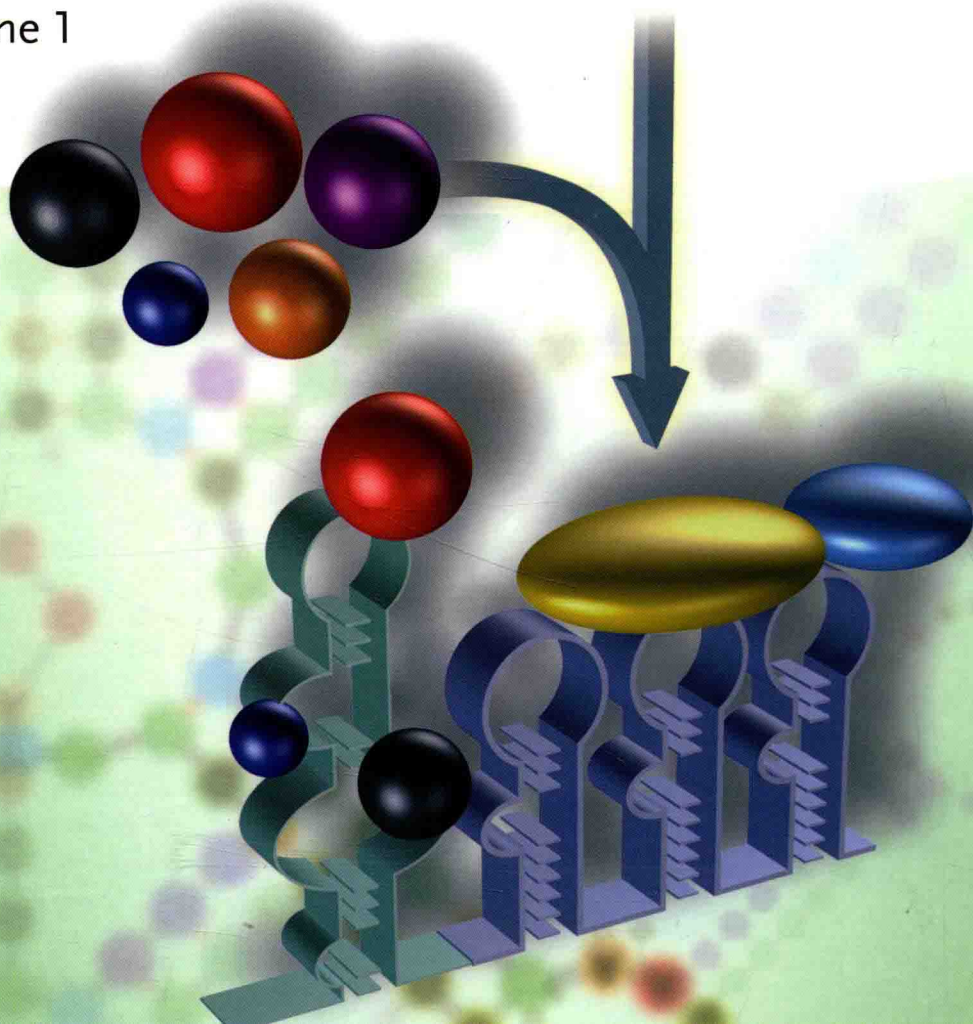


Edited by Roland K. Hartmann, Albrecht Bindereif,
Astrid Schön, and Eric Westhof

Handbook of RNA Biochemistry

Second, Completely Revised and Enlarged Edition

Volume 1



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The Editors

Prof. Dr. Roland K. Hartmann

Philipps-Universität Marburg
Institut für Pharma. Chemie
Marbacher Weg 6
35037 Marburg
Germany

Prof. Dr. Albrecht Bindereif

Justus-Liebig-Universität
Institut für Biochemie
Heinrich-Buff-Ring 58
35392 Giessen
Germany

Dr. Astrid Schön

Universität Leipzig
Molecular Cell Therapy
Deutscher Platz 5
04103 Leipzig
Germany

