**Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/BGD/Laila\_923/2022, complete genome**

GenBank: OM533458.1

[FASTA](https://www.ncbi.nlm.nih.gov/nuccore/OM533458.1?report=fasta) [Graphics](https://www.ncbi.nlm.nih.gov/nuccore/OM533458.1?report=graph)

[Go to:](https://www.ncbi.nlm.nih.gov/nuccore/OM533458.1" \l "goto2189779625_0)

LOCUS OM533458 29765 bp RNA linear VRL 06-FEB-2022

DEFINITION Severe acute respiratory syndrome coronavirus 2 isolate

SARS-CoV-2/human/BGD/Laila\_923/2022, complete genome.

ACCESSION OM533458

VERSION OM533458.1

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 29765)

AUTHORS Banu,L.A.

TITLE Whole genome sequencing of SARRS-CoV-2 at Genomic Research

Laboratory, BSMMU

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 29765)

AUTHORS Banu,L.A., Ahmed,M., Hossain,M. and Hassan,Z.

TITLE Direct Submission

JOURNAL Submitted (06-FEB-2022) Genome research Center, Anatomy, BSMMU,

Bangabandhu Sheikh Mujib Medical University, Bangabandhu Sheikh

Mujib Medical University (BSMMU) Shahbag, Dhaka, Dhaka 1000,

Bangladesh

COMMENT ##Assembly-Data-START##

Assembly Method :: DRAGEN COVID Lineage 3.5.3 v.

05.021.510.3.5.88-85-g1aac5c73 and Bio-IT

Processor Version 0x04261818

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

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

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