



Agilent DNA 1000 Kit Quick Start Guide

Agilent DNA 1000 Kit (reorder number 5067-1504)

DNA Chips

25 DNA Chips

1 Electrode Cleaner

Syringe Kit

1 Syringe

3 Spin Filters

DNA 1000 Reagents (reorder number 5067-1505)

● (yellow) DNA Ladder

● (green) DNA Markers (2 vials)

● (blue) DNA Dye Concentrate (1 vial)

● (red) DNA Gel Matrix (3 vials)

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Research Use Only Not for use in Diagnostic Procedures.

Assay Principles

Agilent DNA kits contain chips and reagents designed for sizing and analysis of DNA fragments. Each Agilent DNA chip contains an interconnected set of microchannels that is used for separation of nucleic acid fragments based on their size as they are driven through it electrophoretically. Agilent DNA kits are designed for use with the Agilent 2100 bioanalyzer only.

Assay Kits

The Agilent DNA 1000 kit provides higher resolution of smaller fragments in comparison of our other DNA sizing kits. It can be used for the following applications:

- Analysis of PCR and RT-PCR products
- RFLP analyses
- Heteroduplex analysis using mismatch cleavage enzymes
- QC of sequencing templates

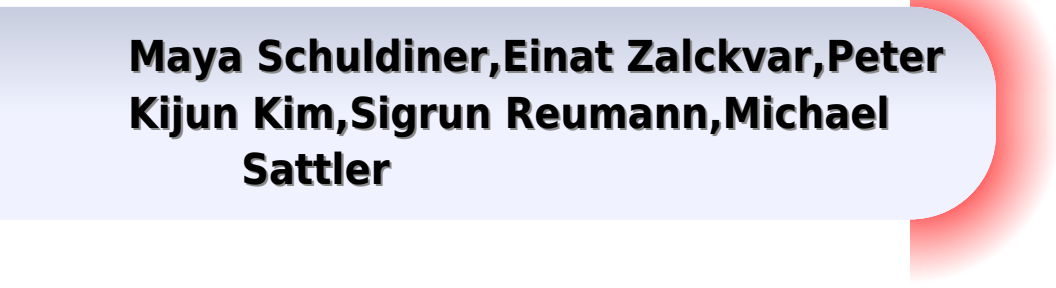
The complete DNA 1000 kit guide can be found in the online help of the 2100 expert software.



Agilent Technologies

Agilent Dna 1000 Kit Quick Start Guide

**Maya Schuldiner, Einat Zalckvar, Peter
Kijun Kim, Sigrun Reumann, Michael
Sattler**



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Hydrogenase: Structure, Function, Maturation, and Application Stefan Frielingsdorf, Francesca Valetti, Constanze Pinske, Chris Greening, 2023-10-24 Molecular hydrogen H₂ is an important molecule in the metabolism of diverse microorganisms. It is used either as energy source or for the disposal of reducing equivalents depending on environmental conditions. Furthermore, H₂ transmits energy between different species within microbial communities. The enzymes that split or evolve H₂ are called hydrogenases, and these metalloproteins can be divided into three phylogenetically unrelated classes distinguishable by the metal composition of their active sites, namely Fe-FeFe and NiFe hydrogenases. Following a century of hydrogenase research, it is now possible to isolate, handle, and investigate these fragile enzymes. There have been numerous advances in understanding the regulation, function, structures, and maturation of these enzymes, as well as their involvement in important processes such as microbial pathogenesis and biogeochemical cycling. The employment of hydrogenases and hydrogenase-based applications could also potentially facilitate the world's transition to a future sustainable H₂-based energy economy.