Prof. Dr. Eric Westhof

CNRS - UPR 9002, Inst. de
Biol. Mol. et Cellulaire
15 rue René Descartes
06708 Strasbourg
France

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Albrecht Bindereif, Astrid Schön,
and Eric Westhof*

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Preface

Why a second edition of the Handbook of RNA Biochemistry about eight years after release of the first edition? We see several profound reasons, the most fundamental one being that new biological and biochemical questions induce new technological advances, which in turn drives our research capabilities and opens up insights into novel RNA functions and mechanistic principles. For example, a multitude of novel non-coding RNAs (ncRNAs) have been uncovered, which entails a need not only for bioinformatic tools to predict their structure and to search for homologs, but also for further developments in biochemical tools for their functional analysis.

In the last decade, research in RNA biology, and here most notably global approaches, experienced an incredible boom, largely driven by new genome-wide and high-throughput technology, as well as RNA bioinformatics. Therefore, high-throughput and deep-sequencing approaches are covered by new chapters in this second edition (Chapters 34, 36–40), and contributions present already in the first edition have been thoroughly updated (Chapters 33 and 35) to keep pace with the fast evolution of these powerful methods.

Although unmodified RNA contains only four different nucleotides, the prediction of RNA secondary and tertiary structures and RNA homology searches are inherently sophisticated tasks of pivotal importance for RNA researchers. Chapters 26–32 are dedicated to these demands. There is also a need for protocols that enable experimental scientists to competently utilize bioinformatic, preferably web-based, tools. This aspect has been taken into account throughout this second edition.

All the chapters already present in the first edition have been updated, which concerns practical details (such as on company names, providers of enzymes and materials, web addresses), methodological details, and protocol streamlining. For example, the topics of RNA ligation or photoaffinity crosslinking to probe RNA structure, each previously represented by two separate chapters, are now consolidated in single chapters (Chapters 3 and 11). In addition, “old,” but very informative, RNA techniques such as gel- or TLC-based approaches to identify modified nucleosides or temperature-gradient gel electrophoresis of RNA, currently out of fashion, have been described in even more detail (Chapters 9 and 21) in order to preserve this kind of more traditional knowledge, which may experience an unforeseen revival at some point in the future.

Methodology in the area of RNA interference is crucial for so many researchers in various fields and is not restricted to RNA specialists, but also essential for RNA-based biotechnology and application in molecular medicine. We have therefore included new chapters on vector-encoded siRNA or miRNA techniques (Chapter 55), miRNA analysis (Chapter 49), and the application of chemically modified siRNAs (Chapter 56).

In summary, we have expanded the number of chapters and protocols, all written by experts in their fields, included new methods and approaches, strengthened the ready-to-use-lab-protocol format, and eliminated some redundancies.

We wish all readers scientific success in the application of our protocols, as well as several *Eureka!* experiences when, or after, consulting this Handbook for experimental strategies to tackle their specific biological questions or problems in RNA research.

March 2013

Roland K. Hartmann
Albrecht Bindereif
Astrid Schön
Eric Westhof

List of Contributors

Andrew J. Andrews

Fox Chase Cancer Center
333 Cottman ave.
Philadelphia,
PA 19111-2497
USA

Minna-Liisa Änkö

Max Planck Institute of
Cell Biology and Genetics
Pfortenhauerstrasse 108
01307 Dresden
Germany

and

Walter and Eliza Hall Institute of
Medical Research
Chemical Biology Division
Parkville, Melbourne
Australia

Manuel Ascano

The Rockefeller University
Laboratory of RNA Molecular
Biology
Howard Hughes Medical
Institute
1230 York Avenue
New York, NY 10065
USA

Pascal Auffinger

Modélisations et Simulations des
Acides Nucléiques
UPR 9002
Institut de Biologie Moléculaire et
Cellulaire du CNRS
15, rue René Descartes
67084 Strasbourg Cedex
France

