

Datasheet for ABIN7566327

SARS-CoV-2 Spike S1 Protein (AA 330-530) (GST tag,His tag)[Go to Product page](#)

Overview

Quantity:	100 µg
Target:	SARS-CoV-2 Spike S1
Protein Characteristics:	AA 330-530
Origin:	SARS Coronavirus-2 (SARS-CoV-2)
Source:	HEK-293 Cells
Protein Type:	Recombinant
Biological Activity:	Active
Purification tag / Conjugate:	This SARS-CoV-2 Spike S1 protein is labelled with GST tag,His tag.

Product Details

Purpose:	SARS-CoV-2 Spike Protein S1 (RBD) (rec.) (GST-His)
Cross-Reactivity:	Human
Characteristics:	Receptor-binding domain (RBD) of SARS-CoV-2 Spike protein S1 (aa 330-530) is fused at the N-terminus to a GST-tag and at the C-terminus to a His-tag.
Purity:	>95 % (SDS-PAGE)
Endotoxin Level:	<0.001EU/µg purified protein (LAL test).
Biological Activity Comment:	Binds to the human ACE2.

Target Details

Target:	SARS-CoV-2 Spike S1
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Target Details

Abstract: [SARS-CoV-2 Spike S1 Products](#)

Background: 2019-nCoV Spike Protein S1 (RBD)

SARS-CoV-2 shares 79.5 % sequence identity with SARS-CoV and is 96.2 % identical at the genome level to the bat coronavirus BatCoV RaTG133, suggesting it had originated in bats. The coronaviral genome encodes four major structural proteins: the Spike (S) protein, Nucleocapsid (N) protein, Membrane/Matrix (M) protein and the Envelope (E) protein. The SARS Envelope (E) protein contains a short palindromic transmembrane helical hairpin that seems to deform lipid bilayers, which may explain its role in viral budding and virion envelope morphogenesis. The SARS Membrane/Matrix (M) protein is one of the major structural viral proteins. It is an integral membrane protein involved in the budding of the viral particles and interacts with SARS Spike (S) protein and the Nucleocapsid (N) protein. The N protein contains two domains, both of them bind the virus RNA genome via different mechanisms. The CoV Spike (S) protein assembles as trimer and plays the most important role in viral attachment, fusion and entry. It is composed of a short intracellular tail, a transmembrane anchor and a large ectodomain that consists of a receptor binding S1 subunit (RBD domain) and a membrane-fusing S2 subunit. Sequence analysis of the SARS-CoV-2 S protein genome showed that it was only 75 % identical with the SARS-CoV S protein. However, analysis of the receptor binding motif (RBM) in the S protein showed that most of the amino acid residues essential for receptor binding were conserved between SARS-CoV and SARS-CoV-2, suggesting that the 2 CoV strains use the same host receptor for cell entry, the receptor angiotensin-converting enzyme 2 (ACE2).

Molecular Weight: ~50kDa (SDS-PAGE, reducing conditions)

Application Details

Restrictions: For Research Use only

Handling

Format: Lyophilized

Reconstitution: 1 mg/mL after reconstitution

Concentration: 1 mg/mL

Buffer: Contains PBS.

Handling Advice: After opening, prepare aliquots and store at -20 °C. Avoid freeze/thaw cycles. Centrifuge lyophilized vial before opening and reconstitution. For maximum product recovery after thawing, centrifuge the vial before opening the cap.

Handling

Storage:	4 °C,-20 °C
Storage Comment:	Short Term Storage: +4°C Long Term Storage: -20°C Use & Stability: Stable for at least 6 months after receipt when stored at -20°C.Working aliquots are stable for up to 3 months when stored at -20°C.