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Titolo	The Handbook of plant functional genomics : concept and protocols // edited by Gunter Kahl and Khalid Meksem
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Descrizione fisica	1 online resource (578 p.)
Collana	Molecular plant biology handbook series The handbook of plant functional genomics
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Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references at the end of each chapters and index.
Nota di contenuto	The Handbook of Plant Functional Genomics; Contents; Preface; List of Contributors; I Transcriptome Analysis; A Whole Genome Expression Analysis; 1 Single Cell Expression Profiling: Transcript and Protein Analyses in Isolated Higher Plant Gametes and Zygotes; 1.1 Introduction; 1.2 Microdissection, Cell Isolation; 1.3 In Vitro Fertilization; 1.4 Techniques for Molecular Analyses of Single Cell Types; 1.4.1 Sampling of Single, Living Cells; 1.4.2 Analyses of Gene Expression; 1.4.2.1 Single Cell Gene-by-Gene Analysis; 1.4.2.2 Amplification of Whole cDNA Populations 1.4.2.3 Quantification of Transcript Levels 1.4.2.4 Library Construction and EST Sequencing; 1.4.2.5 Targeted Approaches Using cDNA Subtraction; 1.4.2.6 Microarray Analyses; 1.5 Analyses of Protein Expression; 1.6 Prospects; References; 2 AFLP-Based RNA Fingerprinting: Novel Variants and Applications; 2.1 Introduction; 2.2 Methods and Protocols; 2.2.1 Theoretical Considerations; 2.2.2 State-of-the-Art cDNA-AFLP Protocol; 2.2.2.1 Isolation of cDNA Fragments; 2.2.2.2 Non-Selective Pre-Amplification; 2.2.2.3 Selective

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 2.2.2.4 Downstream Analysis  
 2.3 Applications of the Technology; 2.3.1 Fruit Development; 2.3.2 Tuber Development; 2.3.3 Transcript BSA; 2.3.4 Domain Profiling; 2.3.5 VIDISCA; 2.4 Perspectives; References; 3 SuperSAGE: The Most Advanced Transcriptome Technology for Functional Genomics; 3.1 Introduction; 3.2 Methods and Protocols; 3.2.1 Linker Preparation; 3.2.2 RNA Sample; 3.2.3 cDNA Synthesis; 3.2.4 Tag Extraction from cDNA; 3.2.5 Purification of Linker-Tag Fragment; 3.2.6 Ditag Formation and Amplification; 3.2.7 Tag Extraction from Sequence Data; 3.3 Applications of the Technology  
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 5.2.1.4 RNaseONE Selection for Full-Length (-) cDNA/RNA Heteroduplex

## Sommario/riassunto

In this incisive, concise overview of this booming field, the editors -- two of the leading figures in the field with a proven track record -- combine their expertise to provide an invaluable reference on the topic. Following a treatment of transcriptome analysis, the book goes on to discuss replacement and mutation analysis, gene silencing and computational analysis. The whole is rounded off with a look at emerging technologies. Each chapter is accompanied by a concise overview, helping readers to quickly identify topics of interest, while important, carefully selected words and concept