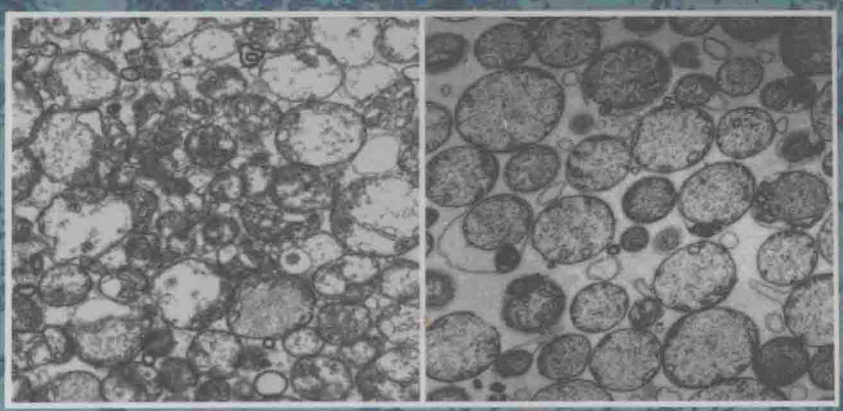
METHODS IN MOLECULAR BIOLOGY™ 432

Organelle Proteomics

Edited by
Delphine Pflieger
Jean Rossier



Humana Press

METHODS IN MOLECULAR BIOLOGY™

Organelle Proteomics

Edited by

Delphine Pflieger

Laboratoire de Neurobiologie et Diversité Cellulaire, CNRS UMR 7637, Ecole Supérieure de Physique et de Chimie Industrielles, Paris, France and Laboratoire d'Analyse et de Modélisation pour la Biologie et l'Environnement, CNRS UMR 8587, Université d'Evry Val d'Essonne, Evry, France

and

Jean Rossier

Laboratoire de Neurobiologie et Diversité Cellulaire, CNRS UMR 7637, Ecole Supérieure de Physique et de Chimie Industrielles, Paris, France

Humana Press

Editor
Delphine Pflieger
Laboratoire de Neurobiologie et Diversité
Cellulaire, CNRS UMR 7637
Ecole Supérieure de Physique et de
Chimie Industrielles
Paris, France
and
Laboratoire d'Analyse et de Modélisation
pour la Biologie et l'Environnement
CNRS UMR 8587, Université d'Evry Val
d'Essonne, Evry, France

Jean Rossier
Laboratoire de Neurobiologie et Diversité
Cellulaire, CNRS UMR 7637
Ecole Supérieure de Physique et de
Chimie Industrielles
Paris, France

Series Editor
John M. Walker
School of Life Sciences
University of Hertfordshire
Hatfield, Herts., AL10 9AB
UK

ISBN: 978-1-58829-779-2 e-ISBN: 978-1-59745-028-7

ISSN: 1064-3745

Library of Congress Control Number: 2007941655

©2008 Humana Press, a part of Springer Science+Business Media, LLC
All rights reserved. This work may not be translated or copied in whole or in part without the written permission of the publisher (Humana Press, 999 Riverview Drive, Suite 208, Totowa, NJ 07512 USA), except for brief excerpts in connection with reviews or scholarly analysis. Use in connection with any form of information storage and retrieval, electronic adaptation, computer software, or by similar or dissimilar methodology now known or hereafter developed is forbidden.
The use in this publication of trade names, trademarks, service marks, and similar terms, even if they are not identified as such, is not to be taken as an expression of opinion as to whether or not they are subject to proprietary rights.
While the advice and information in this book are believed to be true and accurate at the date of going to press, neither the authors nor the editors nor the publisher can accept any legal responsibility for any errors or omissions that may be made. The publisher makes no warranty, express or implied, with respect to the material contained herein.

