Data Sheet (Cat.No.TMAH-01070H)

TargetMol

Anti-SARS-CoV-2 Spike RBD Nanobody Antibody-HRP (5A563)

Product Details

Ig Type:	VHH fusion with human IgG1 Fc
Reactivity:	Human Novel Coronavirus (SARS-CoV-2/ 2019-nCoV)
Conjugation:	HRP
Clone:	5A563
Purification:	Affinity-chromatography

Applications

Application:	ELISA
Recommended	ELISA:1:1000-1:500000.

Properties

Stability & Storage:	Store at -20°C or -80°C for 12 months. Avoid repeated freeze-thaw cycles. Keep away from direct sunlight.
Shipping:	Shipping with blue ice.

Antigen Details

Immunogen:	Recombinant Protein: Human Novel Coronavirus Spike glycoProtein(S) (319-541aa)
Antigen Species:	Human Novel Coronavirus (SARS-CoV-2/ 2019-nCoV)
Uniprot ID:	P0DTC2
Synonyms:	Spike glycoprotein;Peplomer protein;E2;S glycoprotein
Biology Area:	Microbiology

Research Background

attaches the virion to the cell membrane by interacting with host receptor, initiating the infection. Binding to human ACE2 receptor and internalization of the virus into the endosomes of the host cell induces conformational changes in the Spike glycoprotein. Binding to host NRP1 and NRP2 via C-terminal polybasic sequence enhances virion entry into host cell. This interaction may explain virus tropism of human olfactory epithelium cells, which express high level of NRP1 and NRP2 but low level of ACE2. The stalk domain of S contains three hinges, giving the head unexpected orientational freedom. Uses human TMPRSS2 for priming in human lung cells which is an essential step for viral entry. Can be alternatively processed by host furin. Proteolysis by cathepsin CTSL may unmask the fusion peptide of S2 and activate membranes fusion within endosomes. mediates fusion of the virion and cellular membranes by acting as a class I viral fusion protein. Under the current model, the protein has at least three conformational states: pre-fusion native state, pre-hairpin intermediate state, and post-fusion hairpin state. During viral and target cell membrane fusion, the coiled coil regions (heptad repeats) assume a trimer-of-hairpins structure, positioning the fusion peptide in close proximity to the C-terminal region of the ectodomain. The formation of this structure appears to drive apposition and subsequent fusion of viral and target cell membranes. Acts as a viral fusion peptide which is unmasked following S2 cleavage occurring upon virus endocytosis. May down-regulate host tetherin (BST2) by lysosomal degradation, thereby counteracting its antiviral activity.

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