## **PRODUCT** INFORMATION



SARS-CoV-2 Spike Glycoprotein Receptor Binding Domain L452R, T478K variant (rabbit IgG1 Fc-tagged)

Item No. 34837

### **Overview and Properties**

Synonyms:	Delta Variant, SARS-CoV-2 Spike RBD, SARS-CoV-2 Spike Receptor Binding Domain, Severe Acute Respiratory Syndrome Coronavirus 2 Spike Glycoprotein Receptor Binding Domain, Spike S1 RBD
Source:	Active recombinant C-terminal rabbit IgG1 Fc-tagged SARS-CoV-2 spike glycoprotein receptor binding domain L452R, T478K variant expressed in HEK293 cells
Amino Acids:	21-243, 319-541 of PODTC2
Uniprot No.:	PODTC2
Molecular Weight:	50.4 kDa
Storage:	-80°C (as supplied)
Stability:	≥1 year
Purity:	≥90% estimated by SDS-PAGE
Supplied in:	PBS, pH 7.4, with 5% mannitol, 5% D-(+)-trehalose, 0.01% Tween 20, and 10% glycerol
Protein	
Concentration:	<i>batch specific</i> mg/ml
<b>Bioactivity:</b>	SARS-CoV-2 Spike Glycoprotein Receptor Binding Domain L452R, T478K variant (rabbit
	IgG1 Fc-tagged) (Item No. 34837) was captured on an S series Protein G chip and tested
	for binding with gradient concentrations of ACE2 (12.5, 25, 50, 100, and 200 mM) in
	10 mM HEPES, pH 7.4, 150 mM sodium chloride, 0.05% surfactant P20 at 25°C. The
	$k_{ m D}$ value was calculated using the 1:1 (Langmuir) binding model.

Information represents the product specifications. Batch specific analytical results are provided on each certificate of analysis.

#### Images



Lane 1: MWW Markers Lane 2: SARS-CoV-2 Spike Glycoprotein Receptor Binding Domain L452R, T478K variant (4 µg) Lane 2: SARS-CoV-2 Spike Glycoprotein Receptor Binding Domain L452R, T478K variant (2 µg)

SDS-PAGE Analysis of SARS-CoV-2 Spike Glycoprotein Receptor Binding Domain L452R, T478K variant.

Representative gel image shown; actual purity may vary between each batch.



SARS-CoV-2 Spike Glycoprotein Receptor Binding Domain L452R, T478K Specifically Binds ACE2, SARS-CoV-2 Spike Glycoprotein Receptor Binding Domain L452R, T478K was captured on a Protein G Chip S series and SPF analysis was used to determine ACE2 (human, recombinant; Item No. 30587) binding affinity on a Biacore T200, using single cycle kinetics with five concentrations of ACE2.

WARNING THIS PRODUCT IS FOR RESEARCH ONLY - NOT FOR HUMAN OR VETERINARY DIAGNOSTIC OR THERAPEUTIC USE.

#### SAFFTY DATA

This material should be considered hazardous until further information becomes available. Do not ingest, inhale, get in eyes, on skin, or on clothing. Wash thoroughly after handling. Before use, the user must review the complete Safety Data Sheet, which has been sent via email to your institution.

WARRANTY AND LIMITATION OF REMEDY Buyer agrees to purchase the material subject to Cayman's Terms and Conditions. Complete Terms and Conditions including Warranty and Limitation of Liability information can be found on our website.

Copyright Cayman Chemical Company, 12/22/2021

### CAYMAN CHEMICAL

1180 EAST ELLSWORTH RD ANN ARBOR, MI 48108 · USA PHONE: [800] 364-9897 [734] 971-3335 FAX: [734] 971-3640 CUSTSERV@CAYMANCHEM.COM WWW.CAYMANCHEM.COM

