Spike Glycoprotein (Stabilized) from SARS-Related Coronavirus 2, B.1.1.1 Lineage with C-Terminal Histidine and Avi Tags, Recombinant from HEK293 Cells

Catalog No. NR-55615

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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), B.1.1.1 lineage was produced in human embryonic kidney HEK293 cells and purified by immobilized metal affinity chromatography.[1,2,3,4] NR-55615 lacks the signal sequence and contains 1189 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.