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Prepare 5% extra reagent mix if you are preparing multiple samples. 2 Remove the PCR plate from magnetic stand 3 Add 30 μ l of the elution pre-mix to each well of the PCR plate using a single channel or multichannel pipette. 4 Gently pipette the entire volume of each well up and down 10-20 times to mix thoroughly. Ensure

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that the beads are fully resuspended. 5
Seal the PCR plate with a Microseal "B"
adhesive seal.

TruSeq Exome SamplePrep - Harvard
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The TruSeq Exome Kit supports 12-plex

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pre-enrichment library pooling, enabling researchers to maximize sequencing throughput and variant identification by sequencing up to 12 libraries per flow cell lane. This enables sequencing of more exomes per run, so researchers can maximize their budgets.

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TruSeq DNA Exome (formerly TruSeq Exome Kit)

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Rapid solution for ...

TruSeq RNA Exome, previously known as

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the TruSeq RNA Access Library Prep Kit, converts total RNA into template molecules of known strand origin, followed by sequence-specific capture of coding RNA. This provides a low-cost solution for analyzing human RNA isolated from formalin-fixed, paraffin-embedded (FFPE) tissues and other low-

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quality samples. Affordability and focus—Isolating human transcriptome coding regions maximizes discovery power at a fraction of the sequencing depth.

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In her study Elisabeth Salzer describes three novel monogenic diseases. For CD27 deficiency Elisabeth Salzer describes a large cohort of patients. Although all patients shared the same causative missense mutation, they displayed diverse clinical presentations. In another patient she was able to identify a mutation in

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PRKCD resulting in a primary immunodeficiency with severe Lupus-like autoimmunity. The patient exhibited increased mRNA levels of IL6. Therefore, treatment with Tocilizumab, a humanized anti-IL-6 receptor monoclonal antibody was suggested. In a family with a history of deaths due to inflammatory bowel

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disease she identified a missense mutation in IL21. She produced wild type and mutated IL-21 protein and demonstrated a loss of function phenotype. As IL-21 is in clinical trials, she proposed a potentially curative treatment option. These discoveries contributed to the understanding of the multifaceted

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regulatory mechanisms of the immune system and highlighted essential players in these complex signaling networks.

Systems biology combines computational and experimental approaches to analyze complex biological systems and focuses on understanding functional activities

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from a systems-wide perspective. It provides an iterative process of experimental measurements, data analysis, and computational simulation to model biological behavior. This book provides explained protocols for high-throughput experiments and computational analysis procedures central to cancer systems

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biology research and education. Readers will learn how to generate and analyze high-throughput data, therapeutic target protein structure modeling and docking simulation for drug discovery. This is the first practical guide for students and scientists who wish to become systems biologists or utilize the approach for

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cancer research. Contents: Introduction to Cancer Systems Biology (Hsueh-Fen Juan and Hsuan-Cheng Huang) Transcriptome Analysis: Library Construction (Hsin-Yi Chang and Hsueh-Fen Juan) Quantitative Proteome: The Isobaric Tags for Relative and Absolute Quantitation (iTRAQ) (Yi-Hsuan Wu and Hsueh-Fen

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Juan)Phosphoproteome: Sample
Preparation (Chia-Wei Hu and Hsueh-Fen
Juan)Transcriptomic Data Analysis: RNA-
Seq Analysis Using Galaxy (Chia-Lang
Hsu and Chantal Hoi Yin
Cheung)Proteomic Data Analysis:
Functional Enrichment (Hsin-Yi Chang
and Hsueh-Fen Juan)Phosphorylation Data

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Analysis (Chia-Lang Hsu and Wei-Hsuan Wang)
Pathway and Network Analysis (Chen-Tsung Huang and Hsueh-Fen Juan)
Dynamic Modeling (Yu-Chao Wang)
Protein Structure Modeling (Chia-Hsien Lee and Hsueh-Fen Juan)
Docking Simulation (Chia-Hsien Lee and Hsueh-Fen Juan)
Readership: Graduate students

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and researchers entering the cancer systems biology field. Keywords: Systems Biology; Transcriptomics; Proteomics; Network Biology; Dynamic Modeling; Protein Structure Modeling; Docking Simulation; Bioinformatics Review: Key Features: Written by two active researchers in the field Covers both

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experimental and computational areas in cancer systems biology Step-by-step instructions help beginners who are interested in creating biological data and analyzing the data by themselves Readers will gain the skills to generate and analyze omics data and discover potential therapeutic targets and drug candidates

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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

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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

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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

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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.

Bioinformatics: A Practical Guide to
NCBI Databases and Sequence

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Alignments provides the basics of bioinformatics and in-depth coverage of NCBI databases, sequence alignment, and NCBI Sequence Local Alignment Search Tool (BLAST). As bioinformatics has become essential for life sciences, the book has been written specifically to address the need of a large audience

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including undergraduates, graduates, researchers, healthcare professionals, and bioinformatics professors who need to use the NCBI databases, retrieve data from them, and use BLAST to find evolutionarily related sequences, sequence annotation, construction of phylogenetic tree, and the conservative domain of a

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protein, to name just a few. Technical details of alignment algorithms are explained with a minimum use of mathematical formulas and with graphical illustrations. Key Features Provides readers with the most-used bioinformatics knowledge of bioinformatics databases and alignments including both theory and

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application via illustrations and worked examples. Discusses the use of Windows Command Prompt, Linux shell, R, and Python for both Entrez databases and BLAST. The companion website contains tutorials, R and Python codes, instructor materials including slides, exercises, and problems for students. This is the ideal

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textbook for bioinformatics courses taken by students of life sciences and for researchers wishing to develop their knowledge of bioinformatics to facilitate their own research.

