11277081001 **Roche**

Hexanucleotide Mix

solution, pkg of 100 µL, sufficient for 50 labeling reactions

Synonyme(s):
nucleotide mix

Toutes les photos (1)

Documents

FDS

COO/COA

Plus de documents »

Référence	Conditionnement	Disponibilité		Prix	Quantité
11277081001	100 µL	Disponible pour expédition le 01 octobre 2022	Détails...	99,70 €	− +

Demander une commande en gros

Ajouter au panier

PRODUITS RECOMMANDÉS

Roche

11034731001

Primer "random"

lyophilized, sufficient for ≤400 reactions, pkg of 2 mg (Primer, Random pd(N)6 Potassium Salt)

Sigma-Aldrich

H0268

Hexanucleotide Primers

lyophilized powder

Consulter le prix et la disponibilité

Consulter le prix et la disponibilité

PROPRIÉTÉS

Forme	solution
Niveau de qualité	100
Utilisation	sufficient for 50 labeling reactions
Conditionnement	pkg of 100 µL
manufacturer/tradename	Roche
technique(s)	Northern blotting: suitable Southern blotting: suitable cDNA synthesis: suitable (first strand) hybridization: suitable
Expédié(e)(s) dans	dry ice
Temp. de stockage	−20°C

Catégories apparentées

Nucleic Acid Labeling

Roche® Life Science Products

DESCRIPTION

Description générale

Convenient oligonucleotide mixture for rapid random-primed labeling of DNA with radioactive, digoxigenin- or biotin-labeled nucleotides. In this method, the complementary DNA strand is synthesized by Klenow polymerase using the 3′-OH termini of the random oligonucleotides as primers.

Spécificité

Heat inactivation: Stop the reaction by adding 2 µl 0.2 M EDTA (pH 8.0) and/or by heating to 65 °C for 10 minutes.

Application

Hexanucleotide Mix is a mixture of hexanucleotides of all possible sequences for random-primed DNA labeling.
Labeled DNA probes with high specific activity are used in a variety of hybridization techniques:

- Screening of gene libraries
- Southern and northern blots
- *In situ* hybridizations
- RT-PCR
- Generation of cDNA libraries
- Synthesis of first-strand cDNA
- in the determination of vector titer
- Second strand synthesis

Caractéristiques et avantages

The product is a 10x concentrated mixture of random hexanucleotides. Statistically, the mix may contain up to 4,096 different hexanucleotides, but these are probably present in differing amounts.

Contents
10x concentrated mixture of hexanucleotides (62.5 A_{260} units/ml) in reaction buffer [0.5M Tris- HCl, 0.1M $MgCl_2$, 1mM dithioerythritol (DTE), 2mg/ml BSA, pH 7.2 (+20°C)]
Note: The mix is identical to that supplied in vial 5 of the DIG DNA Labeling and Detection Kit and of the DIG DNA Labeling Kit and in vial 6 of the Random Primed DNA Labeling Kit.

Qualité

Function tested in the Random Primed DNA Labeling Kit.

Principe

The "random primed" DNA labeling method developed by Feinberg and Vogelstein is based on the hybridization of a mixture of all possible hexanucleotides to the DNA to be labeled. All sequence combinations are represented in the hexanucleotide primer mixture, which leads to binding of primer to the template DNA in a statistical manner. Thus, an equal degree of labeling along the entire length of the template DNA is guaranteed. The complementary strand is synthesized from the 3′-OH termini of the random hexanucleotide primer using Klenow enzyme, labeling grade. Modified deoxyribonucleoside triphosphates ([^{32}P], [^{35}S],[^{3}H], or [^{125}I] digoxigenin- or biotin-labeled) present in the reaction are incorporated into the newly synthesized complementary DNA strand.

Notes préparatoires

Assay Time
Standard labeling (radioactive): 50 minutes
Labeling assay with digoxigenin-11-dUTP: 80 minutes

Sample Materials

- DNA fragments

- Linearized plasmid DNA
- λDNA

Note: The length of the DNA fragments to be labeled does not influence the reaction. DNA fragments of 100bp length are labeled equally well as linearized plasmid- or λ-DNA. The input DNA serves solely as template for the synthesis of labeled DNA, and is not degraded during the reaction, making it possible to label minimal amounts of DNA (10ng) using this method.

Synthesis: All 4 bases are used to synthesize this random hexanucleotide mix. In the initial reaction, starter nucleotides are linked to a solid phase support. In subsequent coupling reactions, equimolar amounts of the 4 dNTPs are linked to the starter nucleotides until hexamers are generated. The hexamers are then released from the solid phase support.
Post-synthesis: The oligonucleotides are HPLC purified, desalted, and 5′-phosphorylated.

Remarque sur l'analyse

Absorption: 62.5 A_{260} units correspond to 2.5 mg/ml of hexanucleotides.

Autres remarques

For life science research only. Not for use in diagnostic procedures.

INFORMATIONS SUR LA SÉCURITÉ

Code de la classe de stockage	WGK	Flash Point(F)	Point d'éclair C
12 - Non Combustible Liquids	WGK 1	No data available	No data available

DOCUMENTATION

Certificat d'analyse

Saisir un numéro de lot pour rechercher un certificat d'analyse (COA).

Numéro de lot

e.g. 023J5431

Comment saisir un numéro de lot (COA)

Rechercher

Certificat d'origine

Saisir un numéro de lot pour rechercher un certificat d'origine (COO).

Numéro de lot

e.g. 023J5431

Comment saisir un numéro de lot (COO)

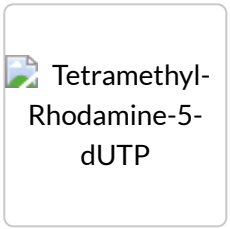
Rechercher

Fiche D'informations Produit

Bulletin - 11277081001

FDS

LES CLIENTS ONT ÉGALEMENT CONSULTÉ



Roche

11534378910

Tetramethyl-Rhodamine-5-dUTP

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11175033910

DIG DNA Labeling Kit

sufficient for 40 labeling reactions, kit of 1 (7 components), suitable for hybridization

Consulter le prix et la disponibilité

ARTICLES REVUS PAR DES PAIRS

Alterations in ribosome biogenesis cause specific defects in C. elegans hermaphrodite gonadogenesis.

Roumen Voutev et al.
Developmental biology, 298(1), 45-58 (2006-08-01)

Ribosome biogenesis is a cell-essential process that influences cell growth, proliferation, and differentiation. How ribosome biogenesis impacts development, however, is poorly understood. Here, we establish a link between ribosome biogenesis and gonadogenesis in Caenorhabditis elegans that affects germline proliferation and

RNA-binding Protein Immunoprecipitation (RIP) to Examine AUF1 Binding to Senescence-Associated Secretory Phenotype (SASP) Factor mRNA.

Elise Alspach et al.
Bio-protocol, 5(10) (2015-05-20)

Immunoprecipitation and subsequent isolation of nucleic acids allows for the investigation of protein:nucleic acid interactions. RNA-binding protein immunoprecipitation (RIP) is used for the analysis of protein interactions with mRNA. Combining RIP with quantitative real-time PCR (qRT-PCR) further enhances the RIP

Identifying microbial fitness determinants by insertion sequencing using genome-wide transposon mutant libraries.

Andrew L Goodman et al.
Nature protocols, 6(12), 1969-1980 (2011-11-19)

Insertion sequencing (INSeq) is a method for determining the insertion site and relative abundance of large numbers of transposon mutants in a mixed population of isogenic mutants of a sequenced microbial species. INSeq is based on a modified mariner transposon

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High-efficiency transduction of liver cancer cells by recombinant adeno-associated virus serotype 3 vectors.

Chen Ling et al.
Journal of visualized experiments : JoVE, (49)(49), doi:10-doi:10 (2011-03-30)

Recombinant vectors based on a non-pathogenic human parvovirus, the adeno-associated virus 2 (AAV2) have been developed, and are currently in use in a number of gene therapy clinical trials. More recently, a number of additional AAV serotypes have also been

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JNK MAPK pathway regulates constitutive transcription of CCL5 by human NK cells through SP1.

Dilip Kumar et al.
Journal of immunology (Baltimore, Md. : 1950), 182(2), 1011-1020 (2009-01-07)

The MAPKs ERK, JNK, and p38 control diverse aspects of the immune response, including regulation of cytotoxin biology in NK cells and CTL. The chemokine CCL5 is coreleased with the cytotoxins, perforin, the granzymes, and granulysin, during the lethal hit

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PRODUITS CONSULTÉS RÉCEMMENT

Roche
11277073910
DIG RNA Labeling Mix
sufficient for 20 reactions, solution

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11277065910
DIG DNA Labeling Mix

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SERVICE TECHNIQUE

Notre équipe de scientifiques dispose d'une expérience dans tous les secteurs de la recherche, notamment en sciences de la vie, science des matériaux, synthèse chimique, chromatographie, analyse et dans de nombreux autres domaines..

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