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Karin Nielsen-Saines

Genetics and Genomics of Eve Disease Xiaovi Raymond Gao, 2019-09-12 Genetics and Genomics of Eye Disease: Advancing to Precision Medicine thoroughly examines the latest genomics methods for studying eye disease, including complex eye disorders associated with multiple genes. GWAS, WES, WGS, RNA-sequencing, and transcriptome analysis as employed in ocular genomics are discussed in-depth, as are genomics findings tied to early-onset glaucoma, strabismus, age-related macular degeneration, adult-onset glaucoma, diabetic retinopathy, keratoconus, and leber congenital amaurosis, among other diseases. Research and clinical specialists offer guidance on conducting preventative screenings and counseling patients, as well as the promise of machine learning, computational statistics and artificial intelligence in advancing ocular genomics research. Offers thorough guidance on conducting genetic and genomic studies of eye disease Examines the genetic basis of a wide range of complex eye diseases and single-gene and Mendelian disorders Discusses the application of genetic testing and genetic risk prediction in eye disease diagnosis and patient counseling

<u>Discovery, Biosynthesis, Regulation, Transport, Release and Engineering of Plant Natural Products</u>
Pan Liao, Milen I. Georgiev, Wei Zhou, 2022-10-12

Resistance to Salinity and Water Scarcity in Higher Plants. Insights From Extremophiles and Stress-Adapted Plants: Tools, Discoveries and Future Prospects Ruth Grene, Nicholas J. Provart, José M. Pardo, 2019-08-15

Crop Improvement by Omics and Bioinformatics Yan Zhao, Jun Li, Zhichao Wu, Xueqiang Wang, 2024-04-11 Crop improvement has been continuously driven by the demand for food security and sustainability. The caloric and nutritional needs of a growing world population require that global food production increase by one billion tons over the next few decades, but the current growth rate falls far short. Moreover, rapid changes in the environment are accelerating land degradation, aggravating pests and diseases, introducing extreme stresses, and reducing crop productivity. Genetic technologies and molecular breeding tools offer novel opportunities for modern crop breeding. In the past few decades, remarkable progress has been achieved in the discovery of genes for crop yield, quality, and resistance and in the dissection of plant molecular mechanisms. With the continuous advancement in sequencing technology, molecular markers, and gene editing, a large number of excellent crop varieties have been cultivated.

Encyclopedia of Bioinformatics and Computational Biology ,2018-08-21 Encyclopedia of Bioinformatics and Computational Biology: ABC of Bioinformatics, Three Volume Set combines elements of computer science, information technology, mathematics, statistics and biotechnology, providing the methodology and in silico solutions to mine biological data and processes. The book covers Theory, Topics and Applications, with a special focus on Integrative —omics and Systems Biology. The theoretical, methodological underpinnings of BCB, including phylogeny are covered, as are more

current areas of focus, such as translational bioinformatics, cheminformatics, and environmental informatics. Finally, Applications provide quidance for commonly asked questions. This major reference work spans basic and cutting-edge methodologies authored by leaders in the field, providing an invaluable resource for students, scientists, professionals in research institutes, and a broad swath of researchers in biotechnology and the biomedical and pharmaceutical industries. Brings together information from computer science, information technology, mathematics, statistics and biotechnology Written and reviewed by leading experts in the field, providing a unique and authoritative resource Focuses on the main theoretical and methodological concepts before expanding on specific topics and applications Includes interactive images, multimedia tools and crosslinking to further resources and databases

<u>Proceedings of the 8th Python in Science</u>
<u>Conference</u> Gaell Varoquaux, Stéfan van der Walt, K.
Jarrod Millman, 2010-02-23 The proceedings of the 8th annual Python for Scientific Computing conference.

Plant Small RNA Praveen Guleria, Vineet Kumar, 2020-02-19 Plant Small RNA: Biogenesis, Regulation and Application describes the biosynthesis of small RNA in plant systems. With an emphasis on the various molecular mechanisms affected by small RNA and their applications in supporting plant growth and survival, this books presents the basics and most recent advancements in small RNA mediated plant genomics, metabolomics, proteomics and physiology. In

addition, it emphasizes the various molecular mechanisms affected by small RNA and their applications in supporting plant growth and survival. Final sections cover the most recent advancements in small RNA mediated plant genomics, metabolomics, proteomics and physiology. Presents foundational information about small RNA biology and regulation in plants Includes small RNA pathway advances Describes the application and scope of small RNA technology for agricultural stability

Field Guidelines for Genetic Experimental Designs in High-Throughput Sequencing Ana M. Aransay, José Luis Lavín Trueba, 2016-06-02 High throughput sequencing (HTS) technologies have conquered the genomics and epigenomics worlds. The applications of HTS methods are wide, and can be used to sequence everything from whole or partial genomes, transcriptomes, non-coding RNAs, ribosome profiling, to single-cell sequencing. Having such diversity of alternatives, there is a demand for information by research scientists without experience in HTS that need to choose the most suitable methodology or combination of platforms and to define their experimental designs to achieve their specific objectives. Field Guidelines for Genetic Experimental Designs in High-Throughput Sequencing aims to collect in a single volume all aspects that should be taken into account when HTS technologies are being incorporated into a research project and the reasons behind them. Moreover, examples of several successful strategies will be analyzed to make the point of the crucial features. This book will be

of use to all scientist that are unfamiliar with HTS and want to incorporate such technologies to their research.