Nathan J. Baird

National Heart
Lung and Blood Institute
National Institutes of Health
50 South Dr.
Bethesda, MD 20892
USA

Thomas Basché

Johannes Gutenberg-Universität
Institute of Physical Chemistry
Duesbergweg 10-14
55099 Mainz
Germany

Benedikt M. Beckmann

European Molecular Biology
Laboratory (EMBL)
Meyerhofstrasse 1
69117 Heidelberg
Germany

Isabelle Behm-Ansmant

Nancy Université
Laboratoire ARN-RNP
Maturation-Structure-Fonction
Enzymologie Moléculaire et
Structurale (AREMS)
UMR 7214 CNRS-UL
Batiment Biopôle
9, avenue de la Forêt de Haye
54506 Vandoeuvre-les-Nancy
France

Hildburg Beier

Universität Würzburg
BEEgroup
Biozentrum
Am Hubland
97074 Würzburg
Germany

Michaela Beitzinger

Universität Regensburg
Lehrstuhl Biochemie I
Universitätsstrasse 31
93053 Regensburg
Germany

Christian Berens

Friedrich-Alexander-Universität
Erlangen-Nürnberg
Lehrstuhl für Mikrobiologie
Department Biologie
Staudtstr. 5
91058 Erlangen
Germany

Ben Berkhout

University of Amsterdam
Laboratory of Experimental
Virology
Department of Medical
Microbiology
Center for Infection and
Immunity Amsterdam (CINIMA)
Academic Medical Center
Meibergdreef 15, K3-113D
1105 AZ Amsterdam
The Netherlands

Albrecht Bindereif

Justus-Liebig-Universität Gießen
Fachbereich Biologie und Chemie
Institut für Biochemie
Heinrich-Buff-Ring 58
35392 Gießen
Germany

Jennifer L. Boots

University of Vienna
Department of Biochemistry and
Molecular Cell Biology
Max F. Perutz Laboratories
Doktor-Bohr-Gasse 9/5
1030 Vienna
Austria

Marc Boudvillain

CNRS
Centre de Biophysique
Moléculaire
rue Charles Sadron
45071 Orleans
France

Marie Bouvier

University of Würzburg
Institute for Molecular Infection
Biology
RNA Biology Group
Josef-Schneider-Strasse 2
97080 Würzburg
Germany

Jesper B. Bramsen

University of Aarhus
Interdisciplinary Nanoscience
Center (iNANO)
Ny Munkegade 118
8000 Aarhus C
Denmark

and

University of Aarhus
Department of Molecular Biology
and Genetics
C. F. Møllers Allé 3
8000 Aarhus C
Denmark

Christiane Branlant

Nancy Université
Laboratoire ARN-RNP
Maturation-Structure-Fonction
Enzymologie Moléculaire et
Structurale (AREMS)
UMR 7214 CNRS-UL
Batiment Biopôle
9, avenue de la Forêt de Haye
54506 Vandoeuvre-les-Nancy
France

Lukas Burger

Biozentrum der Universität Basel
and Swiss Institute of
Bioinformatics (SIB)
Klingelbergstr. 50–70
4056 Basel
Switzerland

Malte Bussiek

University of Kassel
Abt. Genetik and CINSaT
Heinrich-Plett-Str. 40
34132 Kassel
Germany

John C. Castle

Johannes Gutenberg Medical
University of Mainz
TRON –Translational Oncology
Saarstr. 21
55122 Mainz
Germany

Pavol Cekan

The Rockefeller University
Laboratory of RNA Molecular
Biology
Howard Hughes Medical
Institute
1230 York Avenue, Box 186
New York, NY 10065
USA

Clément Chevalier

Université de Strasbourg
Architecture et Réactivité de
l'ARN
UPR 9002 CNRS
IBMC
15, rue René Descartes
67084 Strasbourg
France

Jerzy Ciesiolka

Polish Academy of Sciences
Institute of Bioorganic Chemistry
Laboratory of RNA Biochemistry
Noskowskiego 12/14
61-704 Poznan
Poland

