

**Spike Glycoprotein (Stabilized) from SARS-Related Coronavirus 2, D614G Variant with C-Terminal Histidine Tag, Recombinant from HEK293 Cells**

**Catalog No. NR-55343**  
**BPS Bioscience Catalog No. 100810**

**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 (S) glycoprotein from severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2), D614G variant was produced in human embryonic kidney HEK293 cells and purified by affinity chromatography.<sup>1</sup> NR-55343 lacks the signal sequence (residues 1 to 15) and contains 1195 residues (ectodomain; S1 + S2) of the SARS-CoV-2 S glycoprotein; the recombinant protein was modified to remove the polybasic S1/S2 cleavage site (RRAR to A; residues 682 to 685), stabilized with a pair of mutations (K986P and V987P, wild type numbering) and includes a thrombin cleavage site, T4 foldon trimerization domain and C-terminal hexa-histidine tag.<sup>1</sup> NR-55343 is a variant of SARS-CoV-2 which contains the D614G mutation in the S glycoprotein as compared to the SARS-CoV-2 reference sequence (GenPept: [QHD43416](#)).<sup>1,2,3</sup> The predicted protein sequence is shown in Figure 1.<sup>1</sup> NR-55343 has a theoretical molecular weight of 137,000 daltons. The crystal structure for trimeric S glycoprotein from the SARS-CoV-2 D614G variant has been solved at 3.46 Å resolution (PDB: [6XS6](#)).<sup>3</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>4</sup> The D614G mutation is common to the current variants of interest and concern identified by the Centers for Disease Control and Prevention (CDC). This mutation was one of the first documented in the USA in the initial stages of the pandemic after having initially circulated in Europe.<sup>5</sup> Some evidence suggests that variants with the D614G mutation are more infectious than wild-type.<sup>6</sup>

**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-55343 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 (Stabilized) from SARS-Related Coronavirus 2, D614G Variant with C-Terminal Histidine Tag, Recombinant from HEK293 Cells, NR-55343.”

**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. 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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Figure 1: Predicted Protein Sequence

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1  VNLTRTQLP  PAYTNSFTRG  VYYPDKVFRS  SVLHSTQDLF  LPFFSNVTWF
51  HAIHVSGTNG  TKRFDNPVLP  FNDGVYFAST  EKSNIIRGWI  FGTTLDSTKQ
101  SLLIVNNATN  VVIKVFCEQF  CNDPFLGVYY  HKNNKSWMES  EFRVYSSANN
151  CTFEYVSQPF  LMDLEGKQGN  FKNLREFVFK  NIDGYFKIYS  KHTPINLVRD
201  LPQGFSALEP  LVDLPIGINI  TRFQTLLALH  RSYLTPGDSS  SGWTAGAAAY
251  YVGYLQPRTF  LLKYNENGTI  TDAVDCALDP  LSETKCTLKS  FTVEKGIYQT
301  SNFRVQPTES  IVRFPNITNL  CPFGEVFNAT  RFASVYAWNR  KRISNCVADY
351  SVLYNSASFS  TFKCYGVSPT  KLNDLCFTNV  YADSFVIRGD  EVRQIAPGQT
401  GKIADYNYKL  PDDFTGCVIA  WNSNNLDSKV  GGNYNLYRL  FRKSNLKPFE
451  RDISTEIQYA  GSTPCNGVEG  FNCYFPLQSY  GFQPTNGVGY  QPYRVVLSF
501  ELLHAPATVC  GPKKSTNLVK  NKCWNFNENG  LTGTGVLTES  NKKFLPFQQF
551  GRDIADTTDA  VRDPQLEIL  DITPCSFQGV  SVITPGTNTS  NOVAVLYQGV
601  NCTEVPVAIH  ADQLTPTWRV  YSTGSNVFQT  RAGCLIGAEH  VNNSYECDIP
651  IGAGICASYQ  TQTNPASVA  SQSIIAYTMS  LGAENSVAYS  NNSIAIPTNF
701  TISVTTEILP  VSMTKTSVDC  TMYICGDSTE  CSNLLLQYGS  FCTQLNRALT
751  GIAVEQDKNT  QEVFAQVKQI  YKTPPIKDFG  GFNFSQILPD  PSKPSKRSFI
801  EDLLENKVTL  ADAGFIKQYG  DCLGDIAARD  LICAQKFNGL  TVLPLLLTDE
851  MIAQYTSALL  AGTITSGWTF  GAGAALQIPF  AMQMAYRFNG  IGVTONVLYE
901  NQKLIANQFN  SAIGKIQDSL  SSTASALGKL  QDVVNQNAQA  LNTLVKQLSS
951  NFGAISSVLN  DILSRLDPPE  AEVQIDRLIT  GRLQSLQTYV  TQQLIRAAEI
1001  RASANLAATK  MSECVLGQSK  RVDFCGKGYH  LMSFPQSAPH  GVVFLHVTVV
1051  PAQEKNF'TTA  PAICHGKAH  FPREGVFVSN  GTHWFVTQRN  FYEQIITTD
1101  NTFVSGNCDV  VIGIVNNTVY  DPLQPELDSF  KEELDKYFKN  HTSPDVDLGD
1151  ISGINASVVN  IQKEIDRLNE  VAKNLNESLI  DLQELGKYEQ  YIKWPLVPRG
1201  SGYIPEAPRD  GOAYVRKDGE  WVLLSTFLGG  GHHHHHH
  
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Spike ectodomain – **Residues 1 to 1195** (represents WT amino acid residues 16 to 1213)

RRAR to A substitution of S1/S2 cleavage site – **Residue 667**

KV to PP stabilizing mutations – **Residues 968 and 969**

D614G mutation – **Residue 598**

Thrombin cleavage site – **Residues 1196 to 1201**

T4 foldon trimerization domain – **Residues 1202 to 1228**

Hexa-histidine tag – **Residues 1232 to 1237**