

Spike Glycoprotein Receptor Binding Domain (RBD) from SARS-Related Coronavirus 2, V367F Variant with C-Terminal Avi and Histidine Tags, Recombinant from HEK293 Cells

Catalog No. NR-55342

BPS Bioscience Catalog No. 100770

For research use only. Not for use in humans.

Contributor and Manufacturer:

BPS Bioscience, San Diego, California, USA

Product Description:

A recombinant form of the spike glycoprotein receptor binding domain (RBD) from severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2), V367F variant was produced by transient transfection in human embryonic kidney HEK293 cells, purified by affinity chromatography and biotinylated.¹ NR-55342 lacks the signal sequence, contains 223 residues of the SARS-CoV-2 spike glycoprotein RBD (amino acid residues R319 to F541) and features a C-terminal AviTag™ BirA biotinylation acceptor sequence fused to a hexa-histidine tag. NR-55342 is a variant of SARS-CoV-2 which contains the V367F mutation in the S glycoprotein RBD as compared to the SARS-CoV-2 reference sequence (GenPept: [QHD43416](#)).^{1,2} The predicted protein sequence is shown in Figure 1.¹ NR-55342 has a theoretical molecular weight of 28,000 daltons. The crystal structure for the wild-type S glycoprotein from SARS-CoV-2 has been solved at 2.8 Å resolution (PDB: [6VXX](#)).³

The S glycoprotein mediates viral binding to the host angiotensin converting enzyme 2 (ACE2). This protein forms a trimer, and when bound to a host receptor allows fusion of the viral and cellular membranes.⁴ SARS-CoV-2 variants with the S glycoprotein V367F mutation were found frequently during the early transmission phase and show increased binding affinity to ACE2 compared to wild-type.⁵

Material Provided:

Each vial contains approximately 50 µg of purified recombinant protein in 8 mM phosphate pH 7.4, 110 mM NaCl, 2.2 mM KCl and 20% glycerol. The concentration and volume are shown on the Certificate of Analysis.

Packaging/Storage:

NR-55342 was packaged aseptically in cryovials. The product is provided on dry ice and should be stored at -80°C immediately upon arrival. Storage at warmer temperatures is not recommended due to a low bioburden. Freeze-thaw cycles should be avoided.

Citation:

Acknowledgment for publications should read "The following reagent was obtained through BEI Resources, NIAID, NIH: Spike Glycoprotein Receptor Binding Domain (RBD) from

SARS-Related Coronavirus 2, V367F Variant with C-Terminal Avi and Histidine Tags, Recombinant from HEK293 Cells, NR-55342."

Biosafety Level: 1

Appropriate safety procedures should always be used with this material. Laboratory safety is discussed in the following publication: U.S. Department of Health and Human Services, Public Health Service, Centers for Disease Control and Prevention, and National Institutes of Health. Biosafety in Microbiological and Biomedical Laboratories. 6th ed. Washington, DC: U.S. Government Printing Office, 2020; see www.cdc.gov/biosafety/publications/bmbl5/index.htm.

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References:

1. Zhu, H., Personal Communication.
2. Wu, F., et al. "A New Coronavirus Associated with Human Respiratory Disease in China." Nature 579 (2020): 265-269. PubMed: 32015508.
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BEI Resources

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4. Hulswit, R. J. G., C. A. M. de Haan and B. -J. Bosch. "Coronavirus Spike Protein and Tropism Changes." Adv. Virus Res. 96 (2016): 29-57. PubMed: 27712627.
5. Ou, J., et al. "V367F Mutation in SARS-CoV-2 Spike RBD Emerging During the Early Transmission Phase Enhances Viral Infectivity Through Increased Human ACE2 Receptor Binding Affinity." J. Virol. (2021): *in press*. PubMed: 34105996.
6. Xiao, X. and D. S. Dimitrov. "The SARS-CoV S Glycoprotein." Cell. Mol. Life Sci. 61 (2004): 2428-2430. PubMed: 15526150.
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Figure 1: Predicted Protein Sequence

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1  RVQPTESIVR FPNITNLCPE GEVFNATRFA SVYAWNKRRI SNCVADYSFL
51  YNSASFSTFK CYGVSP TKLN  DLCFTNVYAD SFVIRGDEV R  QIAPGQTGKI
101 ADYNYKLPDD FTGCVIAWNS NNLD SKVGGN  YNYLYRLFRK SNLKPFERDI
151 STEIYQAGST PCNGVEGFNC YFPLQSYGFQ PTNGVGYQPY R VVVLSFELL
201 HAPATVCGPK KSTNLVKNC  VNFEFGGLN  DIFEAQKIEW HEHHHHHHH

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RBD – Residues 1 to 223 (represents amino acid residues 319 to 541)

V367F mutation – **Residue 49**

AviTag™ and hexa-histidine tag – Residues 228 to 248