

**Spike Glycoprotein (Stabilized) from SARS-Related Coronavirus 2, Wuhan-Hu-1 with C-Terminal Histidine and Avi Tags, Recombinant from HEK293F Cells**

**Catalog No. NR-53524**

This reagent is the tangible property of the U.S. Government.

**For research use only. Not for human use.**

**Contributor and 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), Wuhan-Hu-1 (GenPept: [QJE37812](#)) was produced in human embryonic kidney HEK293F cells and purified by immobilized metal affinity and size exclusion chromatography.<sup>1,2,3</sup> NR-53524 lacks the signal sequence and contains 1194 residues (ectodomain) of the SARS-CoV-2 spike 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 (GenPept: [YP\\_009724390](#))] and includes a thrombin cleavage site, T4 foldon trimerization domain and C-terminal hexa-histidine tag fused to an AviTag™ BirA biotinylation acceptor sequence.<sup>1,2,3</sup> The predicted protein sequence is shown in Figure 1.<sup>1</sup> NR-53524 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>4</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. The S protein is a target for neutralizing antibodies.<sup>5</sup>

**Material Provided:**

Each vial contains approximately 50 µL of NR-53524 in phosphate buffered saline (PBS). The concentration, expressed as mg per mL, is shown on the Certificate of Analysis.

**Packaging/Storage:**

NR-53524 was packaged aseptically in cryovials. The product is provided on dry ice and should be stored at -20°C or colder immediately upon arrival. 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, Wuhan-Hu-1 with C-Terminal Histidine and Avi Tags, Recombinant from HEK293F Cells, NR-53524.”

**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. 5th ed. Washington, DC: U.S. Government Printing Office, 2009; see [www.cdc.gov/biosafety/publications/bmbl5/index.htm](http://www.cdc.gov/biosafety/publications/bmbl5/index.htm).

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**References:**

1. Strong, R. K., Personal Communication.

2. Walls, A. C., et al. "Structure, Function, and Antigenicity of the SARS-CoV-2 Spike Glycoprotein." *Cell* 181 (2020): 281-292. PubMed: 32155444.
3. Wu, F., et al. "A New Coronavirus Associated with Human Respiratory Disease in China." *Nature* 579 (2020): 265-269. PubMed: 32015508.
4. Wrapp, D., et al. "Cryo-EM Structure of the 2019-nCoV Spike in the Prefusion Conformation." *Science* 367 (2020): 1260-1263. PubMed: 32075877.
5. 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.

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Figure 1 – Predicted Protein Sequence

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1  QCVNLTTRTQ LPPAYTNSFT RGVYYPDKVF RSSVLHSTQD LFLPFFSNVT
51  WFHAIHVSQT NGTKRFDNPV LPFNDGVYFA STEKSNIIRG WIFGTTLDSK
101 TQSL LIVNNA TNVVIKVECF QFCNDPFLGV YYHKNNKSWM ESEFRVYSSA
151 NNCTFEYVSQ PFLMDLEGKQ GNFKNLREFV FKNIDGYFKI YSKHTPINLV
201 RDL PQGFSAL EPLVDLPIGI NITRFQTLA LHRSYLTPGD SSSGWTAGAA
251 AYYVGYLQPR TFL LKYNENG TITDAVDCAL DPLSETKCTL KSFTVEKGIY
301 QTSNFRVQPT ESIVRFPNIT NLCPFGEVFN ATRFASVYAW NRKRISNCVA
351 DYSVLYNSAS FSTFKCYGVS PTKLNDLCFT NVYADSFVIR GDEVRQIAPG
401 QTGKIADYNY KLPDDFTGCV IAWNSNNLDS KVGGNYNLYL RLFKRKSNLKP
451 FERDISTEIIY QAGSTPCNGV EGFNCYFPLQ SYGFQPTNGV GYQPYRVVVL
501 SFELLHAPAT VCGPKKSTNL VKNKCVNFNF NGLTGTGVL T ESNKKFLPFQ
551 QFGRDIADTT DAVRDPQ TLE ILDITPCSFG GVSVITPGTN TSNQVAVLYQ
601 DVNCTEVPVA IHADQLTPTW RVYSTGSNVF QTRAGCLIGA EHVNNSEYCD
651 IPIGAGICAS YQTQTNPAS VASQSIIAYT MSLGAENVA YSNNIAIPT
701 NFTISVTTEI LPVSMTKTSV DCTMYICGDS TECSNLLLQY GSFCTQLNRA
751 LTGIAVEQDK NTQEVFAQVK QIYKTPPIKD FGGFNFSQIL PDPSKPSKRS
801 FIEDLLFNKV TLADAGFIKQ YGDCLGDIAA RDLICAQKFN GLTVLPPLLT
851 DEMIAQY TSA LLAGTITSGW TFGAGAALQI PFAMQMAYRF NGIGVTQNVL
901 YENQKLIANQ FNSAIGKIQD SLSSTASALG KLQDVVNQNA QALNTLVKQL
951 SSNFGAISSV LNDILSR LDP PEAEVQIDRL ITGRLQSLQT YVTQQLIRAA
1001 EIRASANLAA TKMSECVLQ SKRVDFCGKG YHLMSFPQSA PHGVVFLHVT
1051 YVPAQEKNFT TAPAICHGDK AHFPREGV FV SNGTHWFVTQ RNFYEPQIIT
1101 TDNTEFVSGNC DVVIGIVNNT VYDPLQPELD SFKEELDKYF KNHTSPDIDL
1151 GDISGINASV VNIQKEIDRL NEVAKNLNES LIDLQELGKY EQYIKWPSGR
1201 LVPRGSPGSG YIPEAPRDQ AYVRKDGEWV LLSTFLGHHH HHHGLNDIFE
1251 AQKIEWHE
    
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**Spike ectodomain – Residues 1 to 1197** (representing residues 14 to 1213)  
 Thrombin cleavage site – Residues 1198 to 1206  
 T4 foldon trimerization domain – Residues 1210 to 1236  
 Hexa-histidine tag and AviTag™ – Residues 1238 to 1258