**Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/MEX/COL-4\_6322/2022, complete genome**

GenBank: OQ090605.1

[FASTA](https://www.ncbi.nlm.nih.gov/nuccore/OQ090605.1?report=fasta) [Graphics](https://www.ncbi.nlm.nih.gov/nuccore/OQ090605.1?report=graph)

[Go to:](https://www.ncbi.nlm.nih.gov/nuccore/OQ090605.1" \l "goto2415834610_0)

LOCUS OQ090605 29825 bp RNA linear VRL 20-DEC-2022

DEFINITION Severe acute respiratory syndrome coronavirus 2 isolate

SARS-CoV-2/human/MEX/COL-4\_6322/2022, complete genome.

ACCESSION OQ090605

VERSION OQ090605.1

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 29825)

AUTHORS Zarate,S., Taboada,B., Rosales-Rivera,M., Garcia-Lopez,R.,

Munoz-Medina,J.E., Sanchez-Flores,A., Herrera-Estrella,A.,

Gomez-Gil,B., Selem-Mojica,N., Salas-Lais,A.G., Vazquez-Perez,J.A.,

Cabrera-Gaytan,D.A., Fernandes-Matano,L., Uribe-Noguez,L.A.,

Chale-Dzul,J.B., Maldonado Meza,B.I., Mejia-Nepomuceno,F.,

Perez-Padilla,R., Gutierrez-Rios,R.M., Loza,A., Roche,B., Lopez,S.

and Arias,C.F.

TITLE Omicron-BA.1 dispersion rates in Mexico varied according to the

regional epidemic patterns and the diversity of Delta subvariants

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 29825)

AUTHORS Alvarado-Yaah,J.E., Arias,C.F., Becerril-Vargas,E.,

Cabrera-Gaytan,D.A., Corona-Armenta,G., Chaidez-Quiroz,C.,

Dominguez-Zarate,H., Enciso-Ibarra,J., Espinosa-Ayala,G.,

Fregoso-Rueda,D., Garcia-Gasca,A., Garcia-Lopez,R., Gomez-Gil,B.,

Gonzalez,J.P., Gonzalez-Lopez,I., Grande,R., Herrera-Estrella,A.,

Herrera-Najera,C.I., Jimenez-Moraila,B., Lira-Morales,D.,

Maldonado-Meza,B.I., Marquez-Rosales,M.G., Martinez-Alvarez,J.C.,

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Mejia-Nepomuceno,F., Mireles-Rivera,M.G., Molina-Salinas,G.M.,

Montoya-Fuentes,H., Mujica-Sanchez,M., Munoz-Medina,J.E.,

Nunez-Contreras,J., Salinas-Peralta,I.P., Rivas-Santiago,B.T.,

Rosales-Rivera,M., Salas-Hernandez,J., Salas-Lais,A.G.,

Sanchez-Flores,A., Santacruz-Tinoco,C.E., Selem-Mojica,N.,

Taboada,B., Vazquez,G. and Vazquez-Perez,J.A.

TITLE Direct Submission

JOURNAL Submitted (19-DEC-2022) Genetica del Desarrollo y Fisiologia

Molecular, Instituto de Biotecnologia, Av. Universidad #2001, Col.

Chamilpa, Cuernavaca, Morelos 62210, Mexico

COMMENT ##Assembly-Data-START##

Assembly Method :: ivar v. 1.3.1; bowtie2 v. 2.3.4.3

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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/host="Homo sapiens"

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

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