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Subject: U.S. TRADEMARK APPLICATION NO. 87661190 - SEQUENCING BY BINDING - 720167.210 - Request for Reconsideration Denied - Return to TTAB - Message 2 of 6

Attachment Information:

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Date of Patent: April 3, 2018
Assignee: OMNIOME, INC.
Inventors: Corey M. Dambacher, Michael Van Nguyen

METHOD AND SYSTEM FOR SEQUENCING NUCLEIC ACIDS

Publication number: 20180044727

Abstract: Provided are compositions, methods and systems for determining the sequence of a template nucleic acid using a polymerase-based, sequencing-by-binding procedure. An examination step involves monitoring the interaction between a polymerase and template nucleic acid in the presence of one or more nucleotides. Identity of the next correct nucleotide in the sequence is determined without incorporation of any nucleotide into the structure of the primer by formation of a phosphodiester bond. An optional incorporation step can be used after the examination step to extend the primer by one or more nucleotides, thereby incrementing the template nucleotides that can be examined in a subsequent examination step. The sequencing-by-binding procedure does not require the use of labeled nucleotides or polymerases, but optionally can employ these reagents.

Type: Application
Filed: August 15, 2017
Publication date: February 15, 2018

Applicant: OMNIOME, INC.
Inventors: Kandaswamy VIJAYAN, Corey M. DAMBACHER, Eugene TU, Mark A. BERNARD, Joseph ROKICKI, Kerry WILSON

SEQUENCING METHOD FOR RAPID IDENTIFICATION AND PROCESSING OF COGNATE NUCLEOTIDE PAIRS

Publication number: 20180044715

Abstract: Provided are methods and systems for reducing the time needed for sequencing nucleic acids. The approach relies on detecting formation of nucleotide-specific ternary complexes comprising a polymerase (e.g., a DNA polymerizing enzyme), a primed template nucleic acid molecule, and a nucleotide complementary to the templated base of the primed template nucleic acid. The methods and systems facilitate determination of the next correct nucleotide, as well as the subsequent next correct nucleotide from a cycle of examining four different nucleotides without requiring chemical incorporation of any nucleotide into the primer.

Type: Application
Filed: July 19, 2017

Publication date: February 15, 2018

Publication date: February 15, 2018
Applicant: Omniome, Inc.
Inventors: Pinar Iyidogan, Kandaswamy Vijayan

METHOD OF NUCLEIC ACID SEQUENCE DETERMINATION

Publication number: 20170314072

Abstract: Provided are sequencing-by-binding methods of detecting cognate nucleotides using a crippled DNA polymerizing enzyme that possesses the ability to bind the next correct nucleotide downstream of a primer in a template-dependent fashion, but does not possess the activity needed to promote phosphodiester bond formation. Use of the crippled DNA polymerase permits interrogation of one nucleotide at a time, without incorporation of any nucleotide. Labeled nucleotides, such as fluorescently labeled nucleotides, can be used in conjunction with the crippled DNA polymerase to establish cognate nucleotide identity in a rapid manner.

Type: Application

Filed: April 28, 2017

Publication date: November 2, 2017

Applicant: Omniome, Inc.

Inventors: Kandaswamy Vijayan, Pinar Iyidogan

SEQUENCING METHOD EMPLOYING TERNARY COMPLEX DESTABILIZATION TO IDENTIFY COGNATE NUCLEOTIDES

Publication number: 20170314064

Abstract: Provided are methods and systems for detecting formation of nucleotide-specific ternary complexes comprising a DNA polymerase, a nucleic acid, and a nucleotide complementary to the templated base of the primed template nucleic acid. The methods and systems facilitate determination of the next correct nucleotide without requiring chemical incorporation of the nucleotide into the primer. These results can even be achieved in procedures employing unlabeled, native nucleotides.

Type: Application

Filed: April 28, 2017

Publication date: November 2, 2017

Applicant: Omniome, Inc.

Inventors: Pinar Iyidogan, Kandaswamy Vijayan

SEQUENCING DEVICE

SEQUENCING DEVICE

Publication number: 20170191125

Abstract: Systems and methods for performing DNA sequencing. An example system includes a flow cell, a mechanism to generate fluid flow, a number of reservoirs for containing respective fluids, and a number valves configured such that fluid from any particular one of the plurality of reservoirs can be individually supplied to the flow cell under the impetus of the mechanism to generate fluid flow by opening of the respective valve of the particular reservoir and closing the other valves. Fluids containing test nucleotides may be sequentially flowed through the flow cell and the flow cell imaged at each step to detect binding of the test nucleotides to a sample. The nucleotide sequence of the sample is derived from the images. The sample may be arrayed on a sensing surface of a prism, and the images may be obtained, for example, by surface plasmon resonance imaging (SPRI) of the sensing surface or other techniques.

Type: Application

Filed: December 28, 2016

Publication date: July 6, 2017

Applicant: Omniome, Inc.

Inventors: Kandaswamy Vijayan, Maxim Abashin, Yi Zhang, Espir Kahatt, Kerry Wilson

METHODS FOR DETERMINING SEQUENCE PROFILES

Publication number: 20170137873

Abstract: Provided herein are methods for analyzing a signature sequence in a nucleic acid sample by rapid sequencing of a target nucleic acid region. The method examines the target nucleic acid directly and minimizes the number of examination steps needed to determine a signature that is characteristic of a genetic feature of the nucleic acid sample.

Type: Application

Filed: November 17, 2016

Publication date: May 18, 2017

Applicant: Omniome, Inc.

Inventors: Michael Nguyen, Eugene Tu

NUCLEIC ACID SEQUENCING METHODS AND SYSTEMS

Publication number: 20170022553

Abstract: The present disclosure provides compositions, methods and systems for sequencing a template nucleic acid using a polymerase based, nucleic acid binding reaction involving examination of the interaction between a polymerase and template nucleic acid in the presence of one or more

unlabeled nucleotides. The methods rely, in part, on identifying a base of a template nucleic acid during nucleic acid synthesis by controlling the sequencing reaction conditions. Template nucleic acid bases may be identified during an examination step followed by an optional incorporation step.
Type: Application
Filed: July 21, 2015
Publication date: January 26, 2017
Applicant: OMNIOME, INC.
Inventors: Kandaswamy Vijayan, Eugene Tu, Mark A. Bernard

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