

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property
Organization

International Bureau

(43) International Publication Date
11 November 2021 (11.11.2021)



(10) International Publication Number
WO 2021/226522 A1

(51) International Patent Classification:

G16B 30/10 (2019.01) G16H 50/80 (2018.01)
G16B 20/20 (2019.01)

(21) International Application Number:

PCT/US2021/031389

(22) International Filing Date:

07 May 2021 (07.05.2021)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

63/022,296 08 May 2020 (08.05.2020) US

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(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO,

DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, IT, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, WS, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:

- with international search report (Art. 21(3))
- before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))

(54) Title: GENOME SEQUENCING AND DETECTION TECHNIQUES

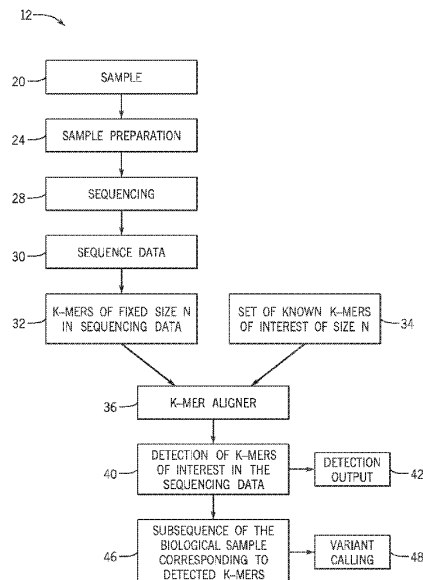


FIG. 1

(57) Abstract: A nucleic acid sequencing technique is described. Sequence data, e.g., generated by a sequencing device, may be analyzed to scan k-mers of a fixed size n in individual reads in the sequence data. Exact matches of the k-mers in the sequence data with reference k-mers are identified. The number of exact matches, their distribution in a reference genome, and/or a number of sequence reads in the sequence data that map to different target regions can be used to determine a characteristic of a sample. In one example, the characteristic is a presence of a pathogen in the sample.

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