

Crystallization Of Nucleic Acids And Proteins A Practical Approach

A review of innovative tools for creative nucleic acid chemists that open the door to novel probes and therapeutic agents Nucleic acids continue to gain importance as novel diagnostic and therapeutic agents. With contributions from noted scientists and scholars, Enzymatic and Chemical Synthesis of Nucleic Acid Derivatives is a practical reference that includes a wide range of approaches for the synthesis of designer nucleic acids and their derivatives. The book covers enzymatic (including chemo-enzymatic) methods, with a focus on the synthesis and incorporation of modified nucleosides. The authors also offer a review of innovative approaches for the non-enzymatic chemical synthesis of nucleic acids and their analogs and derivatives, highlighting especially challenging species. The book offers a concise review of the methods that prepare novel and heavily modified polynucleotides in sufficient amount and purity for most clinical and research applications. This important book: -Presents a timely and topical guide to the synthesis of designer nucleic acids and their derivatives -Addresses the growing market for nucleotide-derived pharmaceuticals used as anti-infectives and chemotherapeutic agents, as well as fungicides and other agrochemicals. -Covers novel methods and the most recent trends in the field -Contains contributions from an international panel of noted scientists Written for biochemists, medicinal chemists, natural products chemists, organic chemists, and biotechnologists, Enzymatic and Chemical Synthesis of Nucleic Acid Derivatives is a practice-oriented guide that reviews innovative methods for the enzymatic as well as non-enzymatic synthesis of nucleic acid species.

Reversible phosphorylation is one of the major mechanisms of controlling protein activity in all eukaryotic cells. This new edition of Protein Phosphorylation: A Practical Approach provides a comprehensive description of current methods used to study protein phosphorylation and the kinases and phosphatases which catalyse it. It includes protocols for studying phosphorylation in intact cells; analysis of signal transduction pathways, kinase specificity, and kinase interactions; assay and purification of kinases and phosphatases; and identification of substrates. Also covered are cloning and expression protocols and advice on the crystallization of kinases and phosphatases. Protein Phosphorylation: A Practical Approach 2e will therefore be of great value to any researcher investigating aspects of reversible protein phosphorylation. Crystallography is the major method of determining structures of biological macromolecules yet crystallization techniques are still regarded as difficult to perform. This new edition of Crystallization of Nucleic Acids and Proteins: A Practical Approach continues in the vein of the first edition by providing a detailed and rational guide to producing crystals of proteins and nucleic acids of sufficient quantity and quality for diffraction studies. It has been thoroughly updated to include all the major new techniques such as the uses of molecular biology in structural biology (maximizing expression systems, sequence modifications to enable crystallization, and the introduction of anomalous scatterers); diagnostic analysis of prenucleation and nucleation by spectroscopic methods; and the two-dimensional electron crystallography of soluble proteins on planar lipid films. As well as an introduction to crystallogenes, the other topics covered are: Handling macromolecular solutions, experimental design, seeding, proceeding from solutions to crystals Crystallization in gels Crystallization of nucleic acid complexes and membrane proteins Soaking techniques Preliminary characterization of crystals in order to tell whether they are suitable for diffraction studies. As with all Practical Approach books the protocols have been written by experienced researchers and are tried and tested methods. The underlying theory is brought together with the laboratory protocols to provide researchers with the conceptual and methodological tools necessary to exploit these powerful techniques. Crystallization of Nucleic Acids and Proteins: A

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Practical Approach 2e will be an invaluable manual of practical crystallization methods to researchers in molecular biology, crystallography, protein engineering, and biological chemistry. Spherical nucleic acids (SNAs) comprise a nanoparticle core and a densely packed and highly oriented nucleic acid shell, typically DNA or RNA. They have novel architecture-dependent properties that distinguish them from all other forms of nucleic acids and make them useful in materials synthesis, catalysis, diagnostics, therapeutics, and optics/plasmonics. This book covers over two decades of the author's research on SNAs and their anisotropic analogues, including synthesis and fundamental properties, and applications in colloidal crystallization, adaptive matter, and nanomedicine, spanning extra- and intracellular diagnostics, gene regulation, and immunomodulation.

