# Recombinant SARS-CoV-2 A.23.1 Spike (GCN4-IZ) His-tag

Catalog Number: 10860-CV

## DESCRIPTION

**Source**

Human embryonic kidney cell, HEK293-derived sars-cov-2 Spike protein

| | | |
|---|---|---|
| SARS-CoV-2 Spike (Val16-Lys1211)(Arg102Ile, Phe157Leu, Val367Phe, Glu484Lys, Gln613His, Pro681Arg)(Arg682Ser, Arg685Ser, Lys986Pro, Val987Pro) Accession # YP_009724390.1 | GCN4-IZ | 6-His tag |

N-terminus C-terminus

| | |
|---|---|
| **N-terminal Sequence Analysis** | Val16 |
| **Predicted Molecular Mass** | 138 kDa |

## SPECIFICATIONS

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|---|---|
| **SDS-PAGE** | 140-166 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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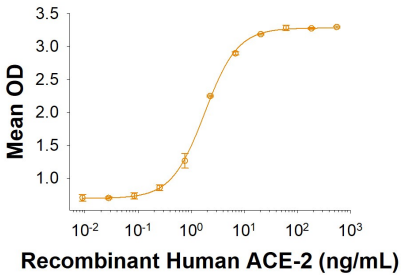
|---|---|
| **Reconstitution** | Reconstitute at 500 µg/mL in PBS. |
| **Shipping** | The product is shipped at ambient temperature. Upon receipt, store it immediately at the temperature recommended below. |
| **Stability & Storage** | **Use a manual defrost freezer and avoid repeated freeze-thaw cycles.**<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. |

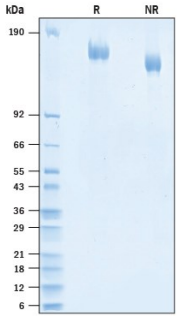
## DATA

**Binding Activity**




**Recombinant SARS-CoV-2 A.23.1 Spike (GCN4-IZ) His-tag Protein Binding Activity.** Recombinant SARS-CoV-2 A.23.1 Spike (GCN4-IZ) His-tag (Catalog # 10860-CV) binds Recombinant Human ACE-2 His-tag (Catalog # 933-ZN) in a functional ELISA.

**SDS-PAGE**




**Recombinant SARS-CoV-2 A.23.1 Spike (GCN4-IZ) His-tag Protein SDS-PAGE.** 2 µg/lane of Recombinant SARS-CoV-2 A.23.1 Spike (GNC4-IZ) His-tag Protein (Catalog # 10860-CV) was resolved with SDS-PAGE under reducing (R) and non-reducing (NR) conditions and visualized by Coomassie® Blue staining, showing bands at 140-166 kDa.



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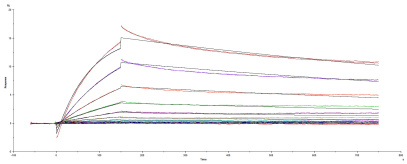
**Surface Plasmon Resonance (SPR)**



**Binding of ACE-2 to SARS-CoV-2 Spike protein mutant A.23.1 variant with E484K by surface plasmon resonance (SPR).** Recombinant SARS-CoV-2 A.23.1 variant with E484K Spike protein His-tag (Catalog #10860-CV) was immobilized on a Biacore Sensor Chip CM5, and binding to recombinant human ACE-2 (Catalog # 933-ZN) was measured at a concentration range between 0.046 nM and 47.2 nM. The double-referenced sensorgram was fit to a 1:1 binding model to determine the binding kinetics and affinity, with an affinity constant of KD=2.29 nM. (Biacore T200).

## 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 (ACE-2), 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 S protein of SARS-CoV-2 shares 75% and 29% amino acid sequence identity with S protein of SARS-CoV-1 and MERS, respectively. A SARS-CoV-2 variant (A.23.1) carrying the amino acid substitution F157L, V367F, E484K, Q613H and P681R in the spike protein region was identified as a prevalent strain in Uganda and is now spread to 26 counties (8). Whether these mutations in spike protein would cause more severe symptom or decrease the efficacy of vaccine-induced immunity is still under investigation.

**References:**

1. Wu, F. *et al.* (2020) Nature **579**:265.
2. Tortorici, M.A. and D. Veesler (2019) Adv. Virus Res. **105**:93.
3. Bosch, B.J. *et al.* (2003). J. Virol. **77**:8801.
4. Belouzard, S. *et al.* (2009) Proc. Natl. Acad. Sci. **106**:5871.
5. Millet, J.K. and G.R. Whittaker (2015) Virus Res. **202**:120.
6. Li, W. *et al.* (2003) Nature **426**:450.
7. Wong, S.K. *et al.* (2004) J. Biol. Chem. **279**:3197.
8. Bugembe, D.L. *et al.* (2021) medRxiv. DOI: 10.1101/2021.02.08.21251393.



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