Active Recombinant SARS-CoV-2 spike S1 Subunit protein, Avi/His-tagged, Biotinylated

Cat. No. Spike-053V **Lot. No.** (See product label)

SPECIFICATION

Product Overview	Biotinylated Recombinant SARS-CoV-2 Spike S1 Subunit(Val16-Pro681) protein, fused to Avi/His tag at the C-terminus, was expressed in CHO cells .
Species	SARS-CoV-2
Source	CHO
ProteinLength	Val16-Pro681
Description	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

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	and flexibility is found in the SARS-CoV-2 RBD (7). Based on amino acid (aa) sequence homology, the SARS-CoV-2 S1 subunit has 65% identity with SARS-CoV-1 S1 subunit, but only 22% homology with the MERS S1 subunit. 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 (ACE-2), but with much higher affinity and faster binding kinetics (9). Before binding to the ACE-2 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 S1 subunit have been shown to inhibit interaction with the ACE-2 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). Our Avi-tag Biotinylated SARS-Cov2 S1 subunit features biotinylation at a single site contained within the Avi-tag, a unique 15 amino acid peptide. Protein orientation will be uniform when bound to streptavidin-coated surface due to the precise control of biotinylation and the rest of the protein is unchanged so there is no interference in the protein's bioactivity.
Predicted N Terminal	Val16
Form	Lyophilized from a 0.2 μm filtered solution in PBS with Trehalose.
Bio-activity	Measured by its binding ability in a functional ELISA with Recombinant Human ACE-2

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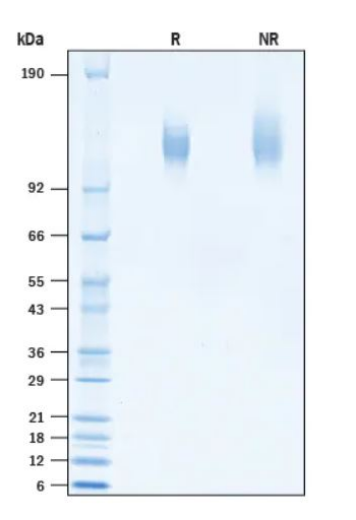
	Fc Chimera.
Molecular Mass	113-127 kDa, under reducing conditions
Endotoxin	<0.10 EU per 1 μg of the protein by the LAL method.
Purity	>95%, by SDS-PAGE visualized with Silver Staining and quantitative densitometry by Coomassie® Blue Staining.
Applications	Bioactivity
Storage	Use a manual defrost freezer 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.3 months, -20 to -70 °C under sterile conditions after reconstitution.
Reconstitution	Reconstitute at 500 μg/mL in PBS.
Conjugation	Biotin

GENE INFORMATION

Gene Name	S surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]
Official Symbol	S
Synonyms	coronavirus spike Protein, 2019-nCoV; cov spike Protein, 2019-nCoV; ncov RBD Protein, 2019-nCoV; ncov s1 Protein, 2019-nCoV; ncov s2 Protein, 2019-nCoV; ncov spike Protein, 2019-nCoV; NCP-CoV RBD Protein, 2019-nCoV; NCP-CoV s1 Protein, 2019-nCoV; NCP-CoV s2 Protein, 2019-nCoV; NCP-CoV Spike Protein, 2019-nCoV; novel coronavirus RBD Protein, 2019-nCoV; novel coronavirus s1 Protein, 2019-

	nCoV; novel coronavirus s2 Protein, 2019-nCoV; novel coronavirus spike Protein, 2019-nCoV; RBD Protein, 2019-nCoV; S1 Protein, 2019-nCoV; S2 Protein, 2019-nCoV; Spike RBD Protein, 2019-nCoV
Gene ID	43740568
Protein Refseq	YP_009724390.1
UniProt ID	P0DTC2
SDS-PAGE	 2 μg/lane Protein was resolved with SDS-PAGE under reducing (R) and non-reducing (NR) conditions and visualized by Coomassie® Blue staining.

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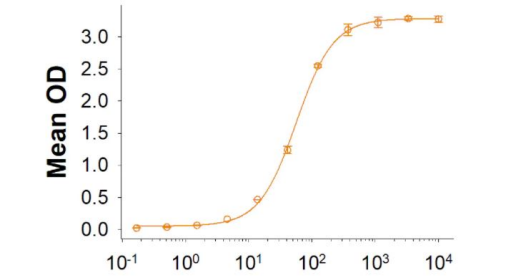
Binding Activity	

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