Synthesizing over thirty years of advances into a comprehensive textbook, Biomolecular Crystallography describes the fundamentals, practices, and applications of protein crystallography. Deftly illustrated in full-color by the author, the text describes mathematical and physical concepts in accessible and accurate language. It distills key co

This text offers in-depth perspectives on every aspect of protein structure identification, assessment, characterization, and utilization, for a clear understanding of the diversity of protein shapes, variations in protein function, and structure-based drug design. The authors cover numerous high-throughput technologies as well as computational methods to study protein structures and residues. A valuable reference, this book reflects current trends in the effort to solve new structures arising from genome initiatives, details methods to detect and identify errors in the prediction of protein structural models, and outlines challenges in the conversion of routine processes into high-throughput platforms.

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Spherical nucleic acids (SNAs) comprise a nanoparticle core and a densely packed and highly oriented nucleic acid shell, typically DNA or RNA. They have novel architecture-dependent properties that distinguish them from all other forms of nucleic acids and make them useful in materials synthesis, catalysis, diagnostics, therapeutics, and optics/plasmonics. This book covers over two decades of Dr. Mirkin's research on SNAs and their anisotropic analogues, including synthesis and fundamental properties, and applications in colloidal crystallization, adaptive matter, and nanomedicine, spanning extra- and intracellular diagnostics, gene regulation, and immunomodulation. It is a reprint volume that compiles 101 key papers from high-impact journals in this research area published by the Mirkin Group at Northwestern University, Illinois, USA, within the International Institute for Nanotechnology, and collaborators. Volume 1 provides an overview and a historical framework of engineering matter from DNA-modified constructs and discusses the enabling features of nucleic acid-functionalized nanomaterials. Volume 2 covers design rules for colloidal crystallization, building blocks for crystal engineering, and DNA and RNA as programmable bonds. Volume 3 discusses colloidal crystallization processes and routes to hierarchical assembly, dynamic nanoparticle superlattices, surface-based and template-confined colloidal crystallization, optics and plasmonics with nanoparticle superlattices, and postsynthetic modification and catalysis with nanoparticle superlattices. Volume 4 covers diagnostic modalities, and intracellular therapeutic and diagnostic schemes based upon nucleic acid-functionalized nanomaterials.

An electrorheological crystalline mass of a molecule is formed by dispersing the molecule in a dispersion fluid and subjecting the molecule dispersion to a uniform electrical field for a period of time during which time an electrorheological crystalline mass is formed. Molecules that may be used to form an electrorheological crystalline

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mass include any organic or inorganic molecule which has a permanent dipole and/or which is capable of becoming an induced dipole in the presence of an electric field. The molecules used to form the electrorheological crystalline mass are preferably macromolecules, such as biomolecules, such as proteins, nucleic acids, carbohydrates, lipoproteins and viruses. Molecules are crystallized by a method in which an electric field is maintained for a period of time after the electrorheological crystalline mass has formed during which time at least some of the molecules making up the electrorheological crystalline mass form a crystal lattice. The three dimensional structure of a molecule is determined by a method in which an electrorheological crystalline mass of the molecule is formed, an x-ray diffraction pattern of the electrorheological crystalline mass is obtained and the three dimensional structure of the molecule is calculated from the x-ray diffraction pattern.

Crystallization is an important separation and purification process used in industries ranging from bulk commodity chemicals to specialty chemicals and pharmaceuticals. In recent years, a number of environmental applications have also come to rely on crystallization in waste treatment and recycling processes. The authors provide an introduction to the field of newcomers and a reference to those involved in the various aspects of industrial crystallization. It is a complete volume covering all aspects of industrial crystallization, including material related to both fundamentals and applications. This new edition presents detailed material on crystallization of biomolecules, precipitation, impurity-crystal interactions, solubility, and design. Provides an ideal introduction for industrial crystallization newcomers Serves as a worthwhile reference to anyone involved in the field Covers all aspects of industrial crystallization in a single, complete volume

The second edition of a highly acclaimed handbook and ready reference. Unmatched in its breadth and quality, around 100 specialists from all over the world share their up-to-date expertise and experiences, including hundreds of protocols, complete with explanations, and hitherto unpublished troubleshooting hints. They cover all modern techniques for the handling, analysis and modification of RNAs and their complexes with proteins. Throughout, they bear the practising bench scientist in mind, providing quick and reliable access to a plethora of solutions for practical questions of RNA research, ranging from simple to highly complex. This broad scope allows the treatment of specialized methods side by side with basic biochemical techniques, making the book a real treasure trove for every researcher experimenting with RNA.

