SARS-Related Coronavirus 2, Isolate hCoV-19/USA/MD-HP50212/2023 (Lineage BA.2.86.1)

Catalog No. NR-59786

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-HP50212/2023
Original Source: Severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2), isolate hCoV-19/USA/MD-HP50212/2023 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-HP50212/2023 is assigned lineage BA.2.86.1 (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-HP50212/2023 has been sequenced (GISAID: EPI_ISL_18679015).[1,2] The following mutations are present in the clinical isolate: Spike A27S, Spike A570V, Spike D614G, Spike D796Y, Spike E554K, Spike F157S, Spike G142D, Spike H69del, Spike H655Y, Spike ins16MPLF, Spike L24del, Spike N679K, Spike N764K, Spike N969K, Spike P25del, Spike P26del, Spike P621S, Spike P681R, Spike P1143L, Spike Q954H, Spike R21T, Spike R158G, Spike S50L, Spike S939F, Spike T19I, Spike V70del, Spike V127F, Spike Y144del, Envelope (E) T9I, Membrane (M) A63T, M A104V, M D3H, M Q19E, M T30A, Nucleocapsid (N) E31del, N G204R, N P13L, N Q229K, N R32del, N R203K, N S33del, N S413R, Non-structural (NS) NS3 T223I, Non-structural protein (NSP)1 A138T, NSP1 S135R, NSP2 A31D, NSP3 A1892T, NSP3 G489S, NSP3 K1155R, NSP3 N1708S, NSP3 T24I, NSP3 V238L, NSP4 L264F, NSP4 T327I, NSP4 T492I, NSP5 P132H, NSP6 F108del, NSP6 G107del, NSP6 S106del, NSP6 V24F, NSP9 T35I, NSP12 P323L, NSP13 R303H, NSP13 R392C, NSP14 I42V, NSP15 T112I.[1,2] It was labeled as a variant of interest (VOI) GRA (BA.2.86+BA.2.86.* excluding JN.1, JN.1.*), and first detected in Denmark/Israel/USA.[1,4]

Note: Stretches of NNNs comprise 4.54% of the overall sequence. Compared to the reference WIV04 sequence, NR-59786 contains an insertion of 12 nucleotides and a gap of 36 nucleotides.

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/MD-HP50212/2023.

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

Packaging/Storage:

NR-59786 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: 2 to 4 days at 37°C and 5% CO_2
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-HP50212/2023 (Lineage BA.2.86.1), NR-59786, 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.

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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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