

PRODUCT INFORMATION



SARS-CoV-2 nsp10 (recombinant)

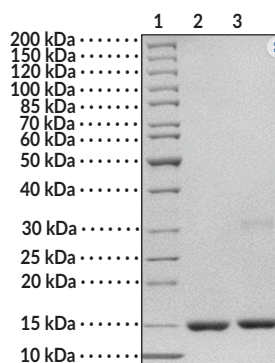
Item No. 40883

Overview and Properties

Synonyms:	SARS-CoV-2 Non-structural Protein 10, Severe Acute Respiratory Syndrome Coronavirus 2 nsp10
Source:	Recombinant SARS-CoV-2 N-terminal His-tagged nsp10 expressed in <i>E. coli</i>
Amino Acids:	1-139 (full length)
Uniprot No.:	P0DTD1
Storage:	-80°C (as supplied); avoid repeated freeze/thaw cycles
Stability:	≥1 year
Purity:	≥90%
Supplied in:	50 mM Tris-HCl, 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:	<i>batch specific</i> mg/ml

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 nsp10 (2 μg)
Lane 3: SARS-CoV-2 nsp10 (10 μg)

SDS-PAGE Analysis of SARS-CoV-2 nsp10

WARNING
THIS PRODUCT IS FOR RESEARCH ONLY - NOT FOR HUMAN OR VETERINARY DIAGNOSTIC OR THERAPEUTIC USE.

SAFETY DATA
This material should be considered hazardous until further information becomes available. Do not ingest, inhale, get in eyes, on skin, or on clothing. Wash thoroughly after handling. Before use, the user must review the [complete](#) Safety Data Sheet, which has been sent via email to your institution.

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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 10 (nsp10) is encoded within *ORF1ab* and is a cofactor for guanine-N7 methyltransferase (guanine-N7 MTase) and 2'-O-methyltransferase (2'-O-MTase).⁶⁻⁸ The amino acid sequence of nsp10 displays few mutations and is highly conserved across SARS-CoV-2 variants.⁷ SARS-CoV-2 nsp10 binds to and stabilizes the disordered N-terminal exoribonuclease domain (ExoN domain) of guanine-N7 MTase and is necessary for accurate exonuclease activity.⁷ It forms a complex with 2'-O-MTase to methylate nascent mRNAs at the ribose 2'-O position, creating a Cap-1 structure that facilitates increased translation of viral mRNAs and reduced innate immune recognition by the host cell.⁸

References

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