Thomas A. Cooper

Baylor College of Medicine
Department of Pathology and
Immunology
One Baylor Plaza
Houston, TX 77030
USA

Simona Cuzic-Feltens

Martin-Luther Universität Halle
Naturwissenschaftliche Fakultät I
– Biowissenschaften
Institut für Biochemie und
Biotechnologie
Kurt-Mothes Str.3
06120 Halle (Saale)
Germany

Andrey Damianov

Justus-Liebig-Universität Giessen
Institut für Biochemie
Heinrich-Buff-Ring 58
35392 Giessen
Germany

and

University of California
at Los Angeles
Howard Hughes Medical
Institute
Los Angeles, CA 90095
USA

Julia Dannenberg

Max Planck Institute of
Biophysical Chemistry
Department of Cellular
Biochemistry
Am Fassberg 11
37077 Göttingen
Germany

François Disdier

Université de Strasbourg
Equipe de Biophysique et
Biologie Structurale
Unité 'Architecture et Réactivité
de l'ARN'
Institut de Biologie Moléculaire et
Cellulaire du CNRS
15, rue René Descartes
67084 Strasbourg
France

Olwen Domingo

Johannes Gutenberg-Universität
Institute of Pharmacy and
Biochemistry
Staudinger Weg 5
55128 Mainz
Germany

Philippe Dumas

Université de Strasbourg
Equipe de Biophysique et
Biologie Structurale
Unité 'Architecture et Réactivité
de l'ARN'
Institut de Biologie Moléculaire et
Cellulaire du CNRS
15, rue René Descartes
67084 Strasbourg
France

Olexandr Dybkov

Max-Planck-Institute for
Biophysical Chemistry
Department of Cellular
Biochemistry
Am Fassberg 11
37077 Göttingen
Germany

Laura E. Easton

MRC Laboratory of Molecular
Biology
Structural Studies Division
Hills Road
Cambridge CB2 0QH
UK

Thomas E. Edwards

University of Iceland
Department of Chemistry
Science Institute
Dunhaga 3
107 Reykjavik
Iceland

David R. Engelke

University of Michigan
Department of Biological
Chemistry
1150 W. Medical Center Drive
Ann Arbor, MI 48109-0600
USA

Markus Englert

Yale University
Department of Molecular
Biophysics and Biochemistry
Howard Hughes Medical
Institute
New Haven, CT 06520-8114
USA

Eric Ennifar

Université de Strasbourg
Equipe de Biophysique et
Biologie Structurale
Unité 'Architecture et Réactivité
de l'ARN'
Institut de Biologie Moléculaire et
Cellulaire du CNRS
15, rue René Descartes
67084 Strasbourg
France

Dirk Eulberg

Neue Welt 14
10247 Berlin
Germany

and

NOXXON Pharma AG
Max-Dohrn-Str. 8-10
10589 Berlin
Germany

Patrizia Fabrizio

Max Planck Institute of
Biophysical Chemistry
Department of Cellular
Biochemistry
37077 Göttingen
Germany

Thalia A. Farazi

The Rockefeller University
Laboratory of RNA Molecular
Biology
Howard Hughes Medical
Institute
1230 York Avenue
New York, NY 10065
USA

Olga Fedorova

Yale University and Howard
Hughes Medical Institute
Department of Molecular Cellular
and Developmental Biology
266 Whitney Avenue
New Haven, CT 06520
USA

Carol A. Fierke

University of Michigan
Department of Chemistry
930 North University
Ann Arbor, MI 48189-1055
USA

Mikko J. Frilander

University of Helsinki
Institute of Biotechnology
PL56 (Viikinkaari 9)
00014 Helsinki
Finland

Daniel Gautheret

Université Paris-Sud
CNRS-UMR8621
Institut de Génétique et
Microbiologie
Bâtiment 400
91405 Orsay Cedex
France

