 1.4.3.2 Regulation of transcription elongation in prokaryotes
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
1.7.5.1 Normalisation (via internal standards)1.7.5.2 Standard curves (via external standards); 1.7.5.3 Alternative methods (via internal standards); 1.7.6 Summary; 1.8 Classification of differential gene expression technologies; 1.8.1 Introduction; 1.8.2 From single genes to transcriptomes; 1.8.3 Methods of classification; 1.8.4 Conclusions; 1.9 Summary; 1.10 References; 2 Sample preparation and supplementary tools; 2.1 Introduction; 2.2 Preparation of cells and tissues; 2.2.1 Immunopurification of cells; 2.2.2 Differential-velocity centrifugation/countercurrent elutriation
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