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Actin is one of the most abundant proteins and ubiquitously expressed in all eukaryotes. In recent years, the analysis of structure and function of such complexes has shed new light on actin's role in cellular and tissue morphogenesis, locomotion and various forms of intracellular motility, but also on its role in nuclear processes like chromatin architecture and transcription. Progress in understanding these different physiological phenomena, but also in unravelling the basis of actin-based pathophysiological processes has been made by combining video microscopy, molecular biology, genetics and biochemistry. Thus, the current research on actin, as ongoing in many international laboratories, is a "hot spot" in basic and translational research in life sciences. In this book on "The Actin Cytoskeleton", twelve internationally renowned authors present specific chapters that cover their recent work concerned with the various roles of actin mentioned above. This comprehensive volume is therefore an attractive handbook for teachers and students in many fields of medicine and pharmacology. This detailed book explores a few of the plethora of techniques and applications

associated with the unique branch of science known as synthetic biology. Chemists, biologists, and engineers engaged in this multidisciplinary field of study will be guided in the creation and regulation of gene circuits, manipulation of biochemical pathways, genome editing and modification, creating genome language and computing, as well as molecular assembly. Written for the highly successful Methods in Molecular Biology series, chapters include introductions to their respective topics, lists of the necessary materials and reagents, step-by-step and readily reproducible protocols, plus troubleshooting tips and explanations of how to avoid pitfalls, all written by experts who have published their work in peer-reviewed journals. Authoritative and practical, Synthetic Biology: Methods and Protocols provides key guidance and ideas for conducting your own synthetic biology projects. This volume of the SALUS series contains author, subject, andgeographic indices for volumes 11-15 of the bibliography. Theauthor listing includes corporate authors and editors as well aspersonal authors. The numbers cited after each entry are theSALUS numbers that were assigned to the documents when theyappeared in the bibliography and can be used to look them up inthe appropriate volume. The book is based on lectures presented on the International Summer School on Biophysics held in Croatia in September 2009. The advantage of the School is that it provides advanced training in very broad scope of areas related to biophysics contrary to other similar schools or workshops that are centered mainly on one topic or technique. In this volume, tenth in the row, the papers in the field of biophysics are presented. The topics are biological phenomena from single protein to macromolecular aggregations structure by using variant physical methods (NMR, EPR, FTIR, Mass Spectrometry, etc.). The interrelationship of supramolecular structures and their functions is enlightened by applications of principals of these physical methods in the biophysical and molecular biology context. This volume details protocols that can be used for generation of knockout animals. Chapters guide the reader through basic protocols for three genome editing technologies, target design tools, and specific protocols for each animal. 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, Genome Editing in Animals: Methods and Protocols aims to ensure successful results in the further study of this vital field. The Nice Classification (NCL), established by the Nice Agreement (1957), is an international classification of goods and services applied for the registration of marks. Battlefields have been the object of fascination for millions of tourists and the subjects of elaborate interpretation projects. This volume will outline the process and results of developing the WWII Maritime Heritage Trail: Battle of Saipan Project. This book will provide examples of how a group of archaeologists, managers and a community took a specific battle and transformed it from a collection of unknown archaeological sites into a comprehensive storied battlescape that reflects the individuals and actions of those who were involved. It will provide an in-depth view of current maritime archaeological research on submerged battlefield sites, the development of a WWII battlefield maritime heritage trail, as well as the problems and solutions of such an effort. It will cover subjects such as: -heritage and dark tourism-conflict or battlefield

archaeology-public interpretation, and community engagement. This volume will serve as a practical review of a project influenced by a range of complementary areas of study and inclusive of many stakeholders, from the public to the professional and beyond. It provides an example of a balanced approach towards research and interpreting archaeological sites through the identification and inclusion of the various stakeholders (professional and community) and an awareness of what was being included, ignored, or inadequately represented in the research and interpretation. Handbook of Discrete and Combinatorial Mathematics provides a comprehensive reference volume for mathematicians, computer scientists, engineers, as well as students and reference librarians. The material is presented so that key information can be located and used quickly and easily. Each chapter includes a glossary. Individual topics are covered in sections and subsections within chapters, each of which is organized into clearly identifiable parts: definitions, facts, and examples. Examples are provided to illustrate some of the key definitions, facts, and algorithms. Some curious and entertaining facts and puzzles are also included. Readers will also find an extensive collection of biographies. This second edition is a major revision. It includes extensive additions and updates. Since the first edition appeared in 1999, many new discoveries have been made and new areas have grown in importance, which are covered in this edition. Space tethers are long cables which can be used for propulsion, momentum exchange, stabilization and altitude control, or maintaining the relative positions of the components of a large dispersed satellite/spacecraft sensor system. Depending on the mission objectives and altitude, spaceflight using this form of spacecraft propulsion may be significantly less expensive than spaceflight using rocket engines. A number of space tethers have been deployed in space missions. Tether satellites can be used for various purposes including research into tether propulsion, tidal stabilisation and orbital plasma dynamics. The use of CRISPR/Cas technology for genome editing suggests many potential applications, including the alteration of the germline of humans, animals and food crops. The speed and efficiency of the CRISPR/Cas system make it a potentially useful system for gene therapy. In this volume expert international authors provide a useful and timely review of the applications of the CRISPR/Cas system across diverse fields and explore further avenues and research directions of this novel and powerful editing technology. The technology and its application are reviewed with respect to reproduction and development, immunity and genetic diseases, system structure and system specificity. Some of the potential problems of the CRISPR/Cas system are also discussed, in particular the specificity of the system: this remains an important topic as improvement could lead to the more direct and efficient use of the CRISPR/Cas system in clinical settings. The authors also debate ethical concerns associated with this powerful new technology. This volume is a rigorous review of the applications and new opportunities for the CRISPR/Cas system and provides a stimulus for current and future research. An invaluable guide for all scientists working in the fields of genome editing and gene therapy the book is also recommended for all life sciences libraries. A collection of stories about those who love and care for horses and the complicated, passionate lives they lead apart from the nine-to-five world opens with a harrowing account of a young woman's abduction. Addressing random vibration of mechanical and structural systems, this work offers techniques for determining

