PATENTS

Nucleic acid sequencing

Recent patents related to sequencing methods and devices.

Patent number	Description	Assignee	Inventor	Date
US 10,191,929	A system comprising a processor and a memory storing instructions executable by the processor creating an index for a nucleic acid sequence. The index comprises a plurality of elements, each corresponding to a permutation of a nucleic acid sequence. Data representing a nucleic acid sequence is received. A subsequence of the nucleic acid sequence is identified in the data at a first position of the nucleic acid sequence. A hash of the subsequence is computed to determine a corresponding element of the index. Position data reflecting the first position is stored in the corresponding element of the index.	Noblis (Reston, VA, USA)	Thomas S, Dellinger N	1/29/2019
US 10,191,011	Miniaturized, fast, highly ruggedized nucleic acid sequencing and separation devices, suitable for use by unskilled or semi-skilled operators and in environmental locations that are controlled or semi-controlled. The devices dramatically reduce the amount of sample and reagent and enable unique microscale chemistries not possible with macroscale instrumentation.	NetBio (Waltham, MA, USA)	Tan E, Lam HC, Kellogg GJ	1/29/2019
US 10,190,161	An apparatus for nucleic acid sequencing, including a base-detection device in a detection site, the base-detection device being configured to detect bases of a portion of a nucleic acid strand at the detection site; and a conveying device, configured to extend the nucleic acid strand and to cause the extended nucleic acid strand to slide through the detection site along a path. The base-detection device includes a plurality of field-effect nanowire detectors, arranged along the path and each including a respective nanowire and nucleic acid probes, which are defined by respective base sequences and are fixed to the respective nanowire.	STMicro-electronics (Agrate Brianza, Italy)	Bianchessi MA, Ferrara F	1/29/2019
US 10,184,147	Compositions and methods for making closed nucleic acid structures in which one or both strands are continuous. The closed nucleic acid structures can be used as sequencing templates, among other applications.	Gen-Probe (San Diego, CA, USA)	Nelson NC, Chelliserry J	1/22/2019
US 10,174,375	Systems, methods and apparatuses for diagnosing auto-immune diseases such as systemic lupus erythematosus (SLE) on the basis of the sizes, methylation levels and/or genomic characteristics of circulating DNA molecules. Massively parallel and/or methylation-aware sequencing can be used on patients' blood or other tissue samples to determine the sizes and methylation levels of individual DNA molecules and identify the number of molecules originating from different genomic regions.	The Chinese University of Hong Kong (Shatin, New Territories, Hong Kong)	Lo Y-MD, Chiu RWK, Chan RWY, Tam LS	1/8/2019
US 10,174,372	A method of sequencing nucleic acid comprising cytosine by providing a sample comprising a template nucleic acid; generating a complementary copy of the template nucleic acid, wherein the generating produces a complementary copy of the template nucleic acid such that cytosine residues in the complementary copy are conversion-resistant cytosine analogs comprising a moiety that inhibits conversion to another base residue; subjecting the template nucleic acid and the complementary copy to conversion treatment to convert cytosine residues in the template nucleic acid into residues comprising the other base, resulting in a converted template nucleic acid and an unconverted complementary copy; and determining the nucleotide sequence of the converted template nucleic acid and the unconverted complementary copy.	Illumina (San Diego, CA, USA)	Kester HA	1/8/2019
US 10,174,368	Methods and systems for sequencing a long nucleic acid fragment, a target polynucleotide with fewer probes, and a target polynucleotide with longer reads. The methods allow low-cost, high-throughput and accurate sequencing of nucleic acids.	Centrillion Technology Holdings (Palo Alto, CA, USA)	Zhou W, Mei R, Matsuzaki H	1/8/2019
US 10,174,363	Methods of sequencing molecules based on luminescence lifetimes and/or intensities. In some aspects, methods of sequencing nucleic acids involve determining the luminescence lifetimes, and optionally luminescence intensities, of a series of luminescently labeled nucleotides incorporated during a nucleic acid sequencing reaction.	Quantum-Si (Guilford, CT, USA)	Rothberg JM, Lackey J, Reed B, Shi X, Huang H	1/8/2019

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