

Spike Glycoprotein N-Terminal Domain (NTD) from SARS-Related Coronavirus 2, N234Q Variant with C-Terminal Histidine Tag, Recombinant from HEK293 Cells

Catalog No. NR-55406

ACROBiosystems Catalog No. S1D-C52H7

For research use only. Not for use in humans.

Contributor and Manufacturer:

ACROBiosystems, Newark, Delaware, USA

Product Description:

A recombinant form of the spike (S) glycoprotein N-terminal domain (NTD) from severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2), N234Q variant was produced by transient transfection in human embryonic kidney HEK293 cells and purified by affinity chromatography.¹ NR-55406 lacks the signal sequence, contains 291 residues of the SARS-CoV-2 S glycoprotein (amino acid residues S13 to L303) and features a C-terminal poly-histidine tag. NR-55406 is a variant of SARS-CoV-2 which contains the N234Q mutation in the S glycoprotein as compared to the SARS-CoV-2 reference sequence (GenPept: [QHD43416](#)).^{1,2} The predicted protein sequence is shown in Figure 1.¹ NR-55406 has a theoretical molecular weight of 34,911 daltons. Representative SDS-PAGE results are shown in Figure 2.¹

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.³ The N234Q mutation has been shown to have decreased sensitivity to some neutralizing monoclonal antibodies.⁴

Material Provided:

Each vial contains approximately 100 µg of purified recombinant protein lyophilized in a sterile phosphate-buffered saline, pH 7.4 and 10% trehalose.

Packaging/Storage:

NR-55406 was packaged aseptically in glass vials. The product is provided lyophilized and should be placed in a closed, dry environment with desiccants and stored at -20°C or colder immediately upon arrival. A frost-free freezer should be avoided, since changes in moisture and temperature may affect protein stability.

Functional Activity:

The biological activity of NR-55406 was measured by its binding ability in a functional ELISA (Figure 3), in which immobilized NR-55406 at 1 µg/mL (100 µL/well) can bind to Anti-SARS-CoV-2 Spike NTD Antibody, Chimeric mAb (ACROBiosystems Cat. No. SPD-M121); the linear range is 0.2 to 6 ng/mL.¹

Reconstitution:

NR-55406 should be reconstituted with 167 µL sterile deionized water to a stock solution of 600 µg/mL. Add sterile deionized water at room temperature with occasional gentle mixing. To avoid surface adsorption loss and inactivation, the reconstituted protein must NOT be aliquoted to less than 10 µg per vial. Carrier protein [e.g. 0.1% (w/v) bovine serum albumin] must be included in the reconstitution buffer if the final protein concentration is lower than recommended or NR-55406 is aliquoted to less than 10 µg per vial. Note: Avoid vigorous shaking or vortexing.

Storage of Reconstituted Protein:

Reconstituted NR-55406 should be stored at -70°C or colder immediately and used within 3 months. Avoid repeated freeze-thaw cycles.

Citation:

Acknowledgment for publications should read “The following reagent was obtained through BEI Resources, NIAID, NIH: Spike Glycoprotein N-Terminal Domain (NTD) from SARS-Related Coronavirus 2, N234Q Variant with C-Terminal Histidine Tag, Recombinant from HEK293 Cells, NR-55406.”

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.

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References:

1. Chen, J., Personal Communication.
2. Wu, F., et al. "A New Coronavirus Associated with Human Respiratory Disease in China." *Nature* 579 (2020): 265-269. PubMed: 32015508.
3. 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.
4. Li, Q; et al. The Impact of Mutations in SARS-CoV-2 Spike on Viral Infectivity and Antigenicity. *Cell.* 182 (2020):1284-1294. PubMed: 32730807.

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Figure 1: Predicted Protein Sequence

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1   SQCVNLTTRT QLPPAYTNSF TRGVYYPDKV FRSSVLHSTQ DLFLPFFSNV
51  TWFHAIHVSG TNGTKRFDNP VLPFNDGVYF ASTEKSNIIR GWIFGTTLDS
101 KTQSL LIVNN ATNVVIK VCE FQFCNDPFLG VYYHKNNKSW MESEFRVYSS
151 ANNCTFEYVS QPFLMDLEGK QGNFKNLREF VFKNIDGYFK IYSKHTPINL
201 VRDLPQGFSA LEPLVDLPIG IQITRFQTL ALHRSYLTPG DSSSGWTAGA
251 AAYYVGYLQP RTFLLKYNEN GTITDAVDCA LDPLSETKCT LGGGSGGGSH
301 HHHHHHHHHH
    
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S protein – **Residues 1 to 291** [represents amino acid residues 13 to 303 of the native protein (GenPept: [QHD43416](#))]
 N234Q mutation – **Residue 222**
 Linker – Residues 292 to 299
 Poly-histidine tag – **Residues 300 to 309**

Figure 2: Representative SDS-PAGE

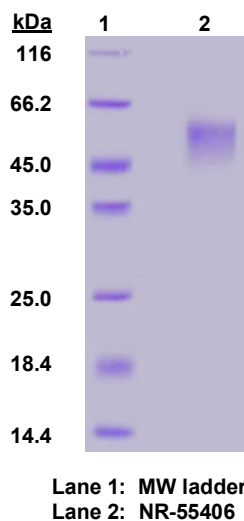


Figure 3: Representative ELISA

