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Title (English)

Development of new methods for multiplexed analysis of biomolecules

Abstract

Efficient methods are required to facilitate the analysis and identification of genes and their transcripts. Today, almost all methods for gene analysis involve PCR followed by a sequence analysis method, or alternatively, nucleic acid samples are applied to dense microarrays of hybridization probes. While PCR offers high specificity and sensitivity, microarrays can be used for multiplex analysis, but at the cost of specificity and sensitivity.

In this work a new method with both the ability of performing multiplex analysis and a high specificity and sensitivity is presented. The method is called random array and it can be used for parallel decoding at the single molecule level of products obtained from rolling circle amplification, in this case amplified padlock probes.

Keywords

Random array, Padlock probes, Rolling circle amplification, Multiplex analysis

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