Cover Illustration: Figure 1, Chapter 4, "Purification of *Saccharomyces cerevisiae* Mitochondria by Zone Electrophoresis in a Free Flow Device," by Hans Zischka, Norbert Kinkl, Ralf J. Braun, and Marius Ueffing

Printed on acid-free paper

9 8 7 6 5 4 3 2 1

springer.com

Organelle Proteomics

METHODS IN MOLECULAR BIOLOGY™

John M. Walker, SERIES EDITOR

435. **Chromosomal Mutagenesis**, edited by *Greg Davis and Kevin J. Kayser, 2008*
434. **Gene Therapy Protocols: Volume 2:** *Design and Characterization of Gene Transfer Vectors*, edited by *Joseph M. LeDoux, 2008*
433. **Gene Therapy Protocols: Volume 1:** *Production and In Vivo Applications of Gene Transfer Vectors*, edited by *Joseph M. LeDoux, 2008*
432. **Organelle Proteomics**, edited by *Delphine Pflieger and Jean Rossier, 2008*
431. **Bacterial Pathogenesis:** *Methods and Protocols*, edited by *Frank DeLeo and Michael Otto, 2008*
430. **Hematopoietic Stem Cell Protocols**, edited by *Kevin D. Bunting, 2008*
429. **Molecular Beacons:** *Signalling Nucleic Acid Probes, Methods and Protocols*, edited by *Andreas Marx and Oliver Seitz, 2008*
428. **Clinical Proteomics:** *Methods and Protocols*, edited by *Antonio Vlahou, 2008*
427. **Plant Embryogenesis**, edited by *Maria Fernanda Suarez and Peter Bozhkov, 2008*
426. **Structural Proteomics:** *High-Throughput Methods*, edited by *Bostjan Kobe, Mitchell Guss, and Huber Thomas, 2008*
425. **2D PAGE: Volume 2:** *Applications and Protocols*, edited by *Anton Posch, 2008*
424. **2D PAGE: Volume 1:** *Sample Preparation and Pre-Fractionation*, edited by *Anton Posch, 2008*
423. **Electroporation Protocols**, edited by *Shulin Li, 2008*
422. **Phylogenomics**, edited by *William J. Murphy, 2008*
421. **Affinity Chromatography:** *Methods and Protocols, Second Edition*, edited by *Michael Zachariou, 2008*
420. **Drosophila:** *Methods and Protocols*, edited by *Christian Dahmann, 2008*
419. **Post-Transcriptional Gene Regulation**, edited by *Jeffrey Wilusz, 2008*
418. **Avidin-Biotin Interactions:** *Methods and Applications*, edited by *Robert J. McMahon, 2008*
417. **Tissue Engineering**, *Second Edition*, edited by *Hannsjörg Hauser and Martin Fussenegger, 2007*
416. **Gene Essentiality:** *Protocols and Bioinformatics*, edited by *Svetlana Gerdes and Andrei L. Osterman, 2008*
415. **Innate Immunity**, edited by *Jonathan Ewbank and Eric Vivier, 2007*
414. **Apoptosis in Cancer:** *Methods and Protocols*, edited by *Gil Mor and Ayesha Alvero, 2008*
413. **Protein Structure Prediction**, *Second Edition*, edited by *Mohammed Zaki and Chris Bystroff, 2008*
412. **Neutrophil Methods and Protocols**, edited by *Mark T. Quinn, Frank R. DeLeo, and Gary M. Bokoch, 2007*
411. **Reporter Genes for Mammalian Systems**, edited by *Don Anson, 2007*
410. **Environmental Genomics**, edited by *Cristofre C. Martin, 2007*
409. **Immunoinformatics:** *Predicting Immunogenicity In Silico*, edited by *Darren R. Flower, 2007*
408. **Gene Function Analysis**, edited by *Michael Ochs, 2007*
407. **Stem Cell Assays**, edited by *Vemuri C. Mohan, 2007*
406. **Plant Bioinformatics:** *Methods and Protocols*, edited by *David Edwards, 2007*
405. **Telomerase Inhibition:** *Strategies and Protocols*, edited by *Lucy Andrews and Trygve O. Tollefsbol, 2007*
404. **Topics in Biostatistics**, edited by *Walter T. Ambrosius, 2007*
403. **Patch-Clamp Methods and Protocols**, edited by *Peter Molnar and James J. Hickman, 2007*
402. **PCR Primer Design**, edited by *Anton Yuryev, 2007*
401. **Neuroinformatics**, edited by *Chiquito J. Crasto, 2007*
400. **Methods in Membrane Lipids**, edited by *Alex Dopico, 2007*
399. **Neuroprotection Methods and Protocols**, edited by *Tiziana Borsello, 2007*
398. **Lipid Rafts**, edited by *Thomas J. McIntosh, 2007*
397. **Hedgehog Signaling Protocols**, edited by *Jamila I. Horabin, 2007*
396. **Comparative Genomics, Volume 2**, edited by *Nicholas H. Bergman, 2007*
395. **Comparative Genomics, Volume 1**, edited by *Nicholas H. Bergman, 2007*
394. **Salmonella:** *Methods and Protocols*, edited by *Heide Schatten and Abraham Eisenstark, 2007*
393. **Plant Secondary Metabolites**, edited by *Harinder P. S. Makkar, P. Siddhuraju, and Klaus Becker, 2007*
392. **Molecular Motors:** *Methods and Protocols*, edited by *Ann O. Sperry, 2007*
391. **MRSA Protocols**, edited by *Yinduo Ji, 2007*
390. **Protein Targeting Protocols**, *Second Edition*, edited by *Mark van der Giezen, 2007*
389. **Pichia Protocols**, *Second Edition*, edited by *James M. Cregg, 2007*
388. **Baculovirus and Insect Cell Expression Protocols**, *Second Edition*, edited by *David W. Murhammer, 2007*
387. **Serial Analysis of Gene Expression (SAGE):** *Digital Gene Expression Profiling*, edited by *Kare Lehmann Nielsen, 2007*
386. **Peptide Characterization and Application Protocols,** edited by *Gregg B. Fields, 2007*
385. **Microchip-Based Assay Systems:** *Methods and Applications*, edited by *Pierre N. Floriano, 2007*
384. **Capillary Electrophoresis:** *Methods and Protocols*, edited by *Philippe Schmitt-Kopplin, 2007*
383. **Cancer Genomics and Proteomics:** *Methods and Protocols*, edited by *Paul B. Fisher, 2007*
382. **Microarrays, Second Edition: Volume 2:** *Applications and Data Analysis*, edited by *Jang B. Rampal, 2007*
381. **Microarrays, Second Edition: Volume 1:** *Synthesis Methods*, edited by *Jang B. Rampal, 2007*
380. **Immunological Tolerance:** *Methods and Protocols*, edited by *Paul J. Fairchild, 2007*

