**Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/USA/VA-CDC-LC0464413/2022, complete genome**

GenBank: OM360636.1

[FASTA](https://www.ncbi.nlm.nih.gov/nuccore/OM360636.1?report=fasta) [Graphics](https://www.ncbi.nlm.nih.gov/nuccore/OM360636.1?report=graph)

[Go to:](https://www.ncbi.nlm.nih.gov/nuccore/OM360636.1" \l "goto2182659029_0)

LOCUS OM360636 29687 bp RNA linear VRL 24-JAN-2022

DEFINITION Severe acute respiratory syndrome coronavirus 2 isolate

SARS-CoV-2/human/USA/VA-CDC-LC0464413/2022, complete genome.

ACCESSION OM360636

VERSION OM360636.1

DBLINK BioProject: [PRJNA716984](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA716984)

BioSample: [SAMN25068874](https://www.ncbi.nlm.nih.gov/biosample/SAMN25068874)

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 29687)

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., Agarwal,M., Almasri,E.,

Boles,D., Burns,A., Charoensri,N., Cohen,O., Countryman,S.,

Cristobal,M.A., Croy,B., Dale,S., Deshmukh,H., Douglas,A.,

Drouillon,V., Eisenberg,M., Engler,H., Ghatti,R., Gupta,P.,

Hicks,S., Humphrey,J., Iyer,L., Pfefferle,L., Jain,M., Robinson,M.,

Kolli,M., Krueger,B., Kuphal,T., Letovsky,S., Levandoski,M.,

Lukasik,C., Meltzer,J., Norvell,B., Nye,M., Parker,S.,

Petropoulos,C., Pruitt,J., Ragan,S., Ryan,S., Sapeta,M.,

Schroth,J., Selvaraju,S.B., Stevovic,G., Suchanek,A., Throop,A.,

Tilson,L., Urban,T., Voshell,J., Wagner,K., Williams,J.,

Williamson,M., Zeng,Q., Zwiefelhofer,T., Paden,C.R. and

MacCannell,D.

TITLE CDC Sars CoV2 Sequencing Baseline Constellation

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 29687)

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., Agarwal,M.,

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Gupta,P., Hicks,S., Humphrey,J., Iyer,L., Pfefferle,L., Jain,M.,

Robinson,M., Kolli,M., Krueger,B., Kuphal,T., Letovsky,S.,

Levandoski,M., Lukasik,C., Meltzer,J., Norvell,B., Nye,M.,

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Schroth,J., Selvaraju,S.B., Stevovic,G., Suchanek,A., Throop,A.,

Tilson,L., Urban,T., Voshell,J., Wagner,K., Williams,J.,

Williamson,M., Zeng,Q., Zwiefelhofer,T., Paden,C.R. and

MacCannell,D.

TITLE Direct Submission

JOURNAL Submitted (19-JAN-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 :: CLC Genomics

Sequencing Technology :: PacBio Sequel II

##Assembly-Data-END##

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