**Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/USA/MN-CDC-IBX322657542052/2022 ORF1ab polyprotein (ORF1ab), ORF1a polyprotein (ORF1ab), surface glycoprotein (S), ORF3a protein (ORF3a), envelope protein (E), membrane glycoprotein (M), ...**

GenBank: OM659585.1

[FASTA](https://www.ncbi.nlm.nih.gov/nuccore/OM659585.1?report=fasta) [Graphics](https://www.ncbi.nlm.nih.gov/nuccore/OM659585.1?report=graph)

[Go to:](https://www.ncbi.nlm.nih.gov/nuccore/OM659585.1" \l "goto2193175724_0)

LOCUS OM659585 29767 bp RNA linear VRL 12-FEB-2022

DEFINITION Severe acute respiratory syndrome coronavirus 2 isolate

SARS-CoV-2/human/USA/MN-CDC-IBX322657542052/2022 ORF1ab polyprotein

(ORF1ab), ORF1a polyprotein (ORF1ab), surface glycoprotein (S),

ORF3a protein (ORF3a), envelope protein (E), membrane glycoprotein

(M), ORF6 protein (ORF6), ORF7a protein (ORF7a), ORF7b (ORF7b),

ORF8 protein (ORF8), nucleocapsid phosphoprotein (N), and ORF10

protein (ORF10) genes, complete cds.

ACCESSION OM659585

VERSION OM659585.1

DBLINK BioProject: [PRJNA731149](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA731149)

BioSample: [SAMN25874861](https://www.ncbi.nlm.nih.gov/biosample/SAMN25874861)

KEYWORDS purposeofsampling:baselinesurveillance.

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 29767)

AUTHORS Howard,D., Batra,D., Cook,P.W., Caravas,J., Rambo-Martin,B.,

Sammons,S., Unoarumhi,Y., Schmerer,M., Lacek,K.A., Kendall,T.,

Caban Figueroa,V., Morrison,S., Gulvick,C., Sula,E., Bixby,C.,

Wang,Y., Schultz,J., Goswami,C., Hager,R., Grimwood,R., Paden,C.R.

and MacCannell,D.

TITLE CDC Sars CoV2 Sequencing Baseline Constellation

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 29767)

AUTHORS Howard,D., Batra,D., Cook,P.W., Caravas,J., Rambo-Martin,B.,

Sammons,S., Unoarumhi,Y., Schmerer,M., Lacek,K.A., Kendall,T.,

Caban Figueroa,V., Morrison,S., Gulvick,C., Sula,E., Bixby,C.,

Wang,Y., Schultz,J., Goswami,C., Hager,R., Grimwood,R., Paden,C.R.

and MacCannell,D.

TITLE Direct Submission

JOURNAL Submitted (12-FEB-2022) Respiratory Viruses Branch, Division of

Viral Diseases, Centers for Disease Control and Prevention, 1600

Clifton Rd, Atlanta, GA 30329, USA

COMMENT ##Assembly-Data-START##

Assembly Method :: DRAGEN Covid Lineage App V3.5.4

Sequencing Technology :: Illumina NovaSeq 6000

##Assembly-Data-END##

FEATURES Location/Qualifiers

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[mat\_peptide](https://www.ncbi.nlm.nih.gov/protein/UKU62187.1?from=819&to=2763) 2695..8529

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stem-loop 1"

[stem\_loop](https://www.ncbi.nlm.nih.gov/nuccore/OM659585.1?from=13454&to=13508) 13454..13508

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stem-loop 2"

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/note="Coronavirus 3' UTR pseudoknot stem-loop 1"

[stem\_loop](https://www.ncbi.nlm.nih.gov/nuccore/OM659585.1?from=29577&to=29605) 29577..29605

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/note="Coronavirus 3' UTR pseudoknot stem-loop 2"

[stem\_loop](https://www.ncbi.nlm.nih.gov/nuccore/OM659585.1?from=29676&to=29690) 29676..29690

/note="Coronavirus 3' stem-loop II-like motif (s2m)"

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