Sheep and Goat Gene Exploration Shaobin Li, Rui Su, Xin Wang, 2022-04-25 *Biostimulants in Agriculture II: Towards a Sustainable Future* Maurizio Ruzzi, Giuseppe Colla, Youssef Rouphael, 2024-06-11 Modern agriculture needs to review and broaden its practices and business models by integrating opportunities coming from different adjacent sectors and value chains, including the bio-based industry, in a fully circular economy strategy. Searching for new tools and technologies to increase crop productivity under optimal and sub-optimal conditions and to improve resources use efficiency is crucial to ensure food security while preserving soil quality, microbial biodiversity, and providing business opportunities for farmers. Biostimulants based on microorganisms or organic substances obtained from renewable materials represent a sustainable, efficient technology or complement to synthetic counterparts to improve nutrient use efficiency and secure crop yield stability. Under the new European Union Regulation 2019/1009, plant biostimulants were defined based on four agricultural functional claims as follows: Plant biostimulants are products that stimulate plant nutrition processes independently of the product's nutrient content, with the sole aim of improving one or more of the following characteristics of the plant and/or the plant rhizosphere: 1. nutrient use efficiency, 2. tolerance/resistance to a biotic stress, 3. quality characteristics, or 4. availability of confined nutrients in the soil or rhizosphere. Many diverse natural substances and chemical derivatives of natural or synthetic compounds, as well as beneficial microorganisms, are cataloged as plant biostimulants, including: i. humic substances, ii. plant or animal-based protein hydrolysates, iii. macro and micro algal extracts, iv. silicon, v. arbuscular mycorrhizal fungi (AMF), and vi. plant growth-promoting rhizobacteria (PGPR) belonging to the *Azotobacter*, *Azospirillum*, and *Rhizobium* genera.

Genetics, Genomics and -Omics of Thermophiles, 2nd Edition Kian Mau Goh, Kok-Gan Chan, Rajesh Kumar Sani, Edgardo Rubén Donati, Anna-Louise Reysenbach, 2019-06-13 This eBook is a collection of articles from a Frontiers Research Topic. Frontiers Research Topics are very popular trademarks of the Frontiers Journals Series; they

are collections of at least ten articles all centered on a particular subject With their unique mix of varied contributions from Original Research to Review Articles Frontiers Research Topics unify the most influential researchers the latest key findings and historical advances in a hot research area Find out more on how to host your own Frontiers Research Topic or contribute to one as an author by contacting the Frontiers Editorial Office frontiersin.org/about/contact

Implications of lipids and modified lipoproteins in atherogenesis: From mechanisms towards novel diagnostic and therapeutic targets Alexander Akhmedov, Chu-Huang Chen, Tatsuya Sawamura, 2023-08-01

Tag-based Next Generation Sequencing Matthias Harbers, Guenter Kahl, 2012-02-13 Tag based approaches were originally designed to increase the throughput of capillary sequencing where concatemers of short sequences were first used in expression profiling New Next Generation Sequencing methods largely extended the use of tag based approaches as the tag lengths perfectly match with the short read length of highly parallel sequencing reactions Tag based approaches will maintain their important role in life and biomedical science because longer read lengths are often not required to obtain meaningful data for many applications Whereas genome re sequencing and de novo sequencing will benefit from ever more powerful sequencing methods analytical applications can be performed by tag based approaches where the focus shifts from sequencing power to better means of data analysis and visualization for common users Today Next Generation Sequence data require powerful bioinformatics expertise that has to be converted into easy to use data analysis tools The book's intention is to give an overview on recently developed tag based approaches along with means of their data analysis together with introductions to Next Generation Sequencing Methods protocols and user guides to be an entry for scientists to tag based approaches for Next Generation Sequencing

The Urogenital Microbiota in Urinary Tract Diseases A. Lenore Ackerman, 2023-01-10

Cells and Materials for Disease Modeling and Regenerative Medicine Ander Abarrategi, Senentxu Lanceros-Mendez, 2021-05-05 Materials science and engineering are strongly developing tools with increasing impact in the biotechnological and biomedical areas Interestingly research in molecular and cellular biology is often at the core of the design and development of materials based approaches providing biological rationale Focused on research relying on biology materials interaction IJMS launched a Special Issue named Cells and Materials for Disease Modeling and Regenerative Medicine The aim of the Special Issue was to generate a compilation of in vitro and in vivo strategies based on cell material interactions This book compiles the papers published in that Special Issue and includes a selection of six original scientific experimental articles and six comprehensive reviews We are convinced that this collection of articles shows representative examples of the state of the art in the field unveiling the relevance of materials research in generating new regenerative medicine and disease modeling approaches

Natural Feed Additives in Animal Nutrition - Their Potential as Functional Feed Iveta Placha, Francesco Gai, Monika Pogány Simonová, 2022-12-02

