Data Sheet (Cat.No.TMPH-03699)

TargetMol

VSIV (strain 94GUB Central America) L Protein (His)

General Information

Synonyms: RNA-directed RNA polymerase L;Transcriptase;Protein L;Replicase;Large structural protein

Protein Construction: 598-784 aa

Species: VSIV

Expression Host: E. coli

Accession: Q8B0H0

Molecular Weight: 25.4 kDa (predicted)

AA Sequence: ICIANHIDYEKWNNHQRKLSNGPVFRVMGQFLGYPSLIERTHEFFEKSLIYYNGRPDLMRVHNNTLVNSTSQR VCWQGQEGGLEGLRQKGWSILNLLVIQREAKIRNTAVKVLAQGDNQVICTQYKTKKSRNVVELQSALNQMV SNNEKIMTAIKIGTGKLGLLINDDETMQSADYLNYGKIPIFRG

QC Testing

Biological Activity: Activity has not been tested. It is theoretically active, but we cannot guarantee it. If you require protein activity, we recommend choosing the eukaryotic expression version first.

Purity: > 85% as determined by SDS-PAGE.

Endotoxin: < 1.0 EU/μg of the protein as determined by the LAL method.

Formulation: Tris-based buffer, 50% glycerol

Preparation and Storage

Reconstitution:

A Certificate of Analysis (CoA) containing reconstitution instructions is included with the products. Please refer to the CoA for detailed information.

Stability & Storage:

Lyophilized powders can be stably stored for over 12 months, while liquid products can be stored for 6-12 months at -80°C. For reconstituted protein solutions, the solution can be stored at -20°C to -80°C for at least 3 months. Please avoid multiple freeze-thaw cycles and store products in aliquots.

Actual storage temperature shall be subject to the COA.

Shipping:

In general, lyophilized powders are shipped with blue ice, while solutions are shipped with dry ice.

Protein Background

Responsible for RNA synthesis (replicase and transcriptase), cap addition, and cap methylation. Performs also the polyadenylation of subgenomic mRNAs by a stuttering mechanism at a slipery stop site present at the end of viral genes. The template is composed of the viral RNA tightly encapsidated by the nucleoprotein (N). The viral polymerase binds to the genomic RNA at the 3' leader promoter, thereby initiating either genome replication or mRNA transcription. In the transcription mode, the polymerase performs the sequential transcription of all mRNAs

using a termination-reinitiation mechanism responding to gene start and gene end signals. Some polymerase disengage from the template at each gene junction, resulting in a decreasing abundance of transcripts from the 3' to the 5' end of the genome. The first gene is the most transcribed, and the last the least transcribed. The viral phosphoprotein helps the polymerase to engage the N-RNA template and acts as processivity factor. Polyribonucleotidyl transferase (PRNTase) adds the cap structure when the nascent RNA chain length has reached few nucleotides. Ribose 2'-O methylation of viral mRNA cap precedes and facilitates subsequent guanine-N-7 methylation, both activities being carried by the viral polymerase. In the replication mode, the polymerase replicates the whole viral genome without recognizing the gene end transcriptional signals. The ability of the polymerase to override the gene end signals as it is producing the antigenome is probably due to replicative RNA becoming encapsidated with nucleoprotein as it is synthesized.

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