Robert Giegerich

Bielefeld University
Faculty of Technology and Center
of Biotechnology
Universitätsstrasse
33501 Bielefeld
Germany

Olaf Gimpl

Bayerische
Julius-Maximilians-Universität
Institut für Biochemie
Biozentrum
Am Hubland
97074 Würzburg
Germany

Markus Gößringer

Philipps-Universität Marburg
Institut für Pharmazeutische
Chemie
Marbacher Weg 6
35037 Marburg
Germany

Arnold Grünweller

Philipps-Universität Marburg
Institute of Pharmaceutical
Chemistry
Marbacher Weg 6
35037 Marburg
Germany

Inna Grishina

Justus-Liebig-Universität Giessen
Institut für Biochemie
Heinrich-Buff-Ring 58
35392 Giessen
Germany

and

Justus-Liebig-Universität Giessen
Biochemisches Institut
Friedrichstrasse 24
35392 Giessen
Germany

Markus Hafner

The Rockefeller University
Howard Hughes Medical
Institute
Laboratory of RNA Molecular
Biology
1230 York Avenue
New York, NY 10065
USA

Dinari A. Harris

University of Michigan
Department of Chemistry
930 N. University
Ann Arbor, MI 48109-1055
USA

Michael E. Harris

Case Western Reserve University
School of Medicine
Department of Biochemistry
10900 Euclid Avenue
Cleveland, OH 44106-4973
USA

Roland K. Hartmann

Philipps-Universität Marburg
Fachbereich Pharmazie
Institut für Pharmazeutische
Chemie
Marbacher Weg 6
Building C
35037 Marburg
Germany

Jean Hausser

University of Basel
Biozentrum
Klingelbergstrasse 50-70
4056 Basel
Switzerland

Corina G. Heidrich

Friedrich-Alexander-Universität
Erlangen-Nürnberg
Lehrstuhl für Mikrobiologie
Department Biologie
Staudtstr. 5
91058 Erlangen
Germany

Anne-Catherine Helfer

Université de Strasbourg
Architecture et Réactivité de
l'ARN
UPR 9002 CNRS
IBMC
15, rue René Descartes
67084 Strasbourg
France

Mark Helm

Johannes Gutenberg-Universität
Mainz
Institut für Pharmazie und
Biochemie
Staudinger Weg 5
55128 Mainz
Germany

Dominik Helmecke

Philipps-Universität Marburg
Institut für Pharmazeutische
Chemie
Marbacher Weg 6
35037 Marburg
Germany

Martin Hengesbach

University of California
Santa Cruz
Department of Chemistry and
Biochemistry
1156 High St
Santa Cruz, CA 95060
USA

Niklas Henriksson

Uppsala University
Department of Cell and
Molecular Biology
BMC
Husargatan 3
751 24 Uppsala
Sweden

Wolfgang R. Hess

University of Freiburg
Faculty of Biology
Genetics & Experimental
Bioinformatics
Institute of Biology III
Schänzlestr. 1
79104 Freiburg
Germany

Gerald Hinze

Johannes Gutenberg-Universität
Institute of Physical Chemistry
Duesbergweg 10-14
55099 Mainz
Germany

Jessica I. Hoell

The Rockefeller University
Laboratory of RNA Molecular
Biology
Howard Hughes Medical
Institute
1230 York Avenue
New York, NY 10065
USA

Alexander Hüttenhofer

Innsbruck Medical University
Section for Genomics and
RNomics
Innsbruck Biocenter
Fritz Pregl Strasse 3
6020 Innsbruck
Austria

Jingyi Hui

Justus-Liebig-Universität Giessen
Institut für Biochemie
Heinrich-Buff-Ring 58
35392 Giessen
Germany

and

Institute of Biochemistry and
Cell Biology
Chinese Academy of Sciences
200031 Shanghai
China

Martin R. Jakobsen

Aarhus University
Department of Molecular Biology
and Genetics
C.F.Møllers Alle
8000 Aarhus C
Denmark