此为试读，需要完整PDF请访问：www.ertongbook.com

Preface

Human genome sequencing has identified about 25,000 genes, most being of unknown function. Localization of the final gene products—that is, the proteins—in a specific organelle is a key to deciphering the proteins' roles within the cell. Over the past 20 years, proteomic analyses have progressively proved to be an invaluable tool to obtain high-throughput protein identification from low-abundance, complex biological samples. These analyses boomed thanks to dramatic technological progresses in mass spectrometry instrumentation, optimization of its coupling to capillary liquid chromatography, and the development of software enabling processing of the vast amount of generated data. In the context of organelle study, such analyses have allowed greater depth in the characterization of the proteins constitutive of, or transiently present in, these large functional modules. For example, in 2002, we published the analysis of a total yeast mitochondrial protein extract by the coupling between capillary liquid chromatography and tandem mass spectrometry, known as liquid chromatography-tandem mass spectrometry (LC-MS/MS) ***(1)***. We were then able to identify 179 proteins (http://mitochondria.cgm.cnrs-gif.fr/) out of about 500 expected mitochondrial constituents. Among these, 132 were already recorded as mitochondrial in the Yeast Protein Database, YPD ***(2)***, 28 were described to be of unknown localization and function, and 19 were described to belong to other subcellular compartments. Among the 28 identified proteins that were uncharacterized in early 2002, eight were further functionally studied by other groups and demonstrated to play a role in mitochondria. For example, Ykr065cp was shown to be involved in the import of mitochondrial matrix proteins ***(3)***, Ylr201cp in ubiquinone biosynthesis ***(4)***, and Ynl177cp was proved to be a mitochondrial ribosomal protein ***(5)***. Another 17 were identified in more recent proteomic analyses of yeast mitochondria (such as reference ***[6]***) confirming our results. Little to no data are currently available in yeast databases to support mitochondrial localization of the three remaining proteins. This study, among many others, illustrates that proteomic analysis of a carefully prepared organelle sample reliably reveals new proteins constitutive of the cellular compartment and paves the way for their detailed functional characterization.

