PATENTS

Metagenomics

Recent patents related to metagenomic analysis for compound identification and sequence assembly.

Patent number	Description	Assignee	Inventor	Date
US 10,184,122	Methods, compositions and kits for using a transposase and a transposon end for generating extensive fragmentation and 5'-tagging of double-stranded target DNA in vitro, then using a DNA polymerase for generating 5'- and 3'-tagged single-stranded DNA fragments without performing a PCR amplification reaction; useful for generating 5'- and 3'-tagged DNA fragments for use in a variety of processes, including processes for metagenomic analysis of DNA in environmental samples, copy number variation analysis of DNA, and comparative genomic sequencing, including massively parallel DNA sequencing.	Epicentre Technologies (Madison, WI, USA)	Grunenwald HL, Caruccio N, Jendrisak J, Dahl G	1/22/2019
US 10,042,976	Systems and methods capable of characterizing populations of organisms within a sample, using probabilistic matching of short strings of sequencing information to identify genomes from a reference genomic database to which the short strings belong. In addition, the system and methods may enable rapid identification of organisms including both pathogens and commensals in clinical samples, and the identification may be achieved by a comparison of many (e.g., hundreds to millions) metagenomic fragments, which have been captured from a sample and sequenced, to many (e.g., millions or billions) pieces of archived sequence information of genomes (i.e., reference genomic databases).	CosmosID (Rockville, MD, USA)	Colwell RR, Livingston BT, Jakupciak D, Hasan NA, Jakupciak JP, Brenner D	8/7/2018
US 9,963,688	EstATII, an esterase that is halotolerant, thermophilic and resistant to a spectrum of heavy metals, including toxic concentration of metals, isolated with a fosmid metagenomic library using DNA isolated from the lowest convective layer of the Atlantis II Red Sea brine pool.	American University in Cairo (New Cairo, Egypt), King Abdullah University of Science and Technology (Thuwal, Saudi Arabia)	El Dorry H, Siam R, Mohamed YM	5/8/2018
US 9,944,914	A method for selectively obtaining a natural variant of an enzyme having activity, including (1) detecting an ORF sequence of a protein having enzymatic activity from a genome database including base sequences of metagenomic DNA of environmental microbiota; (2) obtaining at least one PCR clone including the ORF sequence having a full-length sequence of the ORF, a partial sequence of the ORF, or a base sequence encoding an amino acid sequence that is formed by deletion, substitution, or addition of at least one amino acid residue in an amino acid sequence encoded by the ORF sequence, by performing PCR cloning on at least one metagenomic DNA of the environmental microbiota by using a primer design based on the ORF sequence; (3) determining a base sequence and an amino acid sequence that is encoded by the base sequence for each PCR clone obtained in step 2; and (4) selecting a natural variant of an enzyme having activity by measuring enzyme activity of proteins encoded by each PCR clone obtained in step 2.	Honda Motor Co. (Tokyo)	Suda M, Okuma J, Yamaguchi A, Hirose Y, Kondo Y	4/17/2018
US 9,881,135	A model to identify an individual having or at risk of developing type 2 diabetes using metagenomic clusters, wherein said model is characterized by using different metagenomic clusters for different population groups, and the use of such a model in the identification of a person having risk for developing type 2 diabetes.	Metabogen (Gothenburg, Sweden)	Backhed F, Karlsson FH, Nielson J, Fagerberg B, Tremaroli V	1/30/2018
US 9,783,859	A method of detecting and quantifying various enzymatic activities using a constructed artificial genetic circuit GESS (genetic enzyme screening system) for sensing phenolic compounds and a method of screening a trace of activities of target enzymes from a metagenome using the artificial genetic circuit, thereby securing target enzyme genes. When the method for screening and quantifying target enzymatic activity is used, useful genes can be screened from various genetic communities, including environmental or metagenomic libraries, at a single-cell level in high throughput (million per day).	Korea Research Institute of Bioscience and Biotechnology (Daejeon, Republic of Korea)	Lee SG, Rha E, Choi SL, Song JJ, Choi JH, Kim HS	10/10/2017
US 9,372,959	Systems and methods for assembly of metagenomic sequences. In one embodiment, a plurality of metagenomic sequences is represented in three-dimensional space to obtain a plurality of sequence vectors. On the basis of a plurality of the sequence vectors, a cuboid having a plurality of grids is defined in the three-dimensional space such that it encompasses the plurality of metagenomic sequences. Further, the plurality of metagenomic sequences is assembled into one or more contigs based on traversal of the plurality of grids. In one implementation, the one or more contigs are assembled such that a contig includes metagenomic sequences probably originating from the same genome.	Tata Consultancy Services (Mumbai)	Mande SS, Ghosh TS, Mehra V	6/21/2016

Source: United States Patent and Trademark Office (<http://www.uspto.gov>).

Published online: 3 May 2019

<https://doi.org/10.1038/s41587-019-0118-y>