Data Sheet (Cat.No.TMAH-01070)

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

Product Details

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

Applications

Verified Activity:	1. The Binding Activity of SARS-CoV-2 Spike RBD Nanobody with SARS-CoV-2-S1-RBD Activity: Measured by its binding ability in a functional ELISA. Immobilized SARS-CoV-2-S1-RBD at 2 μg/ml can bind SARS-CoV-2 Spike RBD Nanobody, the EC50 is 0.8674 ng/ml. 2. In the Colloidal Gold Immunochromatography Assay detection system, the background of antibody (TMAH-01070) is clean, the detection limit can be as low as 25ng/ml (1.75ng/0.07ml), and the sensitivity is very good. 3. SARS-CoV-2 Spike RBD Nanobody (TMAH-01070) competed with ACE2-HRP conjugate for binding to SARS-CoV-2-S1-RBD. The binding signal of SARS-CoV-2-S1-RBD and ACE2-HRP conjugate was gradually reduced as the SARS-CoV-2 Spike RBD Nanobody concentrations increased. It indicated that this SARS-CoV-2 Spike RBD Nanobody effectively inhibited the SARS-CoV-2-S1-RBD/ACE2 binding. And the IC50 of this SARS-CoV-2 Spike RBD Nanobody is 1.296 nM. 4. SARS-CoV-2 Spike RBD Nanobody (TMAH-01070) competitively prevented SARS-CoV-2-S1-RBD from binding to ACE2-HRP conjugate. The inhibition efficacy of the SARS-CoV-2-S1-RBD/ACE2 binding was positively proportionally to the SARS-CoV-2 Spike RBD Nanobody concentrations. It showed that this SARS-CoV-2 Spike RBD Nanobody effectively inhibited the SARS-CoV-2-S1-RBD/ACE2 binding. And the IC50 of this SARS-CoV-2 Spike RBD Nanobody is 0.1074 μg/ml. 5. SARS-CoV-2 Spike protein RBD His/Sumostar Tag captured on COOH chip binding to the SARS-CoV-2 Spike RBD Nanobody (TMAH-01070), increases the local refractive index (RI), leading to a red shift of the LSPR peak position. The higher concentrations of SARS-CoV-2 Spike RBD Nanobody, the larger the wavelength shift. The detected affinity constant of SARS-CoV-2 Spike protein RBD/SARS-CoV-2 Spike RBD Nanobody binding is 28.2nM. 6. ELISA: Immobilize various types of SARS proteins at concentration of 2μg/ml on solid substrate, then react with SARS-CoV-2 Spike RBD Nanobody at concentration of 100μg/ml, 10μg/ml and 1μg/ml. It shows the SARS-CoV-2 Spike RBD Nanobody (TMAH-01070) is specific for SARS-CoV-2-S1-RBD protein, without any cross-reactivity with MERS-CoV, SARS-CoV, HCoV-OC43 or HCoV-229E.
Application:	ELISA, GICA

Recommended ELISA:1:10000-1:100000; GICA:1:10000-1:40000; Neutralising:1:100-1:10000.

Properties

Stability & Storage: Store at -20°C or -80°C for 12 months. Avoid repeated freeze-thaw cycles.

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: E2;Spike glycoprotein;S glycoprotein;Peplomer protein

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.