


Rev03  
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**DATASHEET**

# SARS-CoV-2 Spike protein (RBD, E484K, K417N, N501Y, Avi & His Tag)-HRP

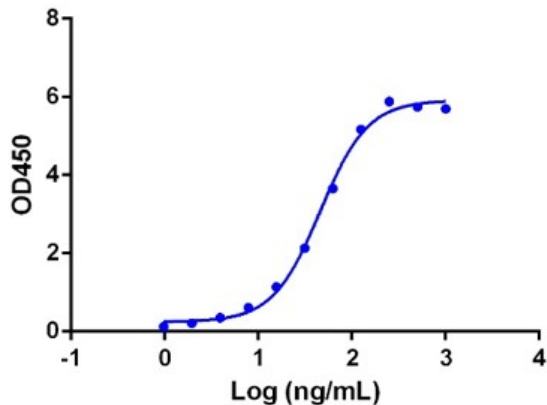
Cat. No.: Z03596

## Product Introduction

<b>Species</b>	SARS-CoV-2
<b>Protein Construction</b>	Expressed with the mutations of E484K, K417N, N501Y. 
<b>Conjugate</b>	HRP
<b>Biological Activity</b>	This protein is validated to bind with human ACE2 (Cat. No. <a href="#">Z03516</a> ) in functional ELISA assay.
<b>Expression System</b>	Human Cells
<b>Application</b>	The optimal dilution ratio should be determined by the end user for specific applications. ELISA 1:1000
<b>Formulation</b>	Supplied as a solution in PBS, pH 7.4, 0.1% ProClin 300.
<b>Storage &amp; Stability</b>	Upon receiving, this product remains stable for up to 3 months at 2-8°C. Protect from light.

## Examples

### SA RBD-HRP with ACE-2



SARS-CoV-2 Spike protein (RBD, E484K, K417N, N501Y, Avi & His tag)-HRP can bind with ACE-2 Fc Chimera, Human (Cat. No.[Z03516](#)) in a functional ELISA.

## Background

**Target Background :** SARS-CoV-2 (Severe Acute Respiratory Syndrome Coronavirus 2) also known as 2019-nCoV (2019 Novel Coronavirus) is a virus that causes illnesses ranging from the common cold to severe diseases. The spike protein mutation N501Y (UK variant) is one of six key contact residues within the receptor-binding domain (RBD) and has been identified as increasing binding affinity to human and murine ACE. Recently, more SARS-CoV-2 variants have been identified, such as the B.1.351 lineage, first identified in South Africa in December 2020, carrying amino acid mutations N501Y, K417N, and E484K in the RBD domain. The B.1.351 lineage is reported to enter cells more easily due to its enhanced affinity to ACE-2 receptor. It is also reported to reduce the efficacy of neutralizing antibody.

**Synonyms :** SARS-CoV-2 SP RBD E484K, K417N, N501Y; South Africa variant; B.1.351; Beta variant

### References :

1. [Emergence and rapid spread of a new severe acute respiratory syndrome-related coronavirus 2 \(SARS-CoV-2\) lineage with multiple spike mutations in South Africa.](#)
2. [Molecular dynamic simulation reveals E484K mutation enhances spike RBD-ACE2 affinity and the combination of E484K, K417N and N501Y mutations \(501Y.V2 variant\) induces conformational change greater than N501Y mutant alone, potentially resulting in an escape mutant.](#)
3. [SARS-CoV-2 501Y.V2 escapes neutralization by South African COVID-19 donor plasma.](#)

**For laboratory research use only. Direct human use, including taking orally and injection and clinical use are forbidden.**