PRODUCT INFORMATION

SARS-CoV-2 nsp14 Methyltransferase (recombinant)

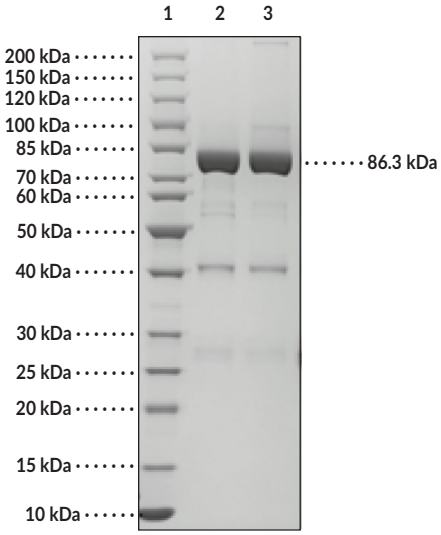
Item No. 40884

Overview and Properties

Synonyms:	SARS-CoV-2 Guanine-N7 Methyltransferase, SARS-CoV-2 Guanine-N7 MTase, SARS-CoV-2 Non-structural Protein 14, Severe Acute Respiratory Syndrome Coronavirus 2 nsp14 Methyltransferase
Source:	Recombinant SARS-CoV-2 N-terminal GST-tagged nsp14 expressed in *E. coli*
Amino Acids:	1-527
Uniprot No.:	P0DTD1
Molecular Weight:	86.3 kDa
Storage:	-80°C (as supplied)
Stability:	≥1 year
Purity:	≥90% estimated by SDS-PAGE
Supplied in:	50 mM Tris, pH 7.5, with 200 mM sodium chloride and 20% glycerol
Endotoxin Testing:	< 1.0 EU/µg, determined by the LAL endotoxin assay
Protein Concentration:	***batch specific*** mg/m
Special Conditions:	Avoid repeated freeze/thaw cycles.

Information represents the product specifications. Batch specific analytical results are provided on each certificate of analysis.

Image



Lane 1: MW Markers
Lane 2: SARS-CoV-2 nsp14 Methyltransferase (2 µg, reduced)
Lane 3: SARS-CoV-2 nsp14 Methyltransferase (10 µg, reduced)

SDS-PAGE Analysis of SARS-CoV-2 nsp14 Methyltransferase.

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Description

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is an enveloped positive-stranded RNA virus and the causative agent of COVID-19, a primarily respiratory illness characterized by fever, cough, and shortness of breath that can lead to life-threatening complications.[1-5] The SARS-CoV-2 genome contains approximately 30 kilobases and 14 open reading frames (ORFs) that encode four structural proteins: spike, envelope, membrane, and nucleocapsid, as well as 16 non-structural proteins and 9 accessory factors.[6] SARS-CoV-2 non-structural protein 14 (nsp14), also known as guanine-N7 methyltransferase (guanine-N7 MTase), is encoded within *ORF1ab* with an amino acid sequence that displays few mutations and is highly conserved across coronaviruses and SARS-CoV-2 variants.[6-8] It is a bifunctional enzyme having an N-terminal exoribonuclease domain (ExoN domain) and a C-terminal methyltransferase domain.[6,7] SARS-CoV-2 nsp14 forms an exonuclease complex with the cofactor nsp10, which binds to and stabilizes the disordered ExoN domain and is a necessary interaction for accurate exoribonuclease and RNA strand proofreading activities.[6-8] It also forms a ternary methylation complex with nsp10 and nsp16 methyltransferase, also known as 2′-O-methyltransferase (2′-O-MTase), and catalyzes guanosine methylation in the viral mRNA 5′-end cap prior to the terminal ribose methylation catalyzed by 2′-O-MTase.[6,9] SARS-CoV-2 nsp14 inhibits IFN-β reporter gene activation induced by the retinoic acid-inducible gene I caspase activation and recruitment domain (RIG-I 2CARD domain) in HEK293FT cells, as well as inhibits global protein translation and expression of IFN-stimulated genes (ISGs) in HEK293T cells expressing SARS-CoV-2 *nsp14*.[7,10]

References

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