Cell proteomics is faced with the extraordinary chemical diversity of expressed proteins and the very large dynamic range of their cellular concentrations. In any given human cell, the most abundant protein is usually actin, present at above 10^8 molecules per cell, whereas cellular receptors, signaling

proteins, and transcription factors may exist at a few hundreds of copies or even less. Yet, the understanding of the diverse cellular processes requires the study of the expression of those proteins—needles in the cellular haystack. To achieve that goal, it is indispensable to enrich such target proteins within a subcellular sample of reduced complexity. To characterize proteins of minor abundance in an organelle, this subcellular compartment can be divided into fractions, such as soluble and insoluble membrane proteins. In one last step of fractionation, the proteomic analysis can be focused on a given protein machinery, such as a single complex. *Organelle Proteomics* focuses on these three levels of subcellular organization by describing the preparation of samples and their proteomic analysis.

This book starts with a chapter by Dr. Edwin Romijn and Prof. John R. Yates III, who introduce the different analytical strategies developed and successfully utilized to study organelle proteomes and detail the use of multidimensional liquid chromatography coupled to tandem mass spectrometry for peptide sample analysis. This book is further composed of two main sections. First, detailed protocols are provided to perform the purification of the various organelles present in eukaryotic cells, as well as to prepare certain subfractions of organelles (Chapters 2–22). In all cases, the samples are aimed to be analyzed by a mass spectrometry technique. Although an exhaustive list of chapters covering all the proteomic analyses of organelles and organelle fractions was not conceivable, we nevertheless wanted to provide analysis examples reflecting the trend toward more specific purifications of organelle subfractions, which will allow reaching the more comprehensive and accurate characterization of the organelle. Most of the chapters cover the whole analytical procedure of organelle characterization, from its purification starting with whole cells up to protein identification using mass spectrometry. In some cases, the chapter may provide a detailed description of the purification process wherein less classical techniques appear, which are implemented by a minority of laboratories (e.g., free flow electrophoresis). Second, however optimized the organelle purification protocol—and skilled the operator—the sample of interest will never consist of the pure targeted organelle. Therefore, among the proteins identified, one has to separate the true from the intruders. The actual subcellular localization of some individual proteins newly attributed to the studied organelle can be evaluated by orthogonal assays, such as microscopy, by expressing the GFP-tagged version of the protein candidates. Yet, this approach is labor-intensive and is usually restricted to a few selected proteins. We devoted the second section of this book to methods enabling a global estimate of the reliability of the protein list assigned to an organelle. An average ratio of proteins wrongly attributed to the organelle of interest is provided by assessing sample purity (Chapter 23). To determine whether every identified protein is

an actual component of the purified organelle, quantitative mass spectrometry methods can be employed (Chapters 24–26). In Chapter 26, Dr. Wei Yan et al. more specifically demonstrate the utility of quantitative approaches to scrutinize protein shuttling between organelles. The examples of quantitative mass spectrometry analysis of organelle fractions presented use a few commercially available isotope-tagged reagents, but many other chemicals, either commercial or prepared in-house, can be utilized. A larger variety of the existing polypeptide-labeling strategies can be found in another volume of this series entitled *Quantitative Proteomics*, edited by Dr. Salvatore Sechi. Finally, the last chapter of this book, by Dr. Wallace F. Marshall, addresses the use of transcriptomic data to identify genes potentially encoding organelle proteomes.

One should keep in mind that some, if not the majority, of peptide sequences assigned by software tools to raw mass spectra must be rejected. The degree of false-positive protein identification can be estimated by statistical interpretation of mass spectrometry results. This aspect, while of greatest importance to generate interlaboratory databases of proteins organized by localization and function, is beyond the scope of this book. It is dealt with in an alternative volume of this series, *Mass Spectrometry Data Analysis in Proteomics*, edited by Dr. Rune Matthiesen.

In terms of chapter format, each chapter begins by introducing the protocol to be described, with its goals and possible advantages over other techniques. In the Materials section, all the equipment and reagents necessary for performing the protocol are listed. The Methods section details the different steps of the protocol while the Notes collect remarks, tricks, and troubleshooting that are likely to help dealing with difficulties that might be encountered during the protocol.

