

SARS-Related Coronavirus 2, Isolate hCoV-19/USA/CA-Stanford-139_S35/2023 (Lineage XBB.1.9)

Catalog No. NR-59441

For research use only. Not for use in humans.

Contributor:

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Manufacturer:

BEI Resources

Product Description:

Virus Classification: *Coronaviridae, Betacoronavirus*

Species: Severe acute respiratory syndrome-related coronavirus 2

Strain/Isolate: hCoV-19/USA/CA-Stanford-139_S35/2023

Original Source: Severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2), isolate hCoV-19/USA/CA-Stanford-139_S35/2023 was isolated from a human nasopharyngeal swab on March 28, 2023, in California, USA.¹

Note: Genome sequence information is provided on the Certificate of Analysis and includes an analysis of all sequence variations observed for each lot.

Comments: Under the nomenclature system introduced by GISAID (Global Initiative on Sharing All Influenza Data), SARS-CoV-2, isolate hCoV-19/USA/CA-Stanford-139_S35/2023 is assigned lineage FL.2 (Pango v.4.3 consensus call), Omicron (XBB.1-like) (Scorpio) and GISAID clade GRA using the Phylogenetic Assignment of Named Global Outbreak lineages (PANGO) tool.^{1,2,3} The complete genome of SARS-CoV-2, isolate hCoV-19/USA/CA-Stanford-139_S35/2023 has been sequenced (GISAID: EPI_ISL_17417339).^{1,2} The following mutations are present in the clinical isolate: Spike A27S, Spike A344S, Spike D405N, Spike D614G, Spike D796Y, Spike E484A, Spike F486P, Spike F490S, Spike G142D, Spike G252V, Spike G339H, Spike G446S, Spike H146Q, Spike H655Y, Spike K417N, Spike L24del, Spike L368I, Spike N440K, Spike N460K, Spike N501Y, Spike N679K, Spike N764K, Spike N969K, Spike P25del, Spike P26del, Spike P681H, Spike Q183E, Spike Q498R, Spike Q954H, Spike R346T, Spike R408S, Spike S371F, Spike S373P, Spike S375F, Spike S477N, Spike T19I, Spike T376A, Spike T478K, Spike V83A, Spike V213E, Spike V445P, Spike Y144del, Spike Y505H, E (Envelope) T9I, E T11A, M (Membrane) A63T, M Q19E, N (Nucleocapsid) G204R, N P13L, N R203K, N S413R, NS3 T223I, NS8 G8stop, NSP1 (Non-structural protein 1) K47R, NSP1 S135R, NSP3 (Non-structural protein 3) G489S, NSP3 G1001S, NSP3 T24I, NSP4 (Non-structural protein 4) L264F, NSP4 L438F, NSP4 T327I, NSP4 T492I, NSP5 (Non-structural protein 5)

P132H, NSP6 (Non-structural protein 6) F108del, NSP6 F216S, NSP6 G107del, NSP6 S106del, NSP9 (Non-structural protein 9) T35I, NSP12 (Non-structural protein 12) G671S, NSP12 P323L, NSP13 (Non-structural protein 13) P504L, NSP13 R392C, NSP13 S36P, NSP14 (Non-structural protein 14) I42V, NSP14 M315T, NSP15 (Non-structural protein 15) T112I.^{1,2} It was labeled as a variant under monitoring (VUM) GRA (XBB.1.9.1+XBB.1.9.1.*) and first detected in Indonesia/Israel/Singapore by the World Health Organization (WHO).^{1,4}

Note: One additional mutation, ORF6 D61L, is present in the GISAID reference sequence, but is not annotated on the GISAID website.

In December 2019, an outbreak of a respiratory illness (COVID-19) began in Wuhan, Hubei Province, China. The outbreak is associated with a seafood market and although environmental samples from the market are positive for the novel coronavirus, an association with a particular animal has not been determined.⁵ SARS-CoV-2 has been isolated from patients from several countries and the sequences of some of these isolates have been deposited with GISAID.

Material Provided:

Each vial contains approximately 0.1 mL of cell lysate and supernatant from *Chlorocebus* (formerly *Cercopithecus*) *aethiops* kidney epithelial cells expressing transmembrane protease, serine 2 and human angiotensin-converting enzyme 2 (Vero E6-TMPRSS2-T2A-ACE2) infected with SARS-CoV-2, isolate hCoV-19/USA/CA-Stanford-139_S35/2023.

Note: If homogeneity is required for your intended use, please purify prior to initiating work.

Packaging/Storage:

NR-59441 was packaged aseptically in screw-capped plastic cryovials. The product is provided frozen and should be stored at -60°C or colder immediately upon arrival. For long-term storage, the vapor phase of a liquid nitrogen freezer is recommended. Freeze-thaw cycles should be avoided.

Growth Conditions:

Host: *Chlorocebus* (formerly *Cercopithecus*) *aethiops* kidney epithelial cells expressing transmembrane protease, serine 2 and human angiotensin-converting enzyme 2 (Vero E6-TMPRSS2-T2A-ACE2; VTA; BEI Resources NR-54970)

Growth Medium: Eagle's Minimum Essential Medium containing Earle's Balanced Salt Solution, non-essential amino acids, 2 mM L-glutamine, 1 mM sodium pyruvate and 1.5 g/L of sodium bicarbonate supplemented with 2% fetal bovine serum, or equivalent

Infection: Cells should be 60% to 70% confluent

Incubation: 3 to 5 days at 37°C and 5% CO₂

Cytopathic Effect: Cell rounding and sloughing

Citation:

Acknowledgment for publications should read "The following reagent was obtained through BEI Resources, NIAID, NIH: SARS-Related Coronavirus 2, Isolate hCoV-19/USA/CA-

Stanford-139_S35/2023 (Lineage XBB.1.9), NR-59441, contributed by Dr. Mehul Suthar.”

Biosafety Level: 3

Appropriate safety procedures should always be used with this material. Laboratory safety is discussed in the following publication: U.S. Department of Health and Human Services, Public Health Service, Centers for Disease Control and Prevention, and National Institutes of Health. [Biosafety in Microbiological and Biomedical Laboratories \(BMBL\)](#). 6th ed. Washington, DC: U.S. Government Printing Office, 2020.

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Use Restrictions:

SARS-CoV-2 materials provided by BEI Resources under the EUSLA are made available for any legitimate purpose, including commercial purposes as long as they are to rapidly prevent, detect, prepare for, and respond to, the spread or transmission of the 2019 SARS-CoV-2. Any further transfer of the original material or any unmodified progeny must be done under the terms of the EUSLA, documented as described above and you must notify BEI Resources of each subsequent transfer. Any new materials made by you that are not the original material or unmodified progeny are excluded from this requirement and you are free to share and commercialize those as your materials.

References:

1. [GISAID](#)
2. Rambaut, A., et al. “A Dynamic Nomenclature Proposal for SARS-CoV-2 Lineages to Assist Genomic Epidemiology.” [Nat. Microbiol.](#) 5 (2020): 1403-1407. PubMed: 32669681.

3. Mercatelli, D. and F. M. Giorgi. “Geographic and Genomic Distribution of SARS-CoV-2 Mutations.” [Front. Microbiol.](#) (2020): doi.org/10.3389/fmicb.2020.01800. PubMed: 32793182.
4. [WHO](#)
5. Gralinski, L. E. and V. D. Menachery. “Return of the Coronavirus: 2019-nCoV.” [Viruses](#) 12 (2020): 135. PubMed: 31991541.

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