

SARS-Related Coronavirus 2, Isolate hCoV-19/USA/MD-HP49081/2023 (Lineage DV.7.1) in VTA Cells

Catalog No. NR-59702

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/MD-HP49081/2023

Original Source: Severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2), isolate hCoV-19/USA/MD-HP49081/2023 was isolated from a human in Maryland, USA, in 2023.¹

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/MD-HP49081/2023 is assigned lineage DV.7.1 (Pango v.4.3.1 consensus call), Omicron (BA.2-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/MD-HP49081/2023 has been sequenced (GISAID: EPI_ISL_18432211).^{1,2} The following mutations are present in the clinical isolate: Spike A27S, Spike D405N, Spike D614G, Spike D796Y, Spike E484A, Spike F157L, Spike F456L, Spike F486S, Spike G142D, Spike G257S, Spike G339H, Spike G446S, Spike H655Y, Spike I210V, Spike K147E, Spike K417N, Spike K444T, Spike L24del, Spike L452R, Spike L455F, Spike L858I, Spike N185D, Spike N440K, Spike N460K, Spike N501Y, Spike N679K, Spike N764K, Spike N969K, Spike P25del, Spike P26del, Spike P681H, Spike Q498R, Spike Q954H, Spike R346T, Spike R408S, Spike S371F, Spike S373P, Spike S375F, Spike S477N, Spike T19I, Spike T376A, Spike T478K, Spike V213G, Spike W152R, Spike Y505H, Envelope (E) T9I, E T11A, Membrane (M) A63T, M Q19E, Nucleocapsid (N) E31del, N G204R, N P13L, N R10Q, N R32del, N R203K, N S33del, N S413R, Non-structural (NS) NS3 A72T, NS3 A110V, NS3 T223I, NS7a A13T, NS8 S69P, Non-structural protein (NSP)1 F143del, NSP1 K141del, NSP1 S135R, NSP1 S142del, NSP2 A247V, NSP2 L448F, NSP3 G489S, NSP3 P822S, NSP3 Q380K, NSP3 S403L, NSP3 T24I, NSP3 T1714I,

NSP4 L264F, NSP4 L438F, NSP4 T327I, NSP4 T492I, NSP5 A285V, NSP5 P132H, NSP6 F108del, NSP6 G107del, NSP6 S106del, NSP8 N118S, NSP9 A22V, NSP12 A529V, NSP12 G671S, NSP12 P323L, NSP13 R392C, NSP14 I42V, NSP14 V182I, NSP15 T112I, NSP16 Q28R.^{1,2} It was labeled as variant under monitoring (VUM) GRA (CH.1.1+CH.1.1.*), and first detected in Austria.^{1,4}

Note: Two additional mutations, ORF6 D61L and ORF10 M1V, are present in the GISAID reference sequence but are 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/MD-HP49081/2023.

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

Packaging/Storage:

NR-59702 was packaged aseptically in 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: 2 to 4 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/MD-HP49081/2023 (Lineage DV.7.1) in VTA Cells, NR-59702, contributed by Dr. Andrew S. Pekosz."

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). Current Edition. Washington, DC: U.S. Government Printing Office.

Disclaimers:

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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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