The crystallization of RiboNucleic Acids (RNA) was studied from the standpoint of mechanisms of crystal growth in three tasks: (1) preparation of high-quality crystals of oligonucleotides for X-ray diffraction, (2) finding pathways to the growth of high-quality crystals for X-ray diffraction and (3) investigation of mechanisms of action of inertial acceleration on crystal growth. In these tasks: (1) RNA crystals were prepared and studied by X-ray diffraction; (2) a pathway to high-quality crystals was discovered and characterized; a combination of kinetic and equilibrium factors could be optimized as described below; and (3) an interplay between purity and gravity was found in a combination of space and ground experiments with nucleic acids and proteins. Most significantly, the rate of concentration of precipitant and RNA can be controlled by membrane-based methods of water removal or by diffusion of multivalent cations across an interface stabilized by a membrane. Oligonucleotide solutions are

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electrokinetically stabilized colloids, and crystals can form by the controlled addition of multivalent cations. Todd, Paul Marshall Space Flight Center NAG8-1165...

X-ray crystallography is the major method of determining biological structures yet the procedures involved in obtaining the required crystals are still seen as something of a black art by many molecular biologists. As with the previous edition this book will dispel this idea by providing a detailed and rational guide to obtaining crystals of proteins and nucleic acids for diffraction studies.

This extensively illustrated book by Alexander McPherson, a master practitioner, accomplishes several important goals: it presents the underlying physical and chemical principles of crystallization in an approachable way; it provides the reader with a biochemical context in which to understand and pursue successful crystal growth; it instructs the reader in practical aspects of the technologies required; and it lays out effective strategies for success that investigators can readily apply to their own experimental questions. This readable volume has been created for every investigator in biomedicine whose studies may require a shift in focus from gene to protein product, as well as chemists and physicists interested in the functions of biologically active macromolecules.

This unique and practical resource provides the most complete and concise summary of underlying principles and approaches to studying nucleic acid structure, including discussion of x-ray crystallography, NMR, molecular modelling, and databases. Its focus is on a survey of structures especially important for biomedical research and pharmacological applications. To aid novices, Principles of Nucleic Acid Structure includes an introduction to technical lingo used to describe nucleic acid structure and conformations (roll, slide, twist, buckle, etc.). This completely updated edition features expanded coverage of the latest advances relevant to recognition of DNA and RNA by small molecules and proteins. In particular, the reader will find extensive new discussions on: RNA folding, ribosome structure and antibiotic interactions, DNA quadruplexes, DNA and RNA protein complexes, and short interfering RNA (siRNA). This handy guide ends with a complete list of resources, including relevant online databases and software. Completely updated with expanded discussion of topics such as RNA folding, ribosome structure and antibiotic interactions, DNA quadruplexes, DNA and RNA protein complexes, and short interfering RNA (siRNA) Includes a complete list of resources, including relevant online databases and software Defines technical lingo for novices

This volume includes comprehensive and up-to-date coverage of all nucleic-acid-specific steps used in X-ray crystallography, from macromolecule production to structure determination. Chapters dedicated to RNA preparation and crystallogenesis will be of interest to beginners, while chapters focused on data collection, phasing and refinement will be particularly useful to researchers with a higher level of expertise. Several functional case studies are also presented in the last part of the book. Written in the highly successful Methods in Molecular Biology series format, chapters include introductions to their respective topics, lists of the necessary materials and reagents, step-by-step, readily reproducible laboratory protocols, and tips on troubleshooting and avoiding known pitfalls. Authoritative and thorough, Nucleic Acid Crystallography: Methods and Protocols presents protocols that are aimed at both researchers and students who are interested in the structural biology of DNA or RNA, alone or in complex with proteins or ligands.

