

Methods in Molecular Biology

VOLUME 176

Steroid Receptor Methods

Protocols and Assays

Edited by
Benjamin A. Lieberman



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Steroid Receptor Methods Protocols And Assays

Lauren Gardner



Steroid Receptor Methods Protocols And Assays:

Steroid Receptor Methods Benjamin A. Lieberman, 2001-08-10 A distinguished team of principal investigators and their associates describe in step by step detail a cross section of the latest research techniques available for studying the endocrine system As a basis for sophisticated biochemical analysis of receptor properties the contributors provide methods for the production and purification of a variety of receptors including progesterone glucocorticoid and androgen Other protocols allow the reader to experiment with DNA binding characteristics hormone binding assays and the use of combinatorial chemistry for drug discovery A series of novel methods utilizing the latest advances in immunochemistry yeast two hybrid screening and fluorescence are included for the detection and analysis of a variety of cellular proteins that influence steroid receptor effectiveness Methods in Molecular Biology: Steroid receptor methods : protocols and assays

John M. Walker, 1984 **Thyroid Hormone Receptors** Aria Baniahmad, 2008-02-05 A panel of outstanding investigators surveys and explains the major cutting edge methods used in thyroid receptor TR research and explains their practical experimental details Described in step by step detail to ensure robust experimental results the techniques presented cover a wide variety of key areas including TR in development and knockout mouse and Xenopus transcriptional regulation by TRs in both cell free systems and in living cells and TR mutant analysis of patients Additional methods provide powerful tools for the isolation of TR regulated protein complexes for studying the oncogene v Erba in blood cell differentiation and for target gene analysis in the brain Microarray chip methods are also presented for analyzing the organs of transgenic mice to identify target genes in the liver *Drug Discovery and Evaluation: Safety and Pharmacokinetic Assays* Franz J. Hock, Michael K. Pugsley, 2024-10-21 Many aspects of drug safety have become an outstanding and even persistent issue and may occur during the process of both drug discovery and development Until 15 years ago drug discovery and evaluation was primarily a sequential process starting with the selection of the most pharmacologically active compound from a series of newly synthesized small molecule chemical series by means of distinctive pharmacological assays Safety aspects were addressed by evaluation of the selected compound at high doses in a series of specific studies directed at indications other than the intended indication of the new compound These tests are then followed by pharmacokinetic studies which are primarily conducted to confirm whether the selected compound possesses a suitable half life for sufficient exposure and efficacy and whether it has the desired properties specificity to the intended route of administration Safety aspects relied predominantly on the conduct of single and repeat toxicology dose studies which inform changes in organ structure rather than organ function Both toxicological and pharmacokinetic studies are adapted to the progress of studies in clinical pharmacology and clinical trials The new edition of this well and broadly accepted reference work contains several innovative and distinguished chapters This sequential strategy has been abandoned with this new version of the book for several reasons Of the possible multitude of negative effects that novel drugs may impart on organ function e g ventricular tachy arrhythmia many are

detected too late in non clinical studies to inform clinicians On the other hand negative findings in chronic toxicity studies in animals may turn out to be irrelevant for human beings New scientific approaches e g high throughput screening human pluripotent stem cells transgenic animals knock out animals in silico models pharmaco genomics and pharmaco proteomics as well as Artificial Intelligence AI methods offered new possibilities There are several examples that show that the druggability of compounds was considerably underestimated when the probability of success of a new project was assessed The success rate in the pharmaceutical industry and the introduction of new chemical entities to the market per year dropped dramatically whereas the development time for a new compound increased sometimes exceeding the patent protection Research and development scientists involving the following changes therefore adopted a change of strategy Parallel instead of sequential involvement of the various disciplines multidimensional compound optimization The term Safety Pharmacology was coined The International Conference on Harmonization ICH founded a Safety Pharmacology Working Group and the Safety Pharmacology Society SPS was launched The discipline provided for evaluation development and validation of a multitude of safety tests outlined in the Core Battery of Studies Characterizing the exposure profile of a drug by conducting pharmacokinetic studies that evaluates the absorption distribution metabolism and excretion should to be investigated at an early stage of development as results contribute to the selection of a compound for further development Advancements in Toxicology were achieved by the introduction of new methods e g in silico methods genetic toxicology computational toxicology and AI The book is a landmark in the continuously changing world of drug research and developments As such it is essential reading for many groups not only for all students of pharmacology and toxicology but also for industry scientists and physicians especially those involved in clinical trials of drugs and for pharmacists who must know the safety requirements of drugs The book is essential for scientists and managers in the pharmaceutical industry who are involved in drug discovery drug development and decision making in the development process In particular the book will be of use to government institutions and committees working on official guidelines for drug evaluation worldwide