Role of Microbiome in Disease Diagnostics and Therapeutics Nar Singh Chauhan, Mitali Mukerji, Shashank Gupta, 2022-10-07

Peroxisome Biology: Breakthroughs, Challenges and Future Directions Maya

Schuldiner, Einat Zalckvar, Peter Kijun Kim, Sigrun Reumann, Michael Sattler, 2021-08-31 **Human Microbiome: Symbiosis to Pathogenesis** Learn-Han Lee, Nurul-Syakima Ab Mutalib, Sunny Hei Wong, Siok-Fong Chin, Vishal Singh, 2021-03-24 **Nanobody** Ulrich Rothbauer, Patrick Chames, 2021-03-30 Nanobodies have become outstanding tools for biomedical research diagnostics and therapy Recent advances in the identification and functionalization of target specific nanobodies now make nanobody based approaches broadly available to many researches in the field This book provides a compilation of original research articles and comprehensive reviews covering important and up to date aspects of research on nanobodies and their applications for immunoassays proteomics protein crystallization and in vitro and in vivo imaging

Forensic Genetic Approaches for Identification of Human Skeletal Remains Angie Ambers, 2022-11-15 Forensic Genetic Approaches for Identification of Human Skeletal Remains Challenges Best Practices and Emerging Technologies provides best practices on processing bone samples for DNA testing The book outlines forensic genetics tools that are available for the identification of skeletal remains in contemporary casework and historical archaeological investigations Although the book focuses primarily on the use of DNA for direct identification or kinship analyses it also highlights complementary disciplines often used in concert with genetic data to make positive identifications such as forensic anthropology forensic odontology and forensic art sculpting Unidentified human remains are often associated with tragic events such as fires terrorist attacks natural disasters war conflicts genocide airline crashes homicide and human rights violations under oppressive totalitarian regimes In these situations extensive damage to soft tissues often precludes the use of such biological samples in the identification process In contrast bone material is the most resilient viable sample type for DNA testing DNA recovered from bone often is degraded and in low quantities due to the effects of human decomposition environmental exposure and the passage of time The complexities of bone microstructure and its rigid nature make skeletal remains one of the most challenging sample types for DNA testing Provides best practices on processing bone samples for DNA testing Presents detailed coverage of proper facilities design for skeletal remains processing selection of optimal skeletal elements for DNA recovery specialized equipment needed preparation and cleaning of bone samples for DNA extraction and more Highlights complementary disciplines often used in concert with genetic data to make positive identifications such as forensic anthropology forensic odontology and forensic art sculpting Molecular Counting Hei-Mun Christina Fan, 2010 The concept of a personal genome stems from the fact that every human genome is unique Measuring the unique features of a personal genome would help uncover the genetic basis of diseases and traits and would be increasingly important in clinical diagnosis especially with the growing emphasis on personalized medicine This thesis focuses on exploring the power of molecular counting to develop novel strategies that address the inadequacy of existing technologies in measuring the unique features of a human genome The first focus of the thesis is aneuploidy detection which has major application in prenatal diagnosis While karyotyping of fetal cells is well established for detecting aneuploidy invasive

sampling of fetal materials impose a small but significant risk to the health of both the mother and the fetus A major research focus in the field of prenatal diagnosis has been to develop a noninvasive test for detecting fetal aneuploidy Here the concept of single molecule counting was applied to the problem of aneuploidy detection The concept was first tested with digital PCR on invasively collected fetal materials and subsequently extended to the noninvasive setting by shotgun sequencing maternal plasma DNA which contains a small amount of fetal DNA The former work led to the development of a polymorphism independent method for rapid invasive diagnosis of aneuploidy while the later work marked the development of the first polymorphism independent method for the noninvasive diagnosis of fetal aneuploidy documented in the literature The second focus of the thesis is molecular haplotyping Present sequencing and other molecular techniques concentrate at identifying variants at isolated locations throughout a genome but largely ignore the haplotypes formed by these variants Direct experimental determination of the haplotypes of an individual is challenging because of the lack of techniques to separate the two highly similar homologous copies of a chromosome Here a whole genome haplotyping method was devised by analyzing amplified materials from single intact chromosomes within single cells made possible by microfluidics Such strategy enabled for the first time completely deterministic measurement of personal whole genome haplotypes It sets the stage for the direct sequencing of the two unique haploid genomes of any individual human which has not been achieved by any personal genomes sequenced to date and can potentially facilitate noninvasive fetal genome sequencing

