Datasheet for ABIN7566343

SARS-CoV-2 Spike S1 Protein (AA 319-541) (Fc Tag)

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Overview

Quantity:	3 x 50 μg
Target:	SARS-CoV-2 Spike S1
Protein Characteristics:	AA 319-541
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 Fc Tag.

Product Details

Purpose:	SARS-CoV-2 Spike Protein S1 (RBD):Fc (human) (rec.) (B.1.1.529 Variant, Omicron)
Cross-Reactivity:	Human
Characteristics:	Receptor-binding domain (RBD) of SARS-CoV-2 Spike protein S1 (aa 319-541) containing the mutations G339D, S371L, S373P, S375F, K417N, N440K, G446S, S477N, T478K, E484A, Q493K, G496S, Q498R, N501Y & Y505H, is fused to the N-terminus of the Fc region of human IgG1.
Purity:	>95 % (SDS-PAGE)
Endotoxin Level:	<0.01EU/μg purified protein (LAL test).
Biological Activity Comment:	Binds to anti-SARS-CoV-2 Spike (RBD) antibodies in serum or plasma. Binds to human ACE2.

Target Details

Target:	SARS-CoV-2 Spike S1
Abstract:	SARS-CoV-2 Spike S1 Products
Background:	2019-nCoV Spike Protein S1 (RBD), Spike Receptor Binding Domain, Omicron Variant, B.1.1.529 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. The S1 subunit contains a receptor binding domain (RBD), which binds to the cell surface receptor angiotensin-converting enzyme 2 (ACE2) present at the surface of epithelial cells. The B.1.1.529 variant, called Omicron was first reported to WHO from South Africa on 24 November 2021. Since then, B.1.1.529 has been detected globally. This variant seems to be at least equally infectious than B.1.617.2 (Delta), has already caused super spreader events and has outcompeted Delta within weeks in most countries. B.1.1.529 hosts an unprecedented number of mutations in its spike gene and early reports have provided evidence for extensive immune escape and reduced vaccine effectiveness.
Molecular Weight:	~60kDa (SDS-PAGE)

Application Details

Restrictions:	For Research Use only

Handling

Format:	Lyophilized
Reconstitution:	1 mg/mL after reconstitution
Concentration:	1 mg/mL

Handling

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.
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.