Fabrice Jossinet

Université de Strasbourg
Architecture et Réactivité de
l'ARN
Institut de Biologie Moléculaire et
Cellulaire du CNRS
67084 Strasbourg
France

Mohsen Khorshid

Biozentrum der Universität Basel
and Swiss Institute of
Bioinformatics (SIB)
Klingelbergstr. 50–70
4056 Basel
Switzerland

Leif A. Kirsebom

Uppsala University
Department of Cell and
Molecular Biology
Biomedical Center
Box 596
751 24 Uppsala
Sweden

Jørgen Kjems

University of Aarhus
Interdisciplinary Nanoscience
Center (iNANO)
Ny Munkegade 118
8000 Aarhus C
Denmark

and

University of Aarhus
Department of Molecular Biology
and Genetics
C. F. Møllers Allé 3
8000 Aarhus C
Denmark

Sven Klussmann

Thrasoltstr. 1
10585 Berlin
Germany

and

NOXXON Pharma AG
Max-Dohrn-Str. 8-10
10589 Berlin
Germany

Karen Köhler

Philipps-Universität Marburg
Institut für Pharmazeutische
Chemie
Marbacher Weg 6
35037 Marburg
Germany

Julian König

MRC Laboratory of Molecular
Biology
Department of Structural Studies
Hills Road
Cambridge CB2 0QH
UK

Jiro Kondo

Sophia University
Department of Materials and
Life Sciences
Faculty of Science and
Technology
7-1 Kioi-cho, Chiyoda-ku
102-8554, Tokyo
Japan

Markus Landthaler

Max-Delbrück-Center for
Molecular Medicine
Berlin Institute for Medical
Systems Biology
Robert-Rössle-Str. 10
13125 Berlin
Germany

Stephen Leong Koan

Université de Montréal
Institute for Research in
Immunology and Cancer (IRIC)
Department of Computer Science
Montréal QC H3C 3J7
Canada

Efthimia Lioliou

Université de Strasbourg
Architecture et Réactivité de
l'ARN
UPR 9002 CNRS
IBMC
15, rue René Descartes
67084 Strasbourg
France

Reinhard Lührmann

Department of Cellular
Biochemistry
Max-Planck-Institute for
Biophysical Chemistry
Am Fassberg 11
37077 Göttingen
Germany

Martin Lützelberger

Technical University of
Braunschweig
Institute of Genetics
Spielmannstr. 7
38 106 Braunschweig
Germany

Peter J. Lukavsky

MRC Laboratory of
Molecular Biology
Structural Studies Division
Hills Road
Cambridge CB2 0QH
UK

and

Masaryk University
CEITEC - Central European
Institute of Technology
Kamenice 5/A4/2.33
62500 Brno
Czech Republic

Christian Maasch

Ernststr. 27
13509 Berlin
Germany

and

NOXXON Pharma AG
Max-Dohrn-Str. 8-10
10589 Berlin
Germany

François Major

Université de Montréal
Institute for Research in
Immunology and Cancer (IRIC)
Department of Computer Science
Montréal QC H3C 3J7
Canada

Virginie Marchand

Nancy Université
Laboratoire ARN-RNP
Maturation-Structure-Fonction
Enzymologie Moléculaire et
Structurale (AREMS)
UMR 7214 CNRS-UL
Batiment Biopôle
9, avenue de la Forêt de Haye
54506 Vandoeuvre-les-Nancy
France

and

European Molecular Biology
Laboratory (EMBL)
Meyerhofstrasse 1
69117 Heidelberg
Germany

Anita Marchfelder

Universität Ulm
Biologie II
Albert-Einstein-Allee 11
89069 Ulm
Germany

Manja Marz

Friedrich-Schiller-University Jena
Faculty of Mathematics and
Computer Science
Leutragraben 1
07743 Jena
Germany

Stefano Marzi

Université de Strasbourg
Architecture et Réactivité de
l'ARN
UPR 9002 CNRS
IBMC
15, rue René Descartes
67084 Strasbourg
France