**Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/USA/MN-MDH-2399/2021, complete genome**

GenBank: MW520923.1

[FASTA](https://www.ncbi.nlm.nih.gov/nuccore/MW520923.1?report=fasta) [Graphics](https://www.ncbi.nlm.nih.gov/nuccore/MW520923.1?report=graph)

[Go to:](https://www.ncbi.nlm.nih.gov/nuccore/MW520923.1" \l "goto1959492885_0)

LOCUS MW520923 29819 bp RNA linear VRL 03-NOV-2021

DEFINITION Severe acute respiratory syndrome coronavirus 2 isolate

SARS-CoV-2/human/USA/MN-MDH-2399/2021, complete genome.

ACCESSION MW520923

VERSION MW520923.1

DBLINK BioProject: [PRJNA628662](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA628662)

BioSample: [SAMN17576091](https://www.ncbi.nlm.nih.gov/biosample/SAMN17576091)

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 29819)

AUTHORS Lorentz,A., Garfin,J., Plumb,M. and Wang,X.

TITLE Direct Submission

JOURNAL Submitted (25-JAN-2021) Public Health Laboratory - Infectious

Disease Lab, Minnesota Department of Health Infectious Disease

Laboratory Submission Group, 601 Robert St. N, St. Paul, MN 55164,

USA

COMMENT ##Assembly-Data-START##

Assembly Method :: StaPH-B Toolkit - Monroe v. 1.1.1

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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stem-loop 1"

[stem\_loop](https://www.ncbi.nlm.nih.gov/nuccore/MW520923.1?from=13443&to=13497) 13443..13497

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SFYEDFLEYHDVRVVLDFI"

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

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

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