
Contents

<i>Preface</i>	<i>v</i>
<i>Contributors</i>	<i>xi</i>

PART I BIOINFORMATICS

1 Prediction of Protein Tertiary Structures Using MUFOLD	3
<i>Jingfen Zhang, Zhiquan He, Qingguo Wang, Bogdan Barz, Ioan Kosztin, Yi Shang, and Dong Xu</i>	
2 Prediction of Protein Functions	15
<i>Roy D. Sleator</i>	
3 Genome-Wide Screens for Expressed Hypothetical Proteins	25
<i>Claus Desler, Jon Ambæk Durhuus, and Lene Juel Rasmussen</i>	
4 Self-Custom-Made SFP Arrays for Nonmodel Organisms	39
<i>Ron Ophir and Amir Sherman</i>	

PART II DNA ANALYSIS

5 Construction and Analysis of Full-Length and Normalized cDNA Libraries from Citrus	51
<i>M. Carmen Marques and Miguel A. Perez-Amador</i>	
6 Assembling Linear DNA Templates for In Vitro Transcription and Translation	67
<i>Viktor Stein, Miriam Kaltenbach, and Florian Hollfelder</i>	
7 Automated Computational Analysis of Genome-Wide DNA Methylation Profiling Data from HELP-Tagging Assays	79
<i>Qiang Jing, Andrew McLellan, John M. Greally, and Masako Suzuki</i>	

PART III RNA ANALYSIS

8 Detection of RNA Editing Events in Human Cells Using High-Throughput Sequencing	91
<i>Iouri Chepelev</i>	
9 Comparative Study of Differential Gene Expression in Closely Related Bacterial Species by Comparative Hybridization	103
<i>Ruisheng An and Parwinder S. Grewal</i>	
10 Whole-Genome RT-qPCR MicroRNA Expression Profiling	121
<i>Pieter Mestdagh, Stefaan Derveaux, and Jo Vandesompele</i>	
11 Using Quantitative Real-Time Reverse Transcriptase Polymerase Chain Reaction to Validate Gene Regulation by PTTG	131
<i>Siva Kumar Panguluri and Sham S. Kakar</i>	

12	FRET-Based Real-Time DNA Microarrays	147
	<i>Arjang Hassibi, Haris Vikalo, José Luis Riechmann, and Babak Hassibi</i>	

PART IV PROTEIN ANALYSIS I: QUANTIFICATION AND IDENTIFICATION

13	2-D Gel Electrophoresis: Constructing 2D-Gel Proteome Reference Maps	163
	<i>Maria Paola Simula, Agata Notarpietro, Giuseppe Toffoli, and Valli De Re</i>	
14	The Use of Antigen Microarrays in Antibody Profiling	175
	<i>Krisztián Papp and József Prechl</i>	
15	Limited Proteolysis in Proteomics Using Protease-Immobilized Microreactors.	187
	<i>Hiroshi Yamaguchi, Masaya Miyazaki, and Hideaki Maeda</i>	
16	Mass Spectrometry for Protein Quantification in Biomarker Discovery	199
	<i>Mu Wang and Jinsam You</i>	

PART V PROTEIN ANALYSIS II: FUNCTIONAL CHARACTERIZATION

17	High-Throughput Microtitre Plate-Based Assay for DNA Topoisomerases	229
	<i>James A. Taylor, Nicolas P. Burton, and Anthony Maxwell</i>	
18	Microscale Thermophoresis as a Sensitive Method to Quantify Protein: Nucleic Acid Interactions in Solution	241
	<i>Karina Zillner, Moran Jerabek-Willemsen, Stefan Duhr, Dieter Braun, Gernot Längst, and Philipp Baaske</i>	
19	Bioluminescence Resonance Energy Transfer: An Emerging Tool for the Detection of Protein–Protein Interaction in Living Cells	253
	<i>Søren W. Gersting, Amelie S. Lotz-Havla, and Ania C. Muntau</i>	
20	LuMPIS: Luciferase-Based MBP-Pull-Down Protein Interaction Screening System	265
	<i>Maria G. Vizoso Pinto and Armin Baiker</i>	
21	Yeast Two-Hybrid Screens: Improvement of Array-Based Screening Results by N- and C-terminally Tagged Fusion Proteins	277
	<i>Thorsten Stellberger, Roman Häuser, Peter Uetz, and Albrecht von Brunn</i>	
22	Inducible microRNA-Mediated Knockdown of the Endogenous Human Lamin A/C Gene	289
	<i>Ina Weidenfeld</i>	
23	Multiple-Gene Silencing Using Antisense RNAs in <i>Escherichia coli</i>	307
	<i>Nobutaka Nakashima, Shan Goh, Liam Good, and Tomohiro Tamura</i>	
24	Functional Screen of Zebrafish Deubiquitylating Enzymes by Morpholino Knockdown and In Situ Hybridization	321
	<i>William Ka Fai Tse and Yun-Jin Jiang</i>	

25	Silencing of Gene Expression by Gymnotic Delivery of Antisense Oligonucleotides	333
	<i>Harris S. Soifer, Troels Koch, Johnathan Lai, Bo Hansen, Anja Hoeg, Henrik Oerum, and C.A. Stein</i>	
26	Polycistronic Expression of Interfering RNAs from RNA Polymerase III Promoters	347
	<i>Laura F. Steel and Viraj R. Sanghvi</i>	

PART VI METABOLITE ANALYSIS

27	Metabolite Analysis of <i>Cannabis sativa</i> L. by NMR Spectroscopy	363
	<i>Isvett Josefina Flores-Sanchez, Young Hae Choi, and Robert Verpoorte</i>	
28	Metabolome Analysis of Gram-Positive Bacteria such as <i>Staphylococcus aureus</i> by GC-MS and LC-MS	377
	<i>Manuel Liebeke, Kirsten Dörries, Hanna Meyer, and Michael Lalk</i>	
29	Metabolic Fingerprinting Using Comprehensive Two-Dimensional Gas Chromatography – Time-of-Flight Mass Spectrometry	399
	<i>Martin F. Almstetter, Peter J. Oefner, and Katja Dettmer</i>	
	<i>Index</i>	413



<http://www.springer.com/978-1-61779-423-0>

Functional Genomics

Methods and Protocols

Kaufmann, M.; Klinger, C. (Eds.)

2012, XV, 418 p., Hardcover

ISBN: 978-1-61779-423-0

A product of Humana Press