Recombinant SARS-CoV-2 NSP14 His-tag

Catalog Number: 10667-CV

DESCRIPTION

Source	*E. coli*-derived sars-cov-2 NSP14 protein Ala1-Gln527 Accession # YP_009725309.1 with a C-terminal 6-His tag
N-terminal Sequence Analysis	Ala1
Predicted Molecular Mass	61 kDa

SPECIFICATIONS

SDS-PAGE	53-62 kDa, under reducing conditions
Endotoxin Level	<1.0 EU per 1 µg of the protein by the LAL method.
Purity	>85%, by SDS-PAGE visualized with Silver Staining and quantitative densitometry by Coomassie® Blue Staining.
Formulation	Supplied as a 0.2 µm filtered solution in Tris, NaCl, TCEP and Glycerol. See Certificate of Analysis for details.

PREPARATION AND STORAGE

Shipping	The product is shipped with polar packs. Upon receipt, store it immediately at the temperature recommended below.
Stability & Storage	**Use a manual defrost freezer and avoid repeated freeze-thaw cycles.** • 6 months from date of receipt, -20 to -70 °C as supplied. • 3 months, -20 to -70 °C under sterile conditions after opening.

BACKGROUND

Non-structural protein 14 (NSP14) is one of several functional proteins released by ORF1a-encoded protease cleavage of the pp1a and pp1ab replicase polyproteins expressed from the coronavirus (CoV) genome (1). The NSPs are involved in the replication and transcription of the viral RNA and not incorporated within the virion particles. Coronaviruses include various highly pathogenic strains such as SARS-CoV, MERS-CoV and SARS-CoV2 that have had significant impact on humans in addition to strains that have negatively impacted livestock. NSP14 is a bifunctional 527 amino acid enzyme. It contains a noncanonical methyltransferase (MTase) domain in the C-terminal portion of the protein that methylates guanosine at the N7 position using S-adenosyl methionine (SAM) as a methyl donor to generate the intermediate cap-O structure of the 5' mRNA cap (2). The viral RNA cap structure protects the viral RNA from degradation, promotes mRNA translation, and prevents recognition by innate immune mechanisms (3). As the MTase active site fold is unique from cellular MTases (4), NSP14 presents an attractive antiviral target. The C-terminal domain is connected via a hinge region to an N-terminal exonuclease domain composed of three highly conserved motifs (5). The 3' to 5' exonuclease function of the N-terminal domain is responsible for the proofreading and high-fidelity replication observed in coronaviruses compared to other RNA viruses (6-8). NSP14 has been shown to form a complex with NSP10; the association with NSP10 was shown to stimulate exonuclease catalytic activity more than 35-fold and is required for the high replication fidelity (9,10). Exonuclease function makes polymerase inhibition via nucleos(t)ide analog (NA) development more challenging because it confers resistance via its error-correcting mechanism for NA incorporated into RNA (6,9). NSP14 exonuclease domain mutation studies showed it is absolutely required for viability and replication of SARSCoV2 (11) suggesting exonuclease activity may serve a more extensive role in replication than proof-reading (11,12). NSP14 was suggested to be involved in mediating recombination frequency and junction site selection in coronavirus (13). Both for the role it plays in resistance to polymerase inhibition and based on absolute requirement for viability, NSP14 is an appealing protein to target for therapeutic and vaccine development (8,11,13,14).

References:

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