SARS-CoV-2 Spike RBD LlaMABody™ Bivalent VHH HulgG$_2$ Fusion Antibody

Recombinant Monoclonal Llama V_HH domain Clone # L009.2.69H

Catalog Number: LMAB10870

DESCRIPTION

Species Reactivity	SARS-CoV-2
Specificity	Clone L009.2.69H is a bivalent Llama V_HH-Human IgG_2 Fusion Antibody that detects SARS-CoV-2 Spike RBD in direct ELISAs. Antibody construct is depicted below.

SARS-CoV-2 Spike RBD Specific Llama V_HH domain	Llama Hinge	Human IgG_2

N-terminus C-terminus

Source	Recombinant Monoclonal Llama V_HH domain Clone # L009.2.69H
Purification	Protein A or G purified from cell culture supernatant
Immunogen	Human embryonic kidney cell HEK293-derived SARS-CoV-2 Spike RBD as immunogen for bivalent Llama VHH-Human IgG_2 Fusion Antibody. Arg319-Phe541 Accession # YP_009724390.1
Endotoxin Level	<0.10 EU per 1 µg of the antibody by the LAL method.
Formulation	Lyophilized from a 0.2 µm filtered solution in PBS with Trehalose. See Certificate of Analysis for details.

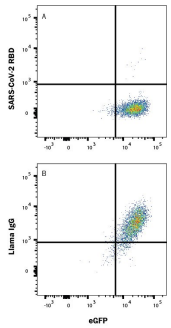
APPLICATIONS

Please Note: *Optimal dilutions should be determined by each laboratory for each application. General Protocols are available in the Technical Information section on our website.*

Blockade of Receptor-ligand Interaction	In a functional flow cytometry test, 50 µg/mL of SARS-Cov-2 Spike RBD Llamabody(Catalog # LMAB10870) will block the binding of Recombinant SARS-Cov-2 Spike 1 Fc-tagged protein (Catalog # 10622-CV) to HEK293 human embryonic kidney cell line transfected with recombinant human ACE-2.

DATA

Blockade of Receptor-ligand Interaction



SARS-Cov-2 Spike 1 protein binding to ACE-2-transfected Human Cell Line is Blocked by SARS-Cov-2 Spike RBD Antibody. In a functional flow cytometry test, Recombinant SARS-Cov-2 Spike 1 Fc-tagged protein (Catalog # 10622-CV) binds to HEK293 human embryonic kidney cell line transfected with recombinant human ACE-2 and eGFP. (A) Binding is completely blocked by 50 µg/mL of SARS-Cov-2 Spike RBD Llamabody VHH His-tag Monoclonal Antibody (Catalog # LMAB10870) but not by (B) Llama IgG1 Control. Protein binding was detected with Mouse Anti-Human IgG Fc APC-conjugated Monoclonal Antibody (Catalog # FAB110A). Staining was performed using our Staining Membrane-Associated Proteins protocol.

PREPARATION AND STORAGE

Reconstitution	Reconstitute at 0.5 mg/mL in sterile PBS.
Shipping	The product is shipped at ambient temperature. Upon receipt, store it immediately at the temperature recommended below.
Stability & Storage	**Use a manual defrost freezer and avoid repeated freeze-thaw cycles.** • 12 months from date of receipt, -20 to -70 °C as supplied. • 1 month, 2 to 8 °C under sterile conditions after reconstitution. • 6 months, -20 to -70 °C under sterile conditions after reconstitution.

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BACKGROUND

SARS-CoV-2, which causes the global pandemic coronavirus disease 2019 (Covid-19), belongs to a family of viruses known as coronaviruses that are commonly comprised of four structural proteins: Spike protein(S), Envelope protein (E), Membrane protein (M), and Nucleocapsid protein (N) (1). SARS-CoV-2 Spike Protein (S Protein) is a glycoprotein that mediates membrane fusion and viral entry. The S protein is homotrimeric, with each ~180-kDa monomer consisting of two subunits, S1 and S2 (2). In SARS-CoV-2, as with most coronaviruses, proteolytic cleavage of the S protein into two distinct peptides, S1 and S2 subunits, is required for activation. The S1 subunit is focused on attachment of the protein to the host receptor while the S2 subunit is involved with cell fusion (3-5). Based on structural biology studies, the receptor binding domain (RBD), located in the C-terminal region of S1, can be oriented either in the up/standing or down/lying state (6). The standing state is associated with higher pathogenicity and both SARS-CoV-1 and MERS can access this state due to the flexibility in their respective RBDs. A similar two-state structure and flexibility is found in the SARS-CoV-2 RBD (7). Based on amino acid (aa) sequence homology, the SARS-CoV-2 S1 subunit RBD has 73% identity with the RBD of the SARS-CoV-1 S1 RBD, but only 22% homology with the MERS S1 RBD. The low aa sequence homology is consistent with the finding that SARS and MERS bind different cellular receptors (8). The S Protein of the SARS-CoV-2 virus, like the SARS-CoV-1 counterpart, binds Angiotensin-Converting Enzyme 2 (ACE2), but with much higher affinity and faster binding kinetics (9). Before binding to the ACE2 receptor, structural analysis of the S1 trimer shows that only one of the three RBD domains in the trimeric structure is in the "up" conformation. This is an unstable and transient state that passes between trimeric subunits but is nevertheless an exposed state to be targeted for neutralizing antibody therapy (10). Polyclonal antibodies to the RBD of the SARS-CoV-2 protein have been shown to inhibit interaction with the ACE2 receptor, confirming RBD as an attractive target for vaccinations or antiviral therapy (11). There is also promising work showing that the RBD may be used to detect presence of neutralizing antibodies present in a patient's bloodstream, consistent with developed immunity after exposure to the SARS-CoV-2 virus (12). Lastly, it has been demonstrated the S Protein can invade host cells through the CD147/EMMPRIN receptor and mediate membrane fusion (13, 14).

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