Recombinant HCoV-229E Nucleocapsid His-tag

Catalog Number: 10708-CV

DESCRIPTION

Source	*Spodoptera frugiperda*, *Sf* 21 (baculovirus)-derived hcov-229e Nucleocapsid protein Met1-Asn389, with a C-terminal 6-His tag Accession # NP_073556.1
N-terminal Sequence Analysis	Ala2, determined by protein ID.
Predicted Molecular Mass	44 kDa

SPECIFICATIONS

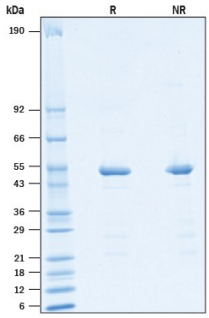
SDS-PAGE	48-53 kDa, under reducing conditions
Activity	Bioassay data are not available.
Endotoxin Level	<0.10 EU per 1 µg of the protein by the LAL method.
Purity	>90%, by SDS-PAGE visualized with Silver Staining and quantitative densitometry by Coomassie® Blue Staining.
Formulation	Lyophilized from a 0.2 µm filtered solution in PBS with Trehalose. See Certificate of Analysis for details.

PREPARATION AND STORAGE

Reconstitution	Reconstitute at 500 µg/mL in PBS.
Shipping	The product is shipped at ambient temperature. Upon receipt, store it immediately at the temperature recommended below.
Stability & Storage	**Use a manual defrost freezer and avoid repeated freeze-thaw cycles.** • 12 months from date of receipt, -20 to -70 °C as supplied. • 1 month, 2 to 8 °C under sterile conditions after reconstitution. • 3 months, -20 to -70 °C under sterile conditions after reconstitution.

DATA

SDS-PAGE



Recombinant HCoV-229E Nucleocapsid His-tag Protein SDS-PAGE. 2 µg/lane of Recombinant HCoV-229E Nucleocapsid His-tag (Catalog # 10708-CV) was resolved with SDS-PAGE under reducing (R) and non-reducing (NR) conditions and visualized by Coomassie® Blue staining, showing bands at 48-53 kDa.

BACKGROUND

HCoV-229E belongs to a family of viruses known as coronaviruses that are commonly comprised of a large plus-strand RNA genome and four structural proteins: Spike protein (S), Envelope protein (E), Membrane protein (M), and Nucleocapsid protein (N). HCoV-229E is a member of the alpha-coronavirus family and was discovered in 1966 (1, 2). Other well-known human coronaviruses include three viruses that cause relatively mild respiratory disease: HCoV-NL63, HCoV-HKU1 and HCov-OC43, plus three viruses that caused the Severe Acute Respiratory Syndrome (SARS-CoV), the Middle East Respirator Syndrome (MERS-CoV), and the global pandemic Covid-19 (SARS-CoV2). While the S, E and M proteins build up the viral envelop, the N protein is involved transcription, replication, and packaging of the viral RNA genome into a helical ribonucleocapsid (RNP) (3). The CoV-229E N protein is a ~50 kDa protein composed of two independent structural domains connected by a linker region. Both the N-terminal and the linker regions contain RNA binding domains, while the C-terminal region is responsible for the oligomerization of the N protein (4). The CoV-229E protein shares 45% amino acid sequence identity with CoV-NL63 N protein. the N protein is an abundant protein during coronavirus infection and displays high immunogenic activity. Cross activity of antibodies among different strains should be rigorously tested when designing serological diagnostic kits (5).

References:

1. Hamre, D. and J.J. Procknow (1966) Proc. Soc. Exp. Biol. Med. **121**:190.
2. Van der Hoek, L. et al. (2004) Nat. Med. **10**:368.
3. Chang, C.K. et al. (2006) J.Biomed. Sci. **13**:59.
4. Lo, Y. et al. (2013) FEBS Letters. **587**:120.
5. Chan, K.H. et al. (2005) Clin. Diagn. Lab. Immunol. **12**:1317.

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