probabilistic characteristics of the response of dynamic systems subjected to random loads or inputs and for calculating probabilities related to system performance or reliability. Antibody–drug conjugates (ADCs) represent one of the most promising and exciting areas of anticancer drug discovery. Five ADCs are now approved in the US and EU [i.e., ado-trastuzumab emtansine (KadcylaTM), brentuximab vedotin (AdcetrisTM), inotuzumab ozogamicin (BesponsaTM), gemtuzumab ozogamicin (MylotargTM) and moxetumomab pasudotox-tdfk (Lumoxiti®)] and over 70 others are in various stages of clinical development, with impressive interim results being reported for many. The technology is based on the concept of delivering a cytotoxic payload selectively to cancer cells by attaching it to an antibody targeted to antigens on the cell surfaces. This approach has several advantages including the ability to select patients as likely responders based on the presence of antigen on the surface of their cancer cells and a wider therapeutic index, given that ADC targeting enables a more efficient delivery of cytotoxic agents to cancer cells than can be achieved by conventional chemotherapy, thus minimising systemic toxicity. Although there are many examples of antibodies that have been developed for this purpose, along with numerous linker technologies used to attach the cytotoxic agent to the antibody, there is presently a relatively small number of payload molecules in clinical use. The purpose of this book is to describe the variety of payloads used to date, along with a discussion of their advantages and disadvantages and to provide information on novel payloads at the research stage that may be used clinically in the future. This reference surveys current best practices in the prevention and management of ventilator-induced lung injury (VILI) and spans the many pathways and mechanisms of VILI including cell injury and repair, the modulation of alveolar-capillary barrier properties, and lung and systemic inflammatory consequences of injurous mechanical ventilation. Considering many emerging therapeutic options, this guide also reviews the wide array of clinical studies on lung protection strategies and approaches to ARDS patients at risk for VILI. During the last ten years, remarkable progress has occurred in the study of molecular evolution. Among the most important factors that are responsible for this progress are the development of new statistical methods and advances in computational technology. In particular, phylogenetic analysis of DNA or protein sequences has become a powerful tool for studying molecular evolution. Along with this developing technology, the application of the new statistical and computational methods has become more complicated and there is no comprehensive volume that treats these methods in depth. Molecular Evolution and Phylogenetics fills this gap and present various statistical methods that are easily accessible to general biologists as well as biochemists, bioinformatists and graduate students. The text covers measurement of sequence divergence, construction of phylogenetic trees, statistical tests for detection of positive Darwinian selection, inference of ancestral amino acid sequences, construction of linearized trees, and analysis of allele frequency data. Emphasis is given to practical methods of data analysis, and methods can be learned by working through numerical examples using the computer program MEGA2 that is provided. In Situ Hybridization Protocols, Fourth Edition contains 21 protocols that utilize the in situ hybridization technology to document or take advantage of the visualization of specific RNA molecules. 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, In Situ Hybridization Protocols, Fourth Edition seeks to aid scientists in the further discovery of new RNA species and uncovering of their cellular functions. Eleven years ago the circular DNA of a novel single-stranded virus has been cloned and partially characterized by Nishizawa and Okamoto and their colleagues. According to the initials of the patient from whom the isolate originated, the virus was named TT virus. This name has been subsequently changed by the International Committee on Taxonomy of Viruses (ICTV) into Torque teno virus, permitting the further use of the abbreviation TTV. Although initially suspected to play a role in non A –E hepatitis, subsequent studies failed to support this notion. Within a remarkably short period of time it became clear that TT viruses are widely spread globally, infect a large proportion of all human populations studied thus far and represent an extremely heterogeneous group of viruses, now labelled as Anelloviruses. TT virus-like infections have also been noted in various animal species. The classification of this virus group turns out to be difficult, their DNA contains between 2200 and 3800 nucleotides, related so-called TT-mini-viruses and a substantial proportion of intragenomic recombinants further complicate attempts to combine these viruses into a unifying phylogenetic concept. Random Vibration in Mechanical Systems focuses on the fundamental facts and theories of random vibration in a form particularly applicable to mechanical engineers. The book first offers information on the characterization and transmission of random vibration. Discussions focus on the normal or Gaussian random process; excitation-response relations for stationary random processes; response of a single-degree-of-freedom system to stationary random excitation; wide-band and narrow-band random processes; and frequency decomposition of stationary random processes. The text then examines failure due to random vibration, including failure due to first excursion up to a certain level; fatigue failure due to a stationary narrow-band random stress process; failure due to an accumulation of damage; failure due to response remaining above a certain level for too great a fraction of the time; and failure mechanisms. The manuscript is a vital reference for mechanical engineers and researchers interested in random vibration in mechanical systems.