# **PRODUCT** INFORMATION



#### Description

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is an enveloped positive-stranded RNA virus, a member of the *Betacoronavirus* genus, and the causative agent of COVID-19.<sup>1-5</sup> The SARS-CoV-2 spike glycoprotein, also known as the surface glycoprotein, is located on the outer envelope of the virion.<sup>3</sup> It is composed of an S1 and S2 subunit divided by a furin S-cleavage site not found in other SARS-CoVs.<sup>6,7</sup> The S1 subunit contains the receptor-binding domain (RBD), which binds to the carboxypeptidase angiotensin-converting enzyme 2 (ACE2), and the S1 and S2 subunits are cleaved by the protease TMPRSS2 to facilitate viral fusion with the host cell membrane.<sup>8-10</sup> In this way, ACE2 acts as the functional receptor for SARS-CoV-2. The SARS-CoV-2 variant of concern (VOC) B.1.617.2, also known as the delta variant, that was originally identified in India, contains the L452R and T478K substitutions.<sup>13</sup> The leucine-to-arginine substitution at position 452 (L452R) increases SARS-CoV-2 affinity for human ACE2, decreases serum neutralization and binding with monoclonal antibodies, and promotes viral infectivity and replication.<sup>11,13</sup> The threonine-to-lysine substitution at position 478 (T478K) also induces structural changes in the receptor- and antibody-binding interfaces.<sup>12</sup> Cayman's SARS-CoV-2 Spike Glycoprotein Receptor Binding Domain L452R, T478K variant (rabbit IgG1 Fc-tagged) protein can be used for ELISA and surface plasmon resonance (SPR) applications.

#### References

- 1. Lu, R., Zhao, X., Li, J., *et al.* Genomic characterisation and epidemiology of 2019 novel coronavirus: Implications for virus origins and receptor binding. *Lancet* **395(10224)**, 565-574 (2020).
- Meo, S.A., Alhowikan, A.M., Al-Khlaiwi, T., *et al.* Novel coronavirus 2019-nCoV: Prevalence, biological and clinical characteristics comparison with SARS-CoV and MERS-CoV. *Eur. Rev. Med. Pharmacol. Sci.* 24(4), 2012-2019 (2020).
- Kandeel, M., Ibrahim, A., Fayez, M., et al. From SARS and MERS CoVs to SARS-CoV-2: Moving toward more biased codon usage in viral structural and nonstructural genes. J. Med. Virol. 92(6), 660-666 (2020).
- 4. Klok, F.A., Kruip, M.J.H.A., van der Meer, N.J.M., *et al.* Incidence of thrombotic complications in critically ill ICU patients with COVID-19. *Thromb. Res.* **191**, 145-147 (2020).
- 5. Yang, F., Shi, S., Zhu, J., *et al.* Analysis of 92 deceased patients with COVID-19. J. Med. Virol. **92(11)**, 2511-2515 (2020).
- 6. Liu, Z., Xiao, X., Wei, X., *et al.* Composition and divergence of coronavirus spike proteins and host ACE2 receptors predict potential intermediate hosts of SARS-CoV-2. *J. Med. Virol.* **92(6)**, 595-601 (2020).
- 7. Walls, A.C., Park, Y.-J., Tortorici, M.A., *et al.* Structure, function, and antigenicity of the SARS-CoV-2 spike glycoprotein. *Cell* **181(2)**, 281-292 (2020).
- 8. Yan, R., Zhang, Y., Li, Y., *et al.* Structural basis for the recognition of the SARS-CoV-2 by full-length human ACE2. *Science* **267(6485)**, 1444-1448 (2020).
- 9. Hoffmann, M., Kleine-Weber, H., Schroeder, S., *et al.* SARS-CoV-2 cell entry depends on ACE2 and TMPRSS2 and is blocked by a clinically proven protease inhibitor. *Cell* **181(2)**, 271-280 (2020).
- 10. Wrapp, D., Wang, N., Corbett, K.S., *et al.* Cryo-EM structure of the 2019-nCov spike in the prefusion conformation. *Science* **367(6483)**, 1260-1263 (2020).
- 11. Motozono, C., Toyoda, M., Zahradnik, J., et al. SARS-CoV-2 spike L452R variant evades cellular immunity and increases infectivity. Cell Host Microbe 29(7), 1124-1136 (2021).
- Baral, P., Bhattarai, N., Hossen, M.L., *et al.* Mutation-induced changes in the receptor-binding interface of the SARS-CoV-2 Delta variant B.1.617.2 and implications for immune evasion. *Biochem. Biophys. Res. Commun.* 574, 14-19 (2021).
- 13. Cherian, S., Potdar, V., Jadhav, S., *et al.* SARS-CoV-2 spike mutations, L452R, T478K, E484Q and P681R, in the second wave of COVID-19 in Maharashtra, India. *Microorganisms* **9(7)**, 1542 (2021).
- 14. Boehm, E., Kronig, I., Neher, R.A., *et al.* Novel SARS-CoV-2 variants: The pandemics within the pandemic. *Clin. Microbiol. Infect.* **27(8)**, 1109-1117 (2021).

#### CAYMAN CHEMICAL

1180 EAST ELLSWORTH RD ANN ARBOR, MI 48108 · USA PHONE: [800] 364-9897 [734] 971-3335 FAX: [734] 971-3640 CUSTSERV@CAYMANCHEM.COM WWW.CAYMANCHEM.COM