



[Go to Product page](#)

Datasheet for ABIN6952670

## SARS-CoV-2 Spike Protein (Trimer) (rho-1D4 tag)

### 5 Images

#### Overview

|                               |  |
|-------------------------------|--|
| Quantity:                     | 100 µg   |
| Target:                       | SARS-CoV-2 Spike   |
| Protein Characteristics:      | Trimer   |
| Origin:                       | SARS Coronavirus-2 (SARS-CoV-2)                                      |
| Source:                       | HEK-293 Cells  |
| Protein Type:                 | Recombinant  |
| Purification tag / Conjugate: | This SARS-CoV-2 Spike protein is labelled with rho-1D4 tag.          |
| Application:                  | ELISA, SDS-PAGE (SDS), Western Blotting (WB), Crystallization (Crys) |

#### Product Details

|                  |  |
|------------------|--|
| Purpose:         | Trimeric, full length Cov-2 spike protein for assay development ("Antibody tests")   |
| Specificity:     | <ul style="list-style-type: none"> <li>• single span transmembrane membrane protein (aa 1-1273)</li> <li>• Furin cleavage site "RRAR" mutated to "GSAS"</li> <li>• trimerization (3 x 142 kDa) shown on native PAGE</li> <li>• expressed in Expi293™ cells</li> <li>• C-terminal Rho1D4 tag for affinity purification</li> <li>• &gt;Solubilization and stabilization in LMNG detergent</li> <li>• 2-step purification via Rho1D4 tag and size exclusion chromatography in LMNG detergent</li> </ul> |
| Characteristics: | <ul style="list-style-type: none"> <li>• Made in Germany - from design to production - by highly experienced protein experts.</li> <li>• Full length SARS Cov-2 spike protein expressed in Expi293™ cells to assure native state glycosylation.</li> <li>• Purification by a multi-step, protein-specific protocol to ensure crystallization grade.</li> <li>• State-of-the-art algorithm used for plasmid design (Gene synthesis).</li> </ul>   |

## Product Details

---

The concentration of our recombinant proteins is measured using the absorbance at 280nm. The protein's absorbance will be measured in several dilutions and is measured against its specific reference buffer.

The concentration of the protein is calculated using its specific absorption coefficient. We use the Expasy's protparam tool to determine the absorption coefficient of each protein.

|                  |   |
|------------------|---|
| Purification:    | <p>The protein is purified from the cleared cell lysate using Rho1D4 capture materials. Eluate fractions are analyzed by SDS-PAGE.</p> <p>Protein containing fractions are subjected to a second purification step through size exclusion chromatography. Eluate fractions are analyzed by SDS-PAGE and Western blot.</p> |
| Purity:          | >95 % as determined by SDS PAGE, Size Exclusion Chromatography and Western Blot.  |
| Endotoxin Level: | Protein is endotoxin-free.  |

## Target Details

---

|                   |  |
|-------------------|--|
| Target:           | SARS-CoV-2 Spike   |
| Abstract:         | <a href="#">SARS-CoV-2 Spike Products</a>  |
| Target Type:      | Viral Protein  |
| Background:       | <p>The spike glycoprotein exists as a homotrimeric fusion protein. Each of the trimers contains 66 glycosylation sites for host-derived N-linked glycans. Accordingly, expression of this primary target for SARS-CoV-2 vaccine development in an appropriate, human expression system is of utmost importance. Prior to ACE2 binding, each monomer in the prefusion complex contains an S1 ectodomain including the receptor binding domain (RBD) and an S2 endodomain harboring a transmembrane domain. In the predominant state of the trimer, one of the RBDs is in an "up" position whereas the other two are in a "down" position. Interaction of S-protein and ACE2 only takes place with the RBD in the "up" position. Receptor binding triggers a structural change that leads to separation of the S1 and S2 subunits.</p> |
| Molecular Weight: | 3 x 142 kDa  |
| Gene ID:          | 43740568   |
| UniProt:          | <a href="#">P0DTC2</a>   |

## Application Details

---

|                    |  |
|--------------------|--|
| Application Notes: | In addition to the applications listed above we expect the protein to work for functional studies as well. As the protein has not been tested for functional studies yet we cannot offer a guarantee |
|--------------------|--|

## Application Details

though.