Progress in Nucleic Acid Research and Molecular Biology

Medicinal Chemistry, Volume 75, the latest release in the Advances in Inorganic Chemistry series, presents timely and informative summaries on current progress in a variety of subject areas. This acclaimed serial features reviews written by experts in the field, serving as an indispensable reference to advanced researchers that empowers readers to pursue new

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developments in each field. Users will find this to be a comprehensive overview of recent findings and trends from the last decade that covers various kinds of inorganic topics, from theoretical oriented supramolecular chemistry, to the quest for accurate calculations of spin states in transition metals. Provides the authority and expertise of leading contributors from an international board of authors Presents the latest release in the Advances in Inorganic Chemistry series Includes the latest information on medicinal chemistry

This volume of Current Topics in Membranes focuses on Membrane Protein Crystallization, beginning with a review of past successes and general trends, then further discussing challenges of membranes protein crystallization, cell free production of membrane proteins and novel lipids for membrane protein crystallization. This publication also includes tools to enhance membrane protein crystallization, technique advancements, and crystallization strategies used for photosystem I and its complexes, establishing Membrane Protein Crystallization as a needed, practical reference for researchers.

This volume provides methods for modern macromolecular crystallography, including all steps leading to crystal structure determination and analysis. Written in the highly successful Methods in Molecular Biology series format, chapters include introductions to their respective topics, lists of the necessary materials and reagents, step-by-step, readily reproducible laboratory protocols, and tips on troubleshooting and avoiding known pitfalls. Authoritative and practical, Protein Crystallography aims to ensure successful results in the further study of this vital field.

Researchers in structural genomics continue to search for biochemical and cellular functions of proteins as well as the ways in which proteins assemble into functional pathways and networks using either experimental or computational approaches. Based on the experience of leading international experts, Structural Genomics and High Throughput Stru

Crystallography Made Crystal Clear is designed to meet the need for an X-ray analysis that is between brief textbook sections and complete treatments. The book provides non-crystallographers with an intellectually satisfying explanation of the principles of how protein models are gleaned from X-ray analysis. The understanding of these concepts will foster wise use of the models, including the recognition of the strengths and weaknesses of pictures or computer graphics. Since proteins comprise the majority of the mass of macromolecules in cells and carry out biologically important tasks, the book will be of interest to biologists. Provides accessible descriptions of principles of x-ray crystallography, built on simple foundations for anyone with a basic science background Leads the reader through clear, thorough, unintimidating explanations of the mathematics behind crystallography Explains how to read crystallography papers in research journals If you use computer-generated models of proteins or nucleic acids for: Studying molecular interactions Designing ligands, inhibitors, or drugs Engineering new protein functions Interpreting chemical, kinetic, thermodynamic, or spectroscopic data Studying protein folding Teaching macromolecule structure, and if you want to read new structure papers intelligently; become a wiser user of macromolecular models; and want to introduce undergraduates to the important subject of x-ray crystallography, then this book is for you.

Macromolecular Crystallography is the study of macromolecules (proteins and nucleic acids) using X-ray crystallographic techniques in order to determine their molecular structure. The knowledge of accurate molecular structures is a pre-requisite for rational drug design, and for structure-based function studies to aid the development of effective therapeutic agents and drugs. The successful determination of the complete genome (genetic sequence) of several species (including humans) has recently

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directed scientific attention towards identifying the structure and function of the complete complement of proteins that make up that species; a new and rapidly growing field of study called 'structural genomics'. There are now several important and well-funded global initiatives in operation to identify all of the proteins of key model species. One of the main requirements for these initiatives is a high-throughput crystallization facility to speed-up the protein identification process. The extent to which these technologies have advanced, calls for an updated review of current crystallographic theory and practice. This practical reference book features the latest conventional and high-throughput methods, and includes contributions from a team of internationally recognized leaders and experts. It will be of relevance and use to graduate students, research scientists and professionals currently working in the field of conventional and high-throughput macromolecular crystallography.

