Recombinant SARS-CoV2 Spike1 RBD-His (fragment)

20211213DS

FOR RESEARCH ONLY! NOT FOR HUMAN USE!

Cat.-no:	**400-029**
Size:	25 µg
Lot. No.:	According to product label
Country of origin:	Germany

Scientific Background

Gene:	*S*
Synonyms:	S glycoprotein, E2, Peplomer protein

SARS-CoV2, which causes the global pandemic Corona virus disease 2019 (Covid-19), belongs to a family of viruses known as Corona viruses that are commonly comprised of four structural proteins: Spike protein (S), Envelope protein (E), Membrane protein (M), and Nucleocapsid protein (N). SARS-CoV2 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. In SARS-CoV2 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. 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. 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-CoV2 RBD. Based on amino acid (aa) sequence homology, the SARS-CoV2 S1 subunit RBD has 73% identity with the RBD of the SARS-CoV1 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. The S Protein of the SARS-CoV2 virus, like the SARS-CoV1 counterpart, binds Angiotensin-Converting Enzyme 2 (ACE2), but with much higher affinity and faster binding kinetics.

Sequence

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RVQPTDSIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTF
KCYGVSPTKLNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKLPDDFTGCVIAW
NSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNCYFPLQSY
GFQPTNGVGYQPYRVVVLSFELLHAPATVCGPKKSTNLVKNKCVNFTRHHHHHH
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Database References

Protein RefSeq:	YP_009724390.1
Uniprot ID:	P0DTC2
mRNA RefSeq:	NC_045512.

Product Specifications

Expressed in	Insect cells
Purity	> 98% by SDS-PAGE & Coomassie stain
Buffer	PBS
Stabilizer	None
Formulation	lyophilized
Length (aa):	231
MW:	26,1 kDa (calculated)

Stability: The lyophilized SARS-CoV2 Spike1 RBD is stable for a few weeks at room temperature, but best stored at -20°C. Reconstituted SARS-CoV2 Spike1 RBD is best stored at –20°C to –70°C.

Reconstitution: The lyophilized SARS-CoV2 Spike1 RBD is soluble in water and most aqueous buffers; it should be reconstituted in PBS to a concentration of not lower than 100µg/ml.

AVOID REPEATED FREEZE AND THAW CYCLES!

Biological Activity: Measured by its binding ability in a functional ELISA. Soluble ACE2-Fc binds to the SARS-CoV2 Spike1 RBD protein.

References

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Handling/Application

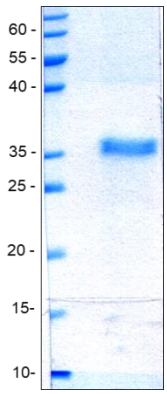

Fig. 1: SDS-PAGE analysis of recombinant SARS-Cov2 Spike1 RBD protein fragment derived from insect cells. Sample was loaded in 15% SDS-polyacrylamide gel under reducing conditions and stained with Coomassie stain.

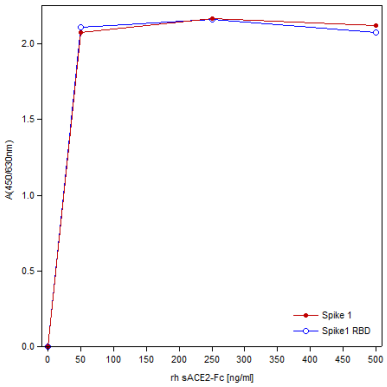

Fig. 2: Binding of sACE2-Fc to recombinant SARS-CoV2 Spike1 proteins in a functional ELISA. Recombinant SARS-CoV2 Spike1 and Spike1 RBD were coated with 1µg/ml in PBS. The sACE2-Fc was added in increasing concentrations.

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