Next-Generation Sequencing Data Analysis Xinkun Wang, 2016-04-06 A Practical Guide to the Highly Dynamic Area of Massively Parallel Sequencing The development of genome and transcriptome sequencing technologies has led to a paradigm shift in life science research and disease diagnosis and prevention. Scientists are now able to see how human diseases and phenotypic changes are connected to DNA mutation, polymorphi

Genome Research ,2008

Comprehensive Foodomics ,2020-11-12 Comprehensive Foodomics, Three Volume Set offers a definitive collection of over 150 articles that provide researchers with innovative answers to crucial questions relating to food quality, safety and its vital and complex links to our health. Topics covered include transcriptomics, proteomics, metabolomics, genomics, green foodomics, epigenetics and noncoding RNA, food safety, food bioactivity and health, food quality and traceability, data treatment and systems biology. Logically structured into 10 focused sections, each article is authored by world leading scientists who cover the whole breadth of Omics and related technologies, including the latest advances and applications. By bringing all this information together in an easily navigable reference, food scientists and nutritionists in both academia and industry will find it the perfect, modern day compendium for frequent reference. List of sections and Section Editors:

Genomics - Olivia McAuliffe, Dept of Food Biosciences, Moorepark, Fermoy, Co. Cork, Ireland Epigenetics & Noncoding RNA - Juan Cui, Department of Computer Science & Engineering, University of Nebraska-Lincoln, Lincoln, NE Transcriptomics -Robert Henry, Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, St Lucia, Australia Proteomics - Jens Brockmeyer, Institute of Biochemistry and Technical Biochemistry, University Stuttgart, Germany Metabolomics - Philippe Schmitt-Kopplin, Research Unit Analytical BioGeoChemistry, Neuherberg, Germany Omics data treatment, System Biology and Foodomics - Carlos Leon Canseco, Visiting Professor, Biomedical Engineering, Universidad Carlos III de Madrid Green Foodomics - Elena Ibanez, Foodomics Lab, CIAL, CSIC, Madrid, Spain Food safety and Foodomics - Djuro Josic, Professor Medicine (Research) Warren Alpert Medical School, Brown University, Providence, RI, USA & Sandra Kraljevic Pavelic, University of Rijeka, Department of Biotechnology, Rijeka, Croatia Food Ouality, Traceability and Foodomics - Daniel Cozzolino, Centre for Nutrition and Food Sciences, The University of Queensland, Queensland, Australia Food Bioactivity, Health and Foodomics -Miguel Herrero, Department of Bioactivity and Food Analysis, Foodomics Lab, CIAL, CSIC, Madrid, Spain Brings all relevant foodomics information together in one place, offering readers a 'one-stop,' comprehensive resource for access to a wealth of information Includes articles written by academics and practitioners from various fields and regions Provides an ideal resource for students.

researchers and professionals who need to find relevant information quickly and easily Includes content from high quality authors from across the globe

In Silico Drug Design Kunal Roy, 2019-02-12 In Silico Drug Design: Repurposing Techniques and Methodologies explores the application of computational tools that can be utilized for this approach. The book covers theoretical background and methodologies of chem-bioinformatic techniques and network modeling and discusses the various applied strategies to systematically retrieve, integrate and analyze datasets from diverse sources. Other topics include in silico drug design methods, computational workflows for drug repurposing, and network-based in silico screening for drug efficacy. With contributions from experts in the field and the inclusion of practical case studies, this book gives scientists, researchers and R&D professionals in the pharmaceutical industry valuable insights into drug design. Discusses the theoretical background and methodologies of useful techniques of cheminformatics and bioinformatics that can be applied for drug repurposing Offers case studies relating to the in silico modeling of FDA-approved drugs for the discovery of antifungal, anticancer, antiplatelet agents, and for drug therapies against diseases Covers tools and databases that can be utilized to facilitate in silico methods for drug repurposing

Variant Calling Charlotte Ng, Salvatore Piscuoglio, 2022-06-25 This volume provides practical guidance on a variety of techniques and steps to ensure successful variant calling. Chapters detail methods for variant calling from single-nucleotide variants to structural variants, variant calling in specialized data types such as RNA-seg and UMI-tagged sequencing, alignment-free genotyping and SNP calling, variant detection in single-cell DNA sequencing data, variant annotation, and preanalytical quality control to ensure successful variant calling. Written in the format of the highly successful Methods in Molecular Biology series, each chapter includes an introduction to the topic, lists step-by-step protocol to execute the algorithms, describes the input and output data, and includes tips on troubleshooting and known pitfalls. Authoritative and cutting-edge, Variant Calling: Methods and Protocols aims to be a foundation for future studies and to be a source of inspiration for new investigations in the field.