Biostatistical Methods Stephen W. Looney, 2008-02-03 Leading biostatisticians and biomedical researchers describe many of the key techniques used to solve commonly occurring data analytic problems in molecular biology and demonstrate how these methods can be used in the development of new markers for exposure to a risk factor or for disease outcomes Major areas of application include microarray analysis proteomic studies image quantitation genetic susceptibility and association evaluation of new biomarkers and power analysis and sample size **DNA-Protein Interactions** Tom Moss, 2008-02-02 Dr Tom Moss assembles the new standard collection of cutting edge techniques to identify key protein DNA interactions and define their components their manner of interaction and their manner of function both in the cell and in the test tube The techniques span a wide range from factor identification to atomic detail and include multiple DNA footprinting analyses including in vivo strategies gel shift EMSA optimization SELEX surface plasmon resonance site specific DNA protein

crosslinking and UV laser crosslinking Comprehensive and broad ranging DNA Protein Interactions Principles and Protocols 2nd Edition offers a stellar array of over 100 up to date and readily reproducible techniques that biochemists and molecular cellular and developmental biologists can use successfully today to understand DNA protein interactions *Protein Structure, Stability, and Folding* Kenneth P. Murphy, 2008-02-04 In Protein Structure Stability and Folding Kenneth P. Murphy and a panel of internationally recognized investigators describe some of the newest experimental and theoretical methods for investigating these critical events and processes Among the techniques discussed are the many methods for calculating many of protein stability and dynamics from knowledge of the structure and for performing molecular dynamics simulations of protein unfolding New experimental approaches presented include the use of co solvents novel applications of hydrogen exchange techniques temperature jump methods for looking at folding events and new strategies for mutagenesis experiments Unique in its powerful combination of theory and practice Protein Structure Stability and Folding offers protein and biophysical chemists the means to gain a more comprehensive understanding of some of this complex area by detailing many of the major techniques in use today *Posttranslational Modification of Proteins* Christoph Kannicht, 2008-02-04 Christoph Kannicht and a panel of highly experienced researchers describe readily reproducible methods for detecting and analyzing the posttranslational modifications of protein particularly with regard to protein function proteome research and the characterization of pharmaceutical proteins *PCR Detection of Microbial Pathogens* Konrad Sachse, Joachim Frey, 2003 Hands on laboratory experts present a set of classic PCR based methods for the identification and detection of important animal and food microbial pathogens including several zoonotic agents These proven techniques can be precisely applied to a wide variety of microbes among them *Campylobacter* spp *Chlamydiae* toxigenic *Clostridia* *Escherichia coli* STEC *Listeria monocytogenes* *Mycoplasmas* *Salmonellae* and *Yersinia enterocolitica* Additional chapters review the specificity and performance of diagnostic PCR analysis the pre PCR processing of samples the critical aspects of standardizing PCR methods and the general issues involved in using PCR technology for microbial diagnosis *High Throughput Screening* William P. Janzen, 2008-02-05 In High Throughput Screening leading scientists and researchers expert in molecular discovery explain the diverse technologies and key techniques used in HTS and demonstrate how they can be applied generically Writing to create precisely the introductory guidebook they wish had been available when they started in HTS these expert seasoned authors illuminate the HTS process with richly detailed tutorials on the biological techniques involved the management of compound libraries and the automation and engineering approaches needed Extensive discussions provide readers with all those key elements of pharmacology molecular biology enzymology and biochemistry that will ensure the identification of suitable targets and screens and detail the technology necessary to mine millions of data points for meaningful knowledge

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