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In light of the rising cost of healthcare and the overall challenges associated with delivering quality care to patients across regions, scientists and pharmacists are exploring new initiatives in drug discovery and design. One such initiative is the adoption of information technology and software applications to improve

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healthcare and pharmaceutical processes. Software Innovations in Clinical Drug Development and Safety is a comprehensive resource analyzing the integration of software engineering for the purpose of drug discovery, clinical trials, genomics, and drug safety testing. Taking a multi-faceted approach to the application

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of computational methods to pharmaceutical science, this publication is ideal for healthcare professionals, pharmacists, computer scientists, researchers, and students seeking the latest information on the architecture and design of software in clinical settings, the impact of clinical technologies on business

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models, and the safety and privacy of patients and patient data. This timely resource features a well-rounded discussion on topics pertaining to the integration of computational methods in pharmaceutical science and practice including, the impact of software integration on business models, patient

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safety concerns, software architecture and design, and data security.

Plant organ abscission is a developmental process regulated by the environment, stress, pathogens and the physiological

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status of the plant. In particular, seed and fruit abscission play an important role in seed dispersion and plant reproductive success and are common domestication traits with important agronomic consequences for many crop species. Indeed, in natural populations, shedding of the seed or fruit at the correct time is

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essential for reproductive success, while for crop species the premature or lack of abscission may be either beneficial or detrimental to crop productivity. The use of model plants, in particular Arabidopsis and tomato, have led to major advances in our understanding of the molecular and cellular mechanisms underlying organ

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abscission, and now many workers pursue the translation of these advances to crop species. Organ abscission involves specialized cell layers called the abscission zone (AZ), where abscission signals are perceived and cell separation takes place for the organ to be shed. A general model for plant organ abscission includes (1) the

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differentiation of the AZ, (2) the acquisition of AZ cells to become competent to respond to various abscission signals, (3) response to signals and the activation of the molecular and cellular processes that lead to cell separation in the AZ and (4) the post-abscission events related to protection of exposed cells after

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the organ has been shed. While this simple four-phase framework is helpful to describe the abscission process, the exact mechanisms of each stage, the differences between organ types and amongst diverse species, and in response to different abscission inducing signals are far from elucidated. For an organ to be shed, AZ

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cells must transduce a multitude of both endogenous and exogenous signals that lead to transcriptional and cellular and ultimately cell wall modifications necessary for adjacent cells to separate. How these key processes have been adapted during evolution to allow for organ abscission to take place in different

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locations and under different conditions is unknown. The aim of the current proposal is to present and be able to compare recent results on our understanding of organ abscission from model and crop species, and to provide a basis to understand both the evolution of abscission in plants and the translation of advances with model

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plants for applications in crop species.

A measure of the success of a journal is that each new issue, or digital alert, includes a couple of papers that pique your interest, perhaps adding a new perspective to your research questions. The collection of papers in this *Frontiers in Ecology and*

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Evolution: 2019 Highlights eBook represents a sample of published papers that attracted the interest of the Specialty Chief Editors and members of the editorial office. While the collection is largely eclectic, it does represent the breadth and methods of enquiry that are published in *Frontiers in Ecology and Evolution*. We

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hope that some of the contributions in this collection similarly interest you.

Cytogenomics demonstrates that chromosomes are crucial in understanding the human genome and that new high-throughput approaches are central to advancing cytogenetics in the 21st

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century. After an introduction to (molecular) cytogenetics, being the basic of all cytogenomic research, this book highlights the strengths and newfound advantages of cytogenomic research methods and technologies, enabling researchers to jump-start their own projects and more effectively gather and

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interpret chromosomal data. Methods discussed include banding and molecular cytogenetics, molecular combing, molecular karyotyping, next-generation sequencing, epigenetic study approaches, optical mapping/karyomapping, and CRISPR-cas9 applications for cytogenomics. The book's second half

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demonstrates recent applications of cytogenomic techniques, such as characterizing 3D chromosome structure across different tissue types and insights into multilayer organization of chromosomes, role of repetitive elements and noncoding RNAs in human genome, studies in topologically associated

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domains, interchromosomal interactions, and chromoanagenesis. This book is an important reference source for researchers, students, basic and translational scientists, and clinicians in the areas of human genetics, genomics, reproductive medicine, gynecology, obstetrics, internal medicine, oncology, bioinformatics,

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medical genetics, and prenatal testing, as well as genetic counselors, clinical laboratory geneticists, bioethicists, and fertility specialists. Offers applied approaches empowering a new generation of cytogenomic research using a balanced combination of classical and advanced technologies Provides a framework for

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interpreting chromosome structure and how this affects the functioning of the genome in health and disease Features chapter contributions from international leaders in the field

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