**Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/USA/MA-Broad-CRSP\_HI2VSRB3HJJCYJLN/2022, complete genome**

GenBank: ON200331.1

[FASTA](https://www.ncbi.nlm.nih.gov/nuccore/ON200331.1?report=fasta) [Graphics](https://www.ncbi.nlm.nih.gov/nuccore/ON200331.1?report=graph)

[Go to:](https://www.ncbi.nlm.nih.gov/nuccore/ON200331.1" \l "goto2221150929_0)

LOCUS ON200331 29804 bp RNA linear VRL 10-APR-2022

DEFINITION Severe acute respiratory syndrome coronavirus 2 isolate

SARS-CoV-2/human/USA/MA-Broad-CRSP\_HI2VSRB3HJJCYJLN/2022, complete

genome.

ACCESSION ON200331

VERSION ON200331.1

DBLINK BioProject: [PRJNA622837](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA622837)

BioSample: [SAMN27411987](https://www.ncbi.nlm.nih.gov/biosample/SAMN27411987)

KEYWORDS .

SOURCE Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)

ORGANISM [Severe acute respiratory syndrome coronavirus 2](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=2697049)

Viruses; Riboviria; Orthornavirae; Pisuviricota; Pisoniviricetes;

Nidovirales; Cornidovirineae; Coronaviridae; Orthocoronavirinae;

Betacoronavirus; Sarbecovirus.

REFERENCE 1 (bases 1 to 29804)

AUTHORS Lemieux,J.E., Siddle,K.J., Shaw,B., Adams,G., Pierce,V.,

Turbett,S., Anahtar,M., Branda,J., Slater,D., Harris,J., Lin,A.E.,

Gladden-Young,A., Lagerborg,K., Rudy,M., DeRuff,K., Carter,A.,

Normandin,E., Bauer,M., Reilly,S., Tomkins-Tinch,C., Loreth,C.,

Chaluvadi,S., Neumann,A., Cusick,C., Chapman,S.B., Gnirke,A.,

Flowers,K., Cerrato,F., Birren,B.W., Gallagher,G., Smole,S.,

Park,D.J., MacInnis,B.L., Ryan,E., LaRocque,R., Rosenberg,E. and

Sabeti,P.C.

TITLE SARS-CoV-2 patient sequencing at the Broad Institute

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 29804)

AUTHORS Lemieux,J.E., Siddle,K.J., Shaw,B., Adams,G., Pierce,V.,

Turbett,S., Anahtar,M., Branda,J., Slater,D., Harris,J., Lin,A.E.,

Gladden-Young,A., Lagerborg,K., Rudy,M., DeRuff,K., Carter,A.,

Normandin,E., Bauer,M., Reilly,S., Tomkins-Tinch,C., Loreth,C.,

Chaluvadi,S., Neumann,A., Cusick,C., Chapman,S.B., Gnirke,A.,

Flowers,K., Cerrato,F., Birren,B.W., Gallagher,G., Smole,S.,

Park,D.J., MacInnis,B.L., Ryan,E., LaRocque,R., Rosenberg,E. and

Sabeti,P.C.

TITLE Direct Submission

JOURNAL Submitted (10-APR-2022) Infectious Disease Program, Broad Institute

of Harvard and MIT, 75 Ames St, Cambridge, MA 02142, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: Broad viral-ngs v. v2.1.33

Coverage :: 4366x

Sequencing Technology :: Illumina NovaSeq 6000

##Assembly-Data-END##

FEATURES Location/Qualifiers

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Sequencing Platform"

/note="Baseline surveillance (random sampling)"

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