

Title (en)

METHOD AND SYSTEM FOR CHARACTERIZATION OF CLOSTRIDIUM DIFFICILE-ASSOCIATED CONDITIONS

Title (de)

VERFAHREN UND SYSTEM ZUR CHARAKTERISIERUNG MIT CLOSTRIDIUM DIFFICILE ASSOZIIERTEN ERKRANKUNGEN

Title (fr)

PROCÉDÉ ET SYSTÈME DE CARACTÉRISATION D'AFFECTIONS ASSOCIÉES À CLOSTRIDIUM DIFFICILE

Publication

**EP 3386592 A4 20190522 (EN)**

Application

**EP 16873997 A 20161209**

Priority

- US 201562265077 P 20151209
- US 201615097862 A 20160413
- US 2016065993 W 20161209

Abstract (en)

[origin: WO2017100688A1] An embodiment of a system and method for characterizing a Clostridium-associated condition in relation to a user includes: a handling network operable to receive containers including material from a set of users, the handling network including a sequencing system operable to determine microbiome sequences from sequencing the material; a processing system operable to generate a microbiome composition dataset and a microbiome functional diversity dataset based on the microbiome sequences, receive a supplementary dataset associated with the Clostridium-associated condition for the set of users; transform the supplementary dataset and features extracted from the microbiome composition dataset and the microbiome functional diversity dataset into a characterization model for the Clostridium-associated condition; and a therapy system operable to promote a therapy to the user based on characterizing the user in relation to the Clostridium-associated condition using the characterization model.

IPC 8 full level

**A61P 31/04** (2006.01); **G16B 50/10** (2019.01); **A61K 38/08** (2019.01); **A61P 43/00** (2006.01); **C12Q 1/6883** (2018.01); **C12Q 1/689** (2018.01); **G16B 40/00** (2019.01); **G16B 40/20** (2019.01); **G16B 50/00** (2019.01); **G16H 10/40** (2018.01); **G16H 50/20** (2018.01); **G16H 50/50** (2018.01); **G16B 50/30** (2019.01)

CPC (source: EP US)

**A61P 31/04** (2018.01 - EP); **A61P 43/00** (2018.01 - EP); **C12Q 1/6883** (2013.01 - EP); **C12Q 1/689** (2013.01 - EP); **G16B 40/00** (2019.02 - EP); **G16B 40/20** (2019.02 - EP US); **G16B 50/00** (2019.02 - EP); **G16B 50/10** (2019.02 - EP US); **G16H 10/40** (2018.01 - EP); **G16H 50/20** (2018.01 - EP); **G16H 50/50** (2018.01 - EP); **G01N 2333/33** (2013.01 - EP); **G16B 50/30** (2019.02 - EP US); **G16H 20/10** (2018.01 - EP); **G16H 20/60** (2018.01 - EP); **Y02A 90/10** (2018.01 - EP)

Citation (search report)

- [IY] US 2015211055 A1 20150730 - APTE ZACHARY [US], et al
- [Y] WO 2015013214 A2 20150129 - WHOLE BIOME INC [US]
- [Y] WO 2015170979 A1 20151112 - IS DIAGNOSTICS LTD [NL]
- [A] XOCHITL C. MORGAN ET AL: "Biodiversity and functional genomics in the human microbiome", TRENDS IN GENETICS., vol. 29, no. 1, 1 January 2013 (2013-01-01), NL, pages 51 - 58, XP055470567, ISSN: 0168-9525, DOI: 10.1016/j.tig.2012.09.005
- See also references of WO 2017100688A1

Designated contracting state (EPC)

AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HR HU IE IS IT LI LT LU LV MC MK MT NL NO PL PT RO RS SE SI SK SM TR

DOCDB simple family (publication)

**WO 2017100688 A1 20170615**; AU 2016366656 A1 20180628; CA 3007503 A1 20170615; CN 108472506 A 20180831; CN 108472506 B 20220329; EP 3386592 A1 20181017; EP 3386592 A4 20190522

DOCDB simple family (application)

**US 2016065993 W 20161209**; AU 2016366656 A 20161209; CA 3007503 A 20161209; CN 201680077988 A 20161209; EP 16873997 A 20161209