# Recombinant SARS-CoV-2 Spike RBD T478K His-tag

Catalog Number: 10875-CV

## DESCRIPTION

| | |
|---|---|
| **Source** | Human embryonic kidney cell, HEK293-derived sars-cov-2 Spike RBD protein<br>Arg319-Phe541 (Thr478Lys), a C-terminal 6-His tag<br>Accession # YP_009724390.1 |
| **N-terminal Sequence Analysis** | Arg319 |
| **Predicted Molecular Mass** | 26 kDa |

## SPECIFICATIONS

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|---|---|
| **SDS-PAGE** | 30-38 kDa, under reducing conditions. |
| **Activity** | Measured by its binding ability in a functional ELISA with Recombinant Human ACE-2 His-tag (Catalog # 933-ZN). |
| **Endotoxin Level** | <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. |
| **Formulation** | Lyophilized from a 0.2 µm filtered solution in PBS with Trehalose. See Certificate of Analysis for details. |

## PREPARATION AND STORAGE

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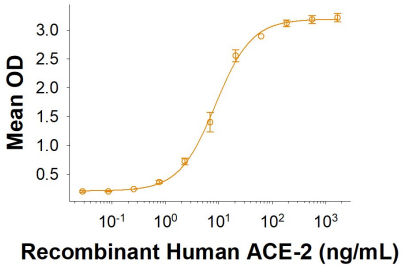
| **Reconstitution** | Reconstitute at 500 µg/mL in PBS. |
| **Shipping** | The product is shipped at ambient temperature. Upon receipt, store it immediately at the temperature recommended below. |
| **Stability & Storage** | **Use a manual defrost freezer and avoid repeated freeze-thaw cycles.**<br>• 12 months from date of receipt, -20 to -70 °C as supplied.<br>• 1 month, 2 to 8 °C under sterile conditions after reconstitution.<br>• 3 months, -20 to -70 °C under sterile conditions after reconstitution. |

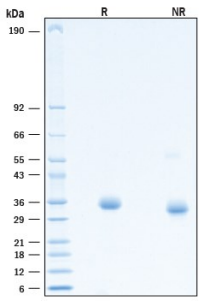
## DATA

### Binding Activity




**Recombinant SARS-CoV-2 T478K Spike RBD His-tag Protein Binding Activity.** Recombinant SARS-CoV-2 T478K Spike RBD (Catalog # 10875-CV) binds Recombinant Human ACE-2 (Catalog # 933-ZN) in a functional ELISA.

### SDS-PAGE




**Recombinant SARS-CoV-2 T478K Spike RBD His-tag Protein SDS-PAGE.** 2 µg/lane of Recombinant SARS-CoV-2 T478K Spike RBD His-tag (Catalog # 10875-CV) was resolved with SDS-PAGE under reducing (R) and non-reducing (NR) conditions and visualized by Coomassie® Blue staining, showing bands at 30-38 kDa.



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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 also include MERS and SARS-CoV-1. Coronaviruses are commonly comprised of four structural proteins: Spike protein (S), Envelope protein (E), Membrane protein (M) and Nucleocapsid protein (N) (1). The SARS-CoV-2 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 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). A metallopeptidase, angiotensin-converting enzyme 2 (ACE2), has been identified as a functional receptor for SARS-CoV-2 through interaction with a receptor binding domain (RBD) located at the C-terminus of S1 subunit (6, 7). The RBD of SARS-CoV-2 shares 73% amino acid (aa) identity with the RBD of the SARS-CoV-1, but only 22% aa identity with the RBD of MERS. SARS-CoV-2 variants carrying the aa substitution T478K in the RBD was first identified in Mexico (8). However, recently it drew a lot attention because this mutation is also present in B.1.617.2, which emerged from India and rapidly spread globally (9) Whether this mutation in RBD would cause more severe symptom or decrease the efficacy of vaccine-induced immunity is still under investigation.

**References:**

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