

# Product Information Sheet for NR-55711

## Spike Glycoprotein (Stabilized) from SARS-Related Coronavirus 2, AY.2 Lineage (Delta Variant) with C-Terminal Histidine and Avi Tags, Recombinant from HEK293 Cells

### Catalog No. NR-55711

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**For research use only. Not for use in humans.**

#### Contributor:

BEI Resources

#### Manufacturer:

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#### Product Description:

A recombinant form of the spike (S) glycoprotein from severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2), AY.2 Lineage (Delta Variant) was produced in human embryonic kidney HEK293 cells and purified by immobilized metal affinity chromatography.<sup>1,2,3,4</sup> NR-55711 lacks the signal sequence and contains 1194 residues (ectodomain) of the SARS-CoV-2 S glycoprotein; the recombinant protein was stabilized by substitution at the furin S1/S2 cleavage site (RRAR→GSAS; residues 682 to 685) and KV→PP mutations (residues 986 and 987; wild type numbering), and includes a T4 foldon trimerization domain, HRV3C protease cleavage site and C-terminal octa-histidine tag fused to an AviTag™ BirA biotinylation acceptor sequence.<sup>1,2,3</sup> NR-55711 includes T19R, V70F, G142D, E156G, delF157-R158, A222V, K417N, L452R, T478K, D614G, P681R and D950N mutations in the S glycoprotein as compared to the SARS-CoV-2 reference sequence (GenPept: [QHD43416](#)).<sup>1,5,6</sup> The predicted protein sequence is shown in Figure 1.<sup>1</sup> NR-55711 has a theoretical molecular weight of 139,600 daltons. The crystal structure for trimeric S glycoprotein from SARS-CoV-2 has been solved at 3.46 Å resolution (PDB: [6VSB](#)).<sup>2</sup>

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.<sup>7</sup> AY.2 is one of several lineages and sublineages designated Delta by the World Health Organization (WHO) and was first identified in India.<sup>8</sup> This lineage contains multiple mutations in the N-terminal domain (NTD) and the receptor-binding domain (RBD), such as L452R which has already been identified in other variants.<sup>8,9</sup> The L452R mutation has been shown to decrease sensitivity to neutralizing antibodies, increase viral infectivity and enhance viral replication capacity.<sup>9,10,11</sup>

#### Material Provided:

Each vial contains approximately 100 microliters of NR-55711 in 10 mM HEPES, pH 7, 150 mM NaCl and 2 mM

ethylenediamine-tetraacetic acid (EDTA). The concentration, expressed as milligrams per milliliter, is shown on the Certificate of Analysis.

#### Packaging/Storage:

NR-55711 was packaged aseptically in cryovials. The product is provided on dry ice and should be stored at -20°C or colder 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 (Stabilized) from SARS-Related Coronavirus 2, AY.2 Lineage (Delta Variant) with C-Terminal Histidine and Avi Tags, Recombinant from HEK293 Cells, NR-55711."

#### 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](http://www.cdc.gov/biosafety/publications/bmbl5/index.htm).

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#### References:

1. Sather, D. N., Personal Communication.
2. Wrapp, D., et al. "Cryo-EM Structure of the 2019-nCoV Spike in the Prefusion Conformation." Science 367 (2020): 1260-1263. PubMed: 32075877.
3. Walls, A. C., et al. "Structure, Function, and Antigenicity of the SARS-CoV-2 Spike Glycoprotein." Cell 181 (2020): 281-292. PubMed: 32155444.
4. Rambaut, A., et al. "A Dynamic Nomenclature Proposal for SARS-CoV-2 Lineages to Assist Genomic Epidemiology." Nat. Microbiol. 5 (2020): 1403-1407. PubMed: 32669681.
5. Wu, F., et al. "A New Coronavirus Associated with Human Respiratory Disease in China." Nature 579 (2020): 265-269. PubMed: 32015508.
6. West, A. P., Jr., et al. "Detection and Characterization of the SARS-CoV-2 Lineage B.1.526 in New York." bioRxiv (2021). doi: 10.1101/2021.02.14.431043. PubMed: 33907745.
7. 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.
8. [WHO](#)
9. Planas, D., et al. "Reduced Sensitivity of SARS-CoV-2 Variant Delta to Antibody Neutralization." Nature 596 (2021): 276-280. PubMed: 34237773.
10. Motozono, C., et al. "SARS-CoV-2 Spike L452R Variant Evades Cellular Immunity and Increases Infectivity." Cell Host Microbe 29 (2021): 1124-1136.e11. PubMed: 34171266.
11. Li, Q., et al. "The Impact of Mutations in SARS-CoV-2 Spike on Viral Infectivity and Antigenicity." Cell 182 (2020): 1284-1294.e9. PubMed: 32730807.