Biology has entered an era in which interdisciplinary cooperation is at an all-time high, practical applications follow basic discoveries more quickly than ever before, and new technologies--recombinant DNA, scanning tunneling microscopes, and more--are revolutionizing the way science is conducted. The potential for scientific breakthroughs with significant implications for society has never been greater. Opportunities in Biology reports on the state of the new biology, taking a detailed look at the disciplines of biology; examining the advances made in medicine, agriculture, and other fields; and pointing out promising research opportunities. Authored by an expert panel representing a variety of viewpoints, this volume also offers recommendations on how to meet the infrastructure needs--for funding, effective information systems, and other support--of future biology research. Exploring what has been accomplished and what is on the horizon, Opportunities in Biology is an indispensable resource for students, teachers, and researchers in all subdisciplines of biology as well as for research administrators and those in funding agencies.

New found interest in the chromosome G-quadruplexes has emerged as an important focus of research in nucleic acids and as a potential target for cancer therapeutics. Existing literature concerning nucleic acids concentrates on aspects of quadruplex structure and historical research. There exists no single comprehensive resource addressing recent advances in therapeutic application and targeting strategies, until now. Quadruplex Nucleic Acids as Therapeutic Targets will be a vital resource for researchers in biochemistry, molecular biology, chemistry, biotechnology, biophysics, medicine, translational science and pharmacology. This timely publication is the first to offer practical application and direct strategies to meet the needs of emerging research. This is one of the first books dedicated to the emerging field of neutron protein crystallography (NPC). The text covers all of the practical aspects of NPC, from the basic background of neutron scattering and diffraction, to the technical details of neutron facilities, growth of high-quality crystals, and data analysis. The final chapter is devoted to providing many examples of using NPC to investigate a wide range of different proteins. It demonstrates how NPC can explore hydrogen bonds, protonation and deprotonation of amino acid residues, hydration structures, and hydrogen-to-deuterium exchange ratios. To avoid redundancy with other textbooks on X-ray protein crystallography (XPC), this book assumes a familiarity with the basics of XPC and strives to highlight and explain the differences between XPC and NPC. It is therefore especially useful for X-ray protein crystallographers who are eager to have a sound,

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scientific basis for judging if NPC is the right technique for furthering their experimental programs.

Nucleic acids play important roles in living systems by storing and transferring genetic information and directing protein synthesis. Recently, it was found that nucleic acids can catalyze chemical and biochemical reactions similar to protein enzymes. In addition, they can also serve as drug targets for the treatment of deadly diseases such as AIDS and cancers. As a result, the 3D structure study of nucleic acids and protein-nucleic acids complexes by X-ray crystallography has become one of the most active research areas. However, the two intrinsic bottlenecks of macromolecule X-ray crystallography, including crystallization and phase determination, have significantly limited its application in study and discovery of the new structures and folds, as well as in exploration of the biological mechanisms. So far, the selenium derivatization (Se-Met) of proteins and multiple anomalous dispersion (MAD) or single anomalous dispersion (SAD) technology have revolutionized the protein crystallography field by providing a rational solution to solve the phase determination problem. Similarly, it is important and urgent to develop a corresponding methodology for nucleic acid X-ray crystallography. The work presented here includes two general research directions: the selenium derivatized nucleic acids (SeNA) and tellurium derivatized nucleic acids (TeNA): 1) The SeNA strategy by site-specifically replacing oxygen with selenium at the 2' and 4 positions of thymidine and uridine has been developed. We found that the selenium derivatization at both sites are relatively stable and doesn't cause significant structure perturbations by comparing with their corresponding native counterparts. In addition to the phase determination, the 2'-Se modification can also facilitate crystal growth of many oligonucleotides. Moreover, we have observed colorful DNAs and RNAs with the 4-Se modification for the first time. 2) The TeNA strategy by covalently incorporating tellurium functionalities into different positions of nucleic acids, particularly at the 2' and 5 position of thymidine, has been developed. We have demonstrated the compatibility of the tellurium modification and solid-phase synthesis, as well as the potential application of the tellurium modifications in anti-viral drug synthesis and DNA-damage investigation.