Regulation by non-coding RNAs Volume 1 Nicholas Delihas, 2018-10-09 Printed Edition of the Special Issue Published in IJMS

Gene Expression Fumiaki Uchiumi,2022-10-05 Gene expression is dependent on multiple steps, including transcription, RNA processing, and translation. Importantly, recent studies revealed that gene expression is regulated by chromatin structures and non-coding RNA profiles. Elucidating the molecular mechanisms may contribute to the development of novel therapeutics for aging-related diseases, including cancer and neurodegenerative diseases. This book provides a comprehensive overview of gene expression and its role in human disease. It

consists of nine chapters organized into two sections on molecular mechanisms in controlling gene expression and the relationships between transcriptional control and human disease.

AACR 2016: Abstracts 1-2696 American Association for Cancer Research (AACR), 2016-03-28 The AACR Annual Meeting is a must-attend event for cancer researchers and the broader cancer community. This year's theme, Delivering Cures Through Cancer Science, reinforces the inextricable link between research and advances in patient care. The theme will be evident throughout the meeting as the latest, most exciting discoveries are presented in every area of cancer research. There will be a number of presentations that include exciting new data from cutting-edge clinical trials as well as companion presentations that spotlight the science behind the trials and implications for delivering improved care to patients. This book contains abstracts 1-2696 presented on April 17-18, 2016, at the AACR Annual Meeting.

The Integrative Physiology of Metabolic Downstates Alessandro Silvani, 2021-11-02

Bioinformatics and the Cell Xuhua Xia,2007-05-08 Biological and biomedical sciences are becoming more interdisciplinary, and scientists of the future need inte rdisciplinary training instead of the conventional disciplinary training. Just as Sean Eddy (2005) wiselypointed out that sending monolingual diplomats to the United Nations maynot enhance international collaborations, combining strictly disciplinary scientists trained in either mathematics, computational science or molecular biology will not create a productive inte

rdisciplinary team ready to solve interdisciplinary problems. Molecular biology is an interdiscip linary science back in its heyday, and founders of molecular biology were ofte n interdisciplinary scientists. Indeed, Francis Crick considered himself as "a mixture of crystallographer, biophysicist, biochemist, and geneticist" (Crick, 1965). Because it was too cumbersome to explain to people that he was such a mixture, the term "molecular biologist" came handy. To get the crystallographer, biophysicist, biochemist, and geneticist within hi mself to collaborate with each other probably worked better than a team with a crystallographer, a biophysicist, a biochemist and a geneticist who maynot even be interested in each other's problems.

Bioinformatics for Cancer Immunotherapy Sebastian Boegel, 2021-03-17 This volume focuses on a variety of in silico protocols of the latest bioinformatics tools and computational pipelines developed for neo-antigen identification and immune cell analysis from high-throughput sequencing data for cancer immunotherapy. The chapters in this book cover topics that discuss the two emerging concepts in recognition of tumor cells using endogenous T cells: cancer vaccines against neo-antigens presented on HLA class I and II alleles, and checkpoint inhibitors. 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. Cutting-edge and authoritative, Bioinformatics for Cancer Immunotherapy: Methods and Protocols is a valuable research tool for any scientist and researcher interested in learning more about this exciting and developing field.

Spliceosomal Pre-mRNA Splicing Klemens J. Hertel, 2016-09-03 Providing a guide to classical experimental approaches to decipher splicing mechanisms and experimental strategies that rely on novel multi-disciplinary approaches, Spliceosomal Pre-mRNA Splicing: Methods and Protocols describes the theory of alternative premRNA splicing in seven introductory chapters and then introduces protocols and their theoretical background relevant for a variety of experimental research. These protocol chapters cover basic methods to detect splicing events, analyses of alternative pre-mRNA splicing in vitro and in vivo manipulation of splicing events and highthroughput and bioinformatic analyses of alternative splicing. 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 protocols and tips on troubleshooting and avoiding known pitfalls. Comprehensive and practical, Spliceosomal Pre-mRNA Splicing: Methods and Protocols will aid newcomers and seasoned molecular biologists in understanding the fascinating world of alternative splicing with the ultimate goal of paving the way for many new discoveries to come.

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