Innate Immune Responses in CNS Inflammation Mireia Guerau-de-Arellano, David Pitt, Astrid E. Cardona, 2021-11-30 [Omics in Plant-Insect Interactions](#) Shengli Jing, Guangcun He, Ming-shun Chen, 2024-10-07 Herbivorous insects such as piercing sucking hemipteran insects and chewing Lepidopteran insects must establish close associations with their host plants in order to modulate plant cellular processes to promote feeding and reproduction In response to herbivore attacks plants have developed a complex immune system such as plant signalings plant resistant genes and plant secondary metabolite A sophisticated molecular arms race between plants and insects involves the interaction between different molecules from plants and insects The secondary metabolite and resistant genes of plants can be used as defense tools against the infestation of insects In contrast the various types of detoxification enzymes and effectors from insects can interfere with plant defense at multiple levels for better adaptation These metabolite substances and resistant genes of plants and detoxification enzymes and effectors of insects are involved in complex networks of genetic physical metabolic and molecular interactions between plants and insects And these molecules and genes can be identified by the new omics technologies including genome transcriptome proteome metabolomics and so on Omics analyses have provided new insights and understanding into the relationships between plants and insects as well as the underlying molecular mechanisms of their interactions Understanding the molecular interaction between plants and insects can help develop new and improved plant resistant varieties and novel green control strategies

Quality and Production of Forage Vincenzo Tufarelli, 2019-10-29 The book Quality and

Production of Forage is intended to keep readers updated on the developments occurring in this field. As it is apparent that livestock animals are important throughout the world because of the meat, milk, and egg they produce, knowledge about the forages available to animals must also be considered for increased production quality and efficiency. This book provides information that readers will find considerably invaluable about forage feeds such as grass, legumes, and straw. The book is composed of ten papers focusing on a wide range of research activities and topics that feature the following concepts: forage, the effect of conservation method on forage protein value, microbial composition and mycotoxin content in forage, genetic diversity of forages, timely sowing to maximize yield for both grain and biomass, ensiling treatments on forage quality, the qualitative characteristics of different accessions of new forage species, forage policy influencing feed costs, feeding forage on animal health, high protein tropical forages as alternative sources for poultry, impact of forages in poultry diet, and significance of forages in sustainable poultry production systems. This book will be an invaluable reference for students and professionals in agricultural science and grassland and animal husbandry researches.

Biotechnological Tools in Fisheries and Aquatic Health Management Bijay Kumar Behera, 2023-11-22. This edited book is focused on SDG 14, life below water. This book covers all aspects of fish biotechnology and health management. A detailed description is provided of CRISPR-Cas9 technology application in the development of superior variety of fish with better growth, disease resistance, etc., accompanied by numerous helpful photographs and schematic diagrams. In addition, recent developments in nanotechnology and its application in fisheries production enhancement have been discussed. Further topics include probiotics, immunostimulants, fish genetic markers, bioremediation, metagenomics, transgenerational immune priming, application of cell culture in fisheries, and nano biosensor application on fish disease diagnosis, pollution monitoring, etc., are provided in details. The book is helpful for researchers, teachers, students, farmers, and entrepreneurs in utilizing the knowledge on recent advancements in different aspects of fish genetics and biotechnology for future research and aquaculture production enhancement.

Base Editors Sangsu Bae, Beomjong Song, 2023-01-02. This volume explores base editors (BEs), an invaluable CRISPR-based genome editing tool with a wide variety of versatile applications. Beginning with an overview of BEs, their diverse variants, and computational tools, the book continues with experimental applications of BEs for disease modeling in mammalian cells and generating mutagenic mice, therapeutic base editing strategies which covers delivery methods of BE-encoded DNA plasmids, mRNAs, or ribonucleoproteins through viruses or non-viral lipid nanoparticles, and lastly the use of BEs in plants and bacteria. 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 laboratory protocols, and tips on troubleshooting and avoiding known pitfalls. *Authoritative and practical Base Editors: Methods and Protocols* serves as an ideal guide for researchers looking to use base editors to continue their studies in an array of fields.

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