Reprint. Originally published in 1982 by Wiley. McPherson (biochemistry, U. of Calif. Riverside) provides an interface between the techniques and practices common to most biochemists and the procedures familiar to x-ray diffractionists. Acidic paper. Annotation copyright Book News, Inc. Portland, Or

Macromolecular Crystallography Protocols, now in two volumes, examines major developments that have occurred since publication of the acclaimed first edition nearly a decade ago. Volume 1, Preparation and Crystallization of Macromolecules and Volume 2, Structure Determination, explore recent advances that have accelerated the pace of structural determination and made crystallography accessible to a broader range of investigators. Volume 1 is composed of detailed protocols for the preparation and optimization of crystals, including tips from the experts on the best methods for inducing proteins to adopt their crystalline form. Volume 2 complements the first volume by addressing laboratory techniques for crystal handling and structural characterization, as well as computational techniques for data collection, phasing, and refinement. The volume concludes with a detailed and insightful survey of available crystallographic software. These volumes will be an indispensable reference for obtaining

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macromolecular crystals and determining their three-dimensional structure. International Tables for Crystallography are no longer available for purchase from Springer. For further information please contact Wiley Inc. (follow the link on the right hand side of this page). The purpose of Volume C is to provide the mathematical, physical and chemical information needed for experimental studies in structural crystallography. The volume covers all aspects of experimental techniques, using all three principal radiation types, from the selection and mounting of crystals and production of radiation, through data collection and analysis, to interpretation of results. As such, it is an essential source of information for all workers using crystallographic techniques in physics, chemistry, metallurgy, earth sciences and molecular biology. Concise but complete, this mini-encyclopedia contains over 1,500 entries covering all important concepts, compounds, techniques and acronyms for quick and easy reference. Guiding readers through the ever-increasing jungle of nucleic acid science and technology, the book distills the key information out of the large body of primary literature and presents it in a single volume. A first-stop resource for everyone, from students to established researchers, as both a desktop and library reference.

Thermus—Advances in Research and Application: 2013 Edition is a ScholarlyBrief™ that delivers timely, authoritative, comprehensive, and specialized information about ZZZAdditional Research in a concise format. The editors have built Thermus—Advances in Research and Application: 2013 Edition on the vast information databases of ScholarlyNews.™ You can expect the information about ZZZAdditional Research in this book to be deeper than what you can access anywhere else, as well as consistently reliable, authoritative, informed, and relevant. The content of Thermus—Advances in Research and Application: 2013 Edition has been produced by the world's leading scientists, engineers, analysts, research institutions, and companies. All of the content is from peer-reviewed sources, and all of it is written, assembled, and edited by the editors at ScholarlyEditions™ and available exclusively from us. You now have a source you can cite with authority, confidence, and credibility. More information is available at <http://www.ScholarlyEditions.com/>.

The precise knowledge of the structure of biological macromolecules forms the basis of understanding their function and their mechanism of action. It also lays the foundation for rational protein and drug design. The only method to obtain this knowledge is still crystallography. At present, the structures of about 400 proteins are known at or nearly at atomic proteins. However, only two of them are membrane proteins or complexes of the membrane proteins. The reasons for the difference is not the crystals of membrane proteins resists forming special problems when being analysed. The reason is that the membrane proteins resist into forming into well-ordered crystals. The intention of this book is to help to produce well-ordered crystals proteins and to provide guidelines, it is aimed at both biochemists and protein crystallographer's.

"Protein Structure Analysis - Preparation and Characterization" is a compilation of practical approaches to the structural analysis of proteins and peptides. Here, about 20 authors describe and comment on techniques for sensitive protein purification and analysis. These methods are used worldwide in biochemical and biotechnical research currently being carried out in pharmaceutical and biomedical laboratories or protein sequencing facilities. The chapters have been written by scientists with extensive experience in these fields, and the practical parts are well documented so that the reader

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should be able to easily reproduce the described techniques. The methods compiled in this book were demonstrated in student courses and in the EMBO Practical Course on "Microsequence Analysis of Proteins" held in Berlin September 10-15, 1995. The topics also derived from a FEBS Workshop, held in Halkidiki, Thessaloniki, Greece, in April, 1995. Most of the authors participated in these courses as lecturers and tutors and made these courses extremely lively and successful. Since polypeptides greatly vary depending on their specific structure and function, strategies for their structural analysis must for the most part be adapted to each individual protein. Therefore, advantages and limitations of the experimental approaches are discussed here critically, so that the reader becomes familiar with problems that might be encountered.

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