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Figure 1: Predicted Protein Sequence

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1  SQCVNLRTRT QLPPAYTNSF TRGVYYPDKV FRSSVLHSTQ DLFLPFFSNV
51  TWFHAIHFSG TNGTKRFDNP VLPFNDGVYF ASTEKSNIIR GWIFGTTLDS
101 KTQSILLIVNN ATNVVIKVCE FQFCNDPFLD VYYHKNNKSW MESGVYSSAN
151 NCTFEYVSQP FLMDLEGKQG NFKNLREFVF KNIDGYFKIY SKHTPINLVR
201 DLPQGFSVLE PLVDLPIGIN ITRFQTLLAL HRSYLTPGDS SSGWTAGAAA
251 YYVGYLQPRT FLLKYNENGIT ITDAVDCALD PLSETKCTLK SFTVEKGIYQ
301 TSNFRVQPTE SIVRFPNITN LCPCFGEVFNA TRFASVYAWN RKRISNCVAD
351 YSVLYNSASF STFCKYGVSP TKLNDLCFTN VYADSFVIRG DEVRQIAPGQ
401 TGNIAADYNK LPDDFTGCVI AWNSNNLDSK VGGNYNYR YR LFRKSNLKP
451 ERDISTEIIYQ AGSKPCNGVE GFNCYFPLQS YGFQPTNGVG YQPYRVVLS
501 FELLHAPATV CGPKKSTNLV KNKCVNFNFN GLTGTGVLTE SNKKFLPFQ
551 FGRDIADTTD AVRDPQTLEI LDITPCSFGG VSVITPGTNT SNQVAVLYQ
601 VNCTEVPVAI HADQLTPTWR VYSTGSNVFQ TRAGCLIGAE HVNNSYEC
651 PIGAGICASY QTQTSNRGSA SSVASQSIIA YTMSLGAENS VAYSNN
701 PTNFTISVTT EILPVSMTKT SVDCTMYICG DSTECSNLLL QYGSFCTQ
751 RALTGIAVEQ DKNTQEVFAQ VKQIYKTPPI KDFGGFNFSQ ILPDPSKPSK
801 RSFIEDLLFN KVTIADAGFI KQYGDCLGDI AARDLICAQK FNGTLVLP
851 LTDEMIAQYT SALLAGTITS GWTFGAGAAL QIPFAMQMAY RFNGIGVTQ
901 VLYENQKLI A NQFNSAIGKI QDSLSTASA LGKLQNVVNQ NAQALNTLVK
951 QLSSNFGAIS SVLNDILSRL DPPEAEVQID RLITGRLQSL QTYVTQQLIR
1001 AAEIRASANL AATKMSECVL GQSKRVDFCG KGYHLMSFPQ SAPHGVVFLH
1051 VTYVPAQEK FTTAPAICHG GKAHFPREGV FVSNGTHWV TQRNFYEPQI
1101 ITTDNTFVSG NCDVVIGIVN NTVYDPLQPE LDSFKEELDK YFKNHTSPDV
1151 DLGDISGINA SVVNIQKEID RLNEVAKNLN ESLIDLQELG KYEQGSGYIP
1201 EAPRDGQAYV RKDGEWVLLS TFLGRSLEVL FQGP GS HHHH HHHHGLNDIF
1251 EAQKIEWHE

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Spike ectodomain – **Residues 1 to 194** (represents WT amino acid residues 13 to 1208)

RRAR to GSAS substitution of S1/S2 cleavage site – Residues 668 to 671

KV to PP stabilizing mutations – Residues 972 and 973

T19R, V70F, G142D, E156G, A222V, K417N, L452R, T478K, D614G, P681R and D950N mutations –

**Residues 7, 58, 130, 144, 208, 403, 438, 464, 600, 667 and 936**

T4 foldon trimerization domain – Residues 1197 to 1223

HRV3C protease cleavage site – Residues 1227 to 1234

Octa-histidine tag and AviTag™ – **Residues 1237 to 1259**