Comment:

Further modifications:

- furin cleavage site "682-RRAR|SV-687" mutated to "682-GSAG|PP-687"

- C-terminal Rho1D4 tag fused with spacer "GSSG" to protein sequence

Size: 1286 amino acids (including Rho1D4 tag and linker)

Restrictions:

For Research Use only

## Handling

Buffer:

20 mM HEPES pH 7.5; 150 mM NaCl, 0.001 % LMNG

Handling Advice:

Avoid repeated freeze-thaw cycles.

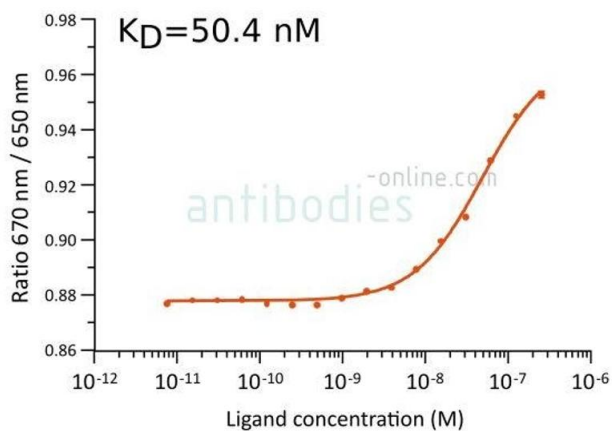
Storage:

-80 °C

Expiry Date:

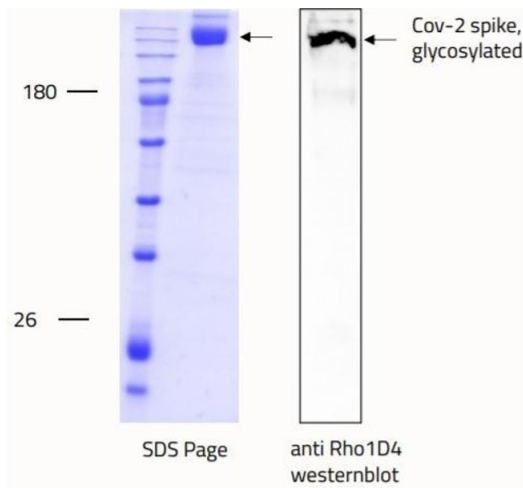
Unlimited (if stored properly)

## Images



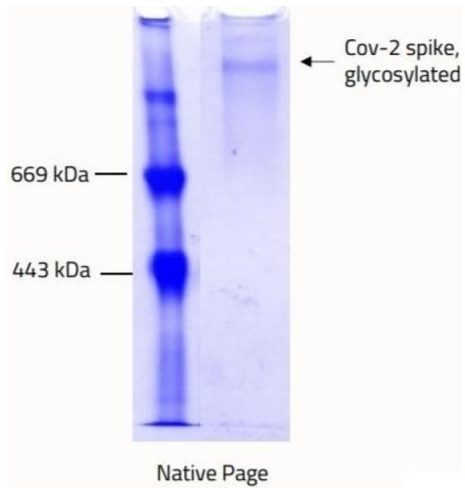
### Binding Studies

**Image 1.** Microscale thermophoresis measurement of binding of anti- SARS-CoV-2 Spike antibody AA 319-541 MM117 (ABIN7042145) to SARS-CoV-2 Spike (Trimer) protein (ABIN6952670). The determined dissociation constant  $K_D$  is indicated.



### Western Blotting

Image 2.



### Blue-native PAGE

Image 3.

Please check the [product details page](#) for more images. Overall 5 images are available for ABIN6952670.