Delphine Pflieger
Jean Rossier

References

1. Pflieger, D., Le Caer, J. P., Lemaire, C., Bernard, B. A., Dujardin, G., Rossier, J. (2002) Systematic identification of mitochondrial proteins by LC-MS/MS. *Anal. Chem.* **74**, 2400–2406.
2. Hodges, P. E., Payne, W. E., Garrels, J. I. (1997) The Yeast Protein Database (YPD): a curated proteome database for *Saccharomyces cerevisiae*. *Nucleic Acids Res.* **26**, 68–72.
3. van der Laan M., Chacinska, A., Lind, M., Perschil, I., Sickmann, A., Meyer, H., et al. (2005) Pam17 is required for architecture and translocation activity of the mitochondrial protein import motor. *Mol. Cell. Biol.* **25**, 7449–7458.

4. Johnson, A., Gin, P., Marbois, B. N., Hsieh, E. J., Wu, M., Barros, M. H., et al. (2005) COQ9, a new gene required for the biosynthesis of coenzyme Q in Saccharomyces cerevisiae. *J. Biol. Chem.* **280**, 31397–31404.
5. Gan X., Kitakawa, M., Yoshino, K., Oshiro, N., Yonezawa, K., Isono, K. (2002) Tag-mediated isolation of yeast mitochondrial ribosome and mass spectrometric identification of its new components. *Eur. J. Biochem.* **269**, 5203–5214.
6. Sickmann, A., Reinders, J., Wagner, Y., Joppich, C., Zahedi, R., Meyer, H. E., et al. (2003) The proteome of Saccharomyces cerevisiae mitochondria. *Proc. Natl. Acad. Sci. U.S.A.* **100**, 13207–13212.

Contributors

RUEDI AEBERSOLD • *Institute for Systems Biology, Seattle, WA; Institute of Molecular Systems Biology, ETH-Zurich, Zurich, Switzerland; and Faculty of Science, University of Zurich, Zurich, Switzerland*

JOHN D. AITCHISON • *Institute for Systems Biology, Seattle, WA*

ERIK ALEXANDERSSON • *Department of Biochemistry, Centre for Chemistry and Chemical Engineering, Lund University, Lund, Sweden*

PHILIP C. ANDREWS • *Department of Biological Chemistry, The University of Michigan, Ann Arbor, MI*

RICK BAGSHAW • *Research Institute, The Hospital for Sick Children, Toronto, Ontario; and Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, Ontario, Canada*

KATJA BERNFUR • *Department of Biochemistry, Centre for Chemistry and Chemical Engineering, Lund University, Lund, Sweden*

ADELE R. BLACKLER • *Department of Pharmacology, University of Colorado School of Medicine, Aurora, CO*

MARIE-PIERRE BOUSQUET-DUBOUCH • *Institut de Pharmacologie et de Biologie Structurale, Centre National de la Recherche Scientifique, Toulouse, France*

RALF J. BRAUN • *GSF-National Research Center for Environment and Health, Institute of Human Genetics, Munich-Neuherberg, Germany*

ODILE BURLET-SCHILTZ • *Institut de Pharmacologie et de Biologie Structurale, Centre National de la Recherche Scientifique, Toulouse, France*

JOHN W. CALLAHAN • *Research Institute, The Hospital for Sick Children, Toronto, Ontario; and Departments of Biochemistry and Pediatrics, University of Toronto, Toronto, Ontario, Canada*

AGNÈS CHAPEL • *CEA, DSV, DRDC, Laboratoire de Chimie des Protéines, Grenoble, France; INSERM, Grenoble, France; and Université Joseph Fourier, Grenoble, France*

JULIE CHAROLLAIS • *Global Health Institute, Ecole Polytechnique Fédérale de Lausanne, Lausanne, Switzerland*

XUEQUN CHEN • *Department of Biological Chemistry, The University of Michigan, Ann Arbor, MI*

HOLLY D. COX • *Department of Pharmaceutical Sciences, University of Montana, Missoula, MT. Current address: Department of Pathology, Salt Lake City, UT*

SANDRINE DA CRUZ • *Department of Cell Biology, University of Geneva, Geneva, Switzerland*

MANUELLE DUCOUX-PETIT • *Institut de Pharmacologie et de Biologie Structurale, Centre National de la Recherche Scientifique, Toulouse, France*

GENEVIÈVE DUJARDIN • *CNRS, Centre de Génétique Moléculaire, Avenue de la Terrasse, Gif sur Yvette, France*

