R&D SYSTEMS
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Recombinant SARS-CoV-2 B.1.2 Nucleocapsid His-tag

Catalog Number: 11000-CV

DESCRIPTION

Source	*Spodoptera frugiperda*, *Sf* 21 (baculovirus)-derived sars-cov-2 Nucleocapsid protein Met1-Ala419 (Pro67Ser, Pro199Leu), with a C-terminal 6-His tag Accession # YP_009724397.2
N-terminal Sequence Analysis	Protein identity confirmed by mass spectrometry.
Predicted Molecular Mass	46 kDa

SPECIFICATIONS

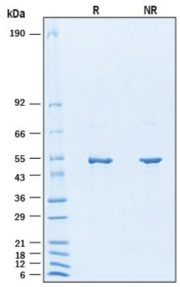
SDS-PAGE	45-55 kDa, under reducing conditions.
Activity	Bioassay data are not available.
Endotoxin Level	<0.10 EU per 1 μg of the protein by the LAL method.
Purity	>95%, by SDS-PAGE visualized with Silver Staining and quantitative densitometry by Coomassie® Blue Staining.
Formulation	Lyophilized from 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 SARS-CoV-2 B.1.2 N His-tag Protein SDS-PAGE. 2 μg/lane of Recombinant SARS-CoV-2 B.1.2 N His-tag Protein (Catalog # 11000-CV) was resolved with SDS-PAGE under reducing (R) and non-reducing (NR) conditions and visualized by Coomassie® Blue staining, showing bands at 45-55 kDa.

BACKGROUND

SARS-Cov-2, which causes the global pandemic coronavirus disease 2019 (Covid-19), belongs to a family of viruses known as coronaviruses that are commonly comprised of four structural proteins: Spike protein (S), Envelope protein (E), Membrane protein (M), and Nucleocapsid protein (N) (1). 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) (2, 3). The SARS-Cov-2 N protein is a ~45 kDa protein composed of two independent structural domains connected by a linker region. The N-terminal region contains an RNA binding domain, the linker region interacts with the M protein and the C-terminal region contains a self-association domain (2,3). The SARS-Cov-2 N protein shares 91% and 47% amino acid sequence identity with SARS-Cov-1 and MERS N protein, respectively. The SARS-Cov-2 N protein displays VSR (viral suppressor of RNA interference) activity in mammalian cells (4). Several emerging SARS-CoV-2 genomes have been identified with mutations compared to the Wuhan-Hu-1 SARS-CoV-2 reference sequence, including the B.1.2 variant. As the N protein is an abundant protein during coronavirus infection and displays high immunogenic activity (5, 6), it has been used to develop diagnostic kit for detecting IgM and IgG antibodies against SARS-Cov-2 (7). Within the N protein, there are 2 mutations in the B.1.2 variant which might make attractive targets for the development of antiviral therapeutics or potential diagnostic tools.

References:

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2. Chang, C. K. *et al.* (2006) J. Biomed. Sci. **13**:59.
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6. Guan, M. *et al.* (2004) Clin. Diagn. Lab. Immunol. **11**:287.
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