

RNA from Machupo Virus, Carvallo

Catalog No. NR-37373

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For research use only. Not for human use.

Contributor and Manufacturer:

World Reference Center for Emerging Viruses and Arboviruses, University of Texas Medical Branch, Galveston, under government contract

Product Description:

RNA was extracted from a preparation of cell lysate and supernatant from Vero E6 cells infected with Machupo virus, Carvallo.¹ The complete genomic sequence of Machupo virus, Carvallo has been determined (GenBank: AY129248² and AY358021³).

NR-37373 was tested for residual virus following the procedure described by Towner et al.⁴ No residual virus was recovered.

Material Provided:

Each vial contains 50 µL of viral RNA in nuclease-free water. The viral RNA is in a background of cellular nucleic acid. The total viral RNA content per vial (µg and copy number) is shown on the Certificate of Analysis for each lot. The vial should be centrifuged prior to opening.

Packaging/Storage:

NR-37373 was packaged aseptically, in screw-capped plastic cryovials. The product is provided frozen and should be stored at -70°C or colder immediately upon arrival. Freeze-thaw cycles should be avoided.

Citation:

Acknowledgment for publications should read "The following reagent was obtained through BEI Resources, NIAID, NIH: RNA from Machupo Virus, Carvallo, NR-37373."

Biosafety Level: 1

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. 5th ed. Washington, DC: U.S. Government Printing Office, 2009; see www.cdc.gov/biosafety/publications/bmbl5/index.htm.

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References:

1. Johnson, K. M., et al. "Virus Isolations from Human Cases of Hemorrhagic Fever in Bolivia." Proc. Soc. Exp. Biol. Med. 118 (1965):113-118. PubMed: 14254520.
2. Charrel, R. N., et al. "Phylogeny of New World Arenaviruses Based on the Complete Coding Sequences of the Small Genomic Segment Identified an Evolutionary Lineage Produced by Intrasegmental Recombination." Biochem. Biophys. Res. Commun. 296 (2002): 1118-1124. PubMed: 12207889.
3. Direct Submission.
4. Towner, J. S., et al. "High-Throughput Molecular Detection of Hemorrhagic Fever Virus Threats with Applications for Outbreak Settings." J. Infect. Dis. 196 Suppl. 2 (2007) S205-S212. PubMed: 17940951.

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