TOM P. J. DUNKLEY • *Cambridge Centre for Proteomics Department of Biochemistry, University of Cambridge, Cambridge, UK*

XIAOLIAN FAN • *Research Institute, The Hospital for Sick Children, Toronto, Ontario, Canada*

MYRIAM FERRO • *CEA, DSV, iRTSV, Laboratoire de l'Etude de la Dynamique des Protéomes, Grenoble, France; INSERM, Grenoble, France; and Université Joseph Fourier, Grenoble, France*

LAURENCE FLORENS • *The Stowers Institute for Medical Research, Kansas City, MO*

KIICHI FUKUI • *Laboratory of Dynamic Cell Biology, Department of Biotechnology, Graduate School of Engineering, Osaka University, Osaka, Japan*

KAZUHIRO FURUKAWA • *Department of Chemistry, Faculty of Science, Niigata University, Niigata, Japan*

JÉRÔME GARIN • *CEA, DSV, DRDC, Laboratoire de Chimie des Protéines, Grenoble, France; INSERM, Grenoble, France; and Université Joseph Fourier, Grenoble, France*

NIKLAS GUSTAVSSON • *Department of Biochemistry, Centre for Chemistry and Chemical Engineering, Lund University, Lund, Sweden*

TSUNEYOSHI HORIGOME • *Department of Chemistry, Faculty of Science, Niigata University, Niigata, Japan*

KATHRYN E. HOWELL • *Department of Cell and Developmental Biology, University of Colorado School of Medicine, Aurora, CO*

DAEHEE HWANG • *Institute for Systems Biology, Seattle, WA. Current address: I-Bio Program & Department of Chemical Engineering, Pohang University of Science and Technology, Kyungbuk, Republic of Korea*

ISABELLE IOST • *Laboratoire de Génétique Moléculaire, Ecole Normale Supérieure, Paris, France*

此为试读,需要完整PDF请访问: www.ertongbook.com

KOHEI ISHII • *Department of Chemistry, Faculty of Science, Niigata University, Niigata, Japan*

MARKUS ISLINGER • *Department of Anatomy and Cell Biology II, University of Heidelberg, Heidelberg, Germany*

AGNÈS JOURNET • *CEA, DSV, DRDC, Laboratoire de Chimie des Protéines, Grenoble, France; INSERM, Grenoble, France; and Université Joseph Fourier, Grenoble, France*

JACQUES JOYARD • *Laboratoire de Physiologie Cellulaire Végétale, Grenoble, France; Université Joseph Fourier/CNRS UMR-5168/INRA/CEA-Grenoble, Grenoble, France; and iRTSV, Grenoble, France*

ADINE KARLSSON • *Department of Biochemistry, Centre for Chemistry and Chemical Engineering, Lund University, Lund, Sweden*

LANI C. KELLER • *Department of Biochemistry & Biophysics, University of California, San Francisco, CA*

JACOB KENNEDY • *ZymoGenetics, Inc, Seattle, WA*

SYLVIE KIEFFER-JAQUINOD • *CEA, DSV, DRDC, Laboratoire de Chimie des Protéines, Grenoble, France; INSERM, Grenoble, France; and Université Joseph Fourier, Grenoble, France*

NORBERT KINKL • *Technical University Munich, Institute of Human Genetics, Munich, Germany; GSF-National Research Center for Environment and Health, Institute of Human Genetics, Munich-Neuherberg, Germany*

PER KJELLBOM • *Department of Biochemistry, Centre for Chemistry and Chemical Engineering, Lund University, Lund, Sweden*

NADIA KORFALI • *The Wellcome Trust Centre for Cell Biology and Institute of Cell Biology, University of Edinburgh, Edinburgh, UK*

CHRISTER LARSSON • *Department of Biochemistry, Centre for Chemistry and Chemical Engineering, Lund University, Lund, Sweden*

CLAIRE LEMAIRE • *CNRS, Centre de Génétique Moléculaire, Gif sur Yvette, France*

KATHRYN S. LILLEY • *Cambridge Centre for Proteomics Department of Biochemistry, University of Cambridge, Cambridge, UK*

MARK S. LOWENTHAL • *Department of Pharmacology, University of Colorado School of Medicine, Aurora, CO*

DON J. MAHURAN • *Research Institute, The Hospital for Sick Children, Toronto, Ontario; and Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, Ontario, Canada*

MARCELLO MARELLI • *Homestead Clinical Corporation, Seattle, WA*

WALLACE F. MARSHALL • *Department of Biochemistry & Biophysics, University of California, San Francisco, CA*

JEAN-CLAUDE MARTINOU • *Department of Cell Biology, University of Geneva, Geneva, Switzerland*

MARIETTE MATONDO • *Institut de Pharmacologie et de Biologie Structurale, Centre National de la Recherche Scientifique, Toulouse, France*

BERNARD MONSARRAT • *Institut de Pharmacologie et de Biologie Structurale, Centre National de la Recherche Scientifique, Toulouse, France*

ALEXEY I. NESVIZHSKII • *Department of Pathology, University of Michigan, Ann Arbor, MI*

DELPHINE PFLIEGER • *Laboratoire Analyse et Modélisation pour la Biologie et l'Environnement, Université d'Evry Val d'Essonne, Evry, France*

THIERRY RABILLOUD • *CEA/DSV/IRTSV/BBSI, UMR CNRS 5092, Biologie et Biophysique des systèmes intégrés, CEA Grenoble, 17 rue des martyrs, Grenoble, France*

NORBERT ROLLAND • *Laboratoire de Physiologie Cellulaire Végétale, Grenoble, France; Université Joseph Fourier/CNRS UMR-5168/INRA/CEA-Grenoble, Grenoble, France; and iRTSV, Grenoble, France*

EDWIN P. ROMIJN • *Philips Research Eindhoven, High Tech Campus, Eindhoven, The Netherlands*

JEAN ROSSIER • *Laboratoire de Neurobiologie et Diversité Cellulaire, CNRS UMR 7637, Ecole Supérieure de Physique et de Chimie Industrielles, Paris, France*

DANIEL SALVI • *Laboratoire de Physiologie Cellulaire Végétale, Grenoble, France; Université Joseph Fourier/CNRS UMR-5168/INRA/CEA-Grenoble, Grenoble, France; iRTSV, Grenoble, France*

ERIC C. SCHIRMER • *The Wellcome Trust Centre for Cell Biology and Institute of Cell Biology, University of Edinburgh, Edinburgh, UK*

HIDEAKI TAKATA • *Laboratory of Dynamic Cell Biology, Department of Biotechnology, Graduate School of Engineering, Osaka University, Osaka, Japan*

CHARLES M. THOMPSON • *Department of Biomedical and Pharmaceutical Sciences, Missoula, MT*

SUSUMU UCHIYAMA • *Laboratory of Dynamic Cell Biology, Department of Biotechnology, Graduate School of Engineering, Osaka University, Osaka, Japan*

MARIUS UEFFING • *Technical University Munich, Institute of Human Genetics, Munich, Germany; GSF-National Research Center for Environment and Health, Institute of Human Genetics, Munich-Neuherberg, Germany*

SANDRINE UTTENWEILER-JOSEPH • *Institut de Pharmacologie et de Biologie Structurale, Centre National de la Recherche Scientifique, Toulouse, France*

JOËLLE VINH • *Laboratoire de Neurobiologie et Diversité Cellulaire, Ecole Supérieure de Physique et de Chimie Industrielles, Paris, France*

GERHARD WEBER • *BD Diagnostics – Preanalytical Systems, Planegg/Martinsried, Germany*

JACEK R. WIŚNIEWSKI • *Department of Proteomics and Signal Transduction, Max-Planck Institute of Biochemistry, Martinsried, Germany*

CHRISTINE C. WU • *Department of Pharmacology, University of Colorado School of Medicine, Aurora, CO*

WEI YAN • *Institute for Systems Biology, Seattle, WA; Department of Pathology, University of Washington, Seattle, WA*

JOHN R. YATES III • *The Scripps Research Institute, La Jolla, CA*

EUGENE C. YI • *ZymoGenetics, Inc, Seattle, WA*

HUIWEN ZHANG • *Research Institute, The Hospital for Sick Children, Toronto, Ontario, Canada*

HANS ZISCHKA • *GSF-National Research Center for Environment and Health, Institute of Toxicology, Munich-Neuherberg, Germany*

Contents

此为试读,需要完整PDF请访问: www.ertongbook.com