Recent patents related to clinical applications of sequencing

Patent number	Description	Assignee	Inventor	Date
US 9,731,266	Systems, devices, methods, and kits for performing an integrated analysis, which can include sample processing, library construction, amplification, and sequencing. The integrated analysis can be performed within one or more modules that are fluidically connected to each other and can be controlled and/or automated by a computer. The integrated analysis can be performed on a tissue sample, a clinical sample, or an environmental sample.	IntegenX (Pleasanton, CA, USA)	Stern S, Jovanovich SB	8/15/2017
US 9,727,692	A computer-implemented method for processing and/or analyzing nucleic acid sequencing data comprising a first data input and a second data input. The first data input comprises untargeted sequencing data generated from a first nucleic acid sample obtained from a subject. The second data input comprises target-specific sequencing data generated from a second nucleic acid sample obtained from the subject. Next, with the aid of a computer processor, the first data input and the second data input are combined to produce a combined dataset. Next, an output derived from the combined dataset is generated. The output is indicative of the presence or absence of one or more polymorphisms of the first nucleic acid sample and/or the second nucleic acid sample. The method provides numerous improvements over existing nanostructure sequencing methods in, for example, clinical applications and high-throughput environments.	Personalis (Menlo Park, CA, USA)	Harris J, Pratt M, West J, Chen R, Li M	8/8/2017
US 9,725,763	Nanostructure-based sequencing methods and systems, including contacting an immobilized RNA polymerase with a double-stranded target nucleic acid molecule under sequencing conditions; detecting the movement of the target nucleic acid molecule and/or one or more nascent strand(s) through, on, or over a nanostructure; repeating the contacting and detecting steps a plurality of times; and determining the sequence of the target nucleic acid molecule based, sequentially, on the presence or absence of a change in the movement in the presence of at least one nucleoside triphosphate. The methods provide numerous improvements over existing nanostructure sequencing technology.	Eve Biomedical (Redwood City, CA, USA)	Kosteroglou T, Papademetriou S	8/8/2017
US 9,725,732	The isolation and sequencing of nucleic acid molecules that encode cytochrome P450 polypeptides from a *Papaver somniferum* cultivar; useful in the production of clinically useful opiate alkaloids such as morphine, codeine, thebaine, noscapine [also known as narcotine], and papaverine, and in the identification of poppy cultivars that include genes that comprise said nucleic acid molecules.	Sun Pharmaceutical Industries (Notting Hill, Victoria, Australia)	Winzer T, Walker TC, Graham IA	8/8/2017
US 9,719,137	Amplification primers with a universal tag and sequencing primers comprising at least one non-natural nucleobase capable of hybridizing to a complementary non-natural nucleobase. Also, nucleic acid amplification and sequencing methods using an amplification primer with a universal tag and sequencing primers, as well as kits and solid supports comprising such primers and tags.	Siemens Healthcare Diagnostics (Tarrytown, NY, USA)	Battersby T, Guettouche T, Hnatyszyn J	8/1/2017
US 9,719,136	Methods of adding adapters to nucleic acids, including combining in a reaction mixture a template nucleic acid, a template switch oligonucleotide, a polymerase, and dNTPs. The methods further include attaching sequencing platform adapter constructs to the ends of the product nucleic acid or a derivative thereof. Aspects of the invention further include compositions and kits. The subject methods find use in a variety of applications, including those that require the presence of particular nucleotide sequences at one or both ends of nucleic acids of interest; useful in areas of basic research and diagnostics (e.g., clinical diagnostics) including the generation of sequencing-ready libraries of nucleic acids of interest, suppression PCR, cloning, detection, library amplification, array hybridization, whole genome amplification, etc.	Takara Bio USA, (Mountain View, CA, USA)	Betts C, Farmer AA	8/1/2017
US 9,708,659	Compositions, methods, and kits for high-sensitivity single-molecule digital counting by stochastic labeling of a collection of identical molecules by attaching a diverse set of labels. Detection may be by a variety of methods including hybridization-based or sequencing. May be useful to estimate the number of separate molecules of a given type or types within a sample and in performing a wide variety of clinical measurements.	Cellular Research (Menlo Park, CA, USA)	Fodor SPA, Fu GK	7/18/2017
US 9,708,657	Sequence-based profiling of nucleic acid populations by multiplex amplification and attachment of one or more sequence tags to anchor copies of target nucleic acids, followed by high-throughput sequencing of the amplification product. Some embodiments of the invention are directed to minimal residual disease analysis of patients being treated for cancer.	Adaptive Biotechnologies (Seattle)	Asbury T, Hervold K, Kotwaliwale C, Faham M, Moorhead M, Weng L, Wittkop T, Zheng J	7/18/2017
US 9,708,654	Sequencing two or more genes expressed in a single cell in a high-throughput manner. More particularly, a method for high-throughput sequencing of pairs of transcripts co-expressed in single cells (e.g., antibody VH and VL coding sequence) to determine pairs of polypeptide chains that comprise immune receptors.	Board of Regents, The University of Texas System (Austin, TX, USA)	Hunicke-Smith S, Dekosky B, Ellington A, Georgiou G	7/18/2017

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