Product Data Sheet

Proteins





SARS-CoV S Protein RBD (HEK293, His-Avi)

Cat. No.: HY-P78346

Synonyms: S protein RBD; S glycoprotein RBD; Spike protein RBD

Species: HEK293 Source:

Accession: P59594 (R306-F527)

Gene ID: 1489668 **Molecular Weight:** 36-46 kDa

PROPERTIES

Biological Activity	Immobilized SARS Spike RBD, His Tag at $2\mu g/ml$ ($100\mu l/well$) on the plate. Dose response curve for Human ACE2, hFc Tag with the EC $_{50}$ of $39.0 ng/ml$ determined by ELISA.
Appearance	Lyophilized powder.
Formulation	Lyophilized from a 0.22 μm filtered solution of PBS, pH 7.4. Normally 5% trehalose is added as protectant before lyophilization.
Endotoxin Level	<1 EU/μg, determined by LAL method.
Reconsititution	It is not recommended to reconstitute to a concentration less than 100 $\mu g/mL$ in ddH $_2$ O.
Storage & Stability	Stored at -20°C for 2 years. After reconstitution, it is stable at 4°C for 1 week or -20°C for longer (with carrier protein). It is recommended to freeze aliquots at -20°C or -80°C for extended storage.

Room temperature in continental US; may vary elsewhere.

DESCRIPTION

Background

Shipping

The SARS-CoV S protein is implicated in down-regulating host tetherin (BST2) through lysosomal degradation, thus counteracting its antiviral activity. In the context of infection, the S protein attaches the virion to the cell membrane by interacting with host receptors, initiating the viral entry process. The binding to human ACE2 and CLEC4M/DC-SIGNR receptors, coupled with the subsequent internalization of the virus into the endosomes of the host cell, induces conformational changes in the S glycoprotein. Additionally, proteolysis by cathepsin CTSL may unmask the fusion peptide of S2, activating membrane fusion within endosomes. These orchestrated events underscore the pivotal role of the SARS-CoV S protein in mediating viral entry and evading host antiviral defenses, shedding light on its significance in the pathogenesis of SARS-CoV infections. Further exploration is crucial to unveil the intricate molecular mechanisms underlying these processes and to identify potential targets for therapeutic interventions.

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