

Title (en)

METHODS FOR IDENTIFYING LOW-ABUNDANCE POLYNUCLEOTIDES AND RELATED COMPOSITIONS

Title (de)

METHODE ZUR IDENTIFIZIERUNG VON IN GERINGEN MENGEN VORHANDENEN NUKLEINSÄURESEQUENZEN UND VERWANDTE ZUSAMMENSETZUNGEN

Title (fr)

METHODES D'IDENTIFICATION DE POLYNUCLEOTIDES PEU ABONDANTS ET COMPOSITIONS CORRESPONDANTES

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Abstract (en)

[origin: WO0212564A2] This invention provides novel methods for producing a plurality of polynucleotides prepared from a polynucleotide sample and the plurality of polynucleotides so produced. In one embodiment, the plurality of polynucleotides is prepared by subtractive hybridization between test and reference polynucleotide samples and is substantially enriched in sequences that are either not present in the reference polynucleotide sample or are present in the reference polynucleotide sample in substantially lower concentration than in the test polynucleotide sample. The plurality of polynucleotides is also substantially enriched in low-abundance sequences, relative to the test polynucleotide sample. The invention also provides kits useful in the methods of the invention and for using the polynucleotides produced thereby. The polynucleotides are useful in a wide variety of applications, such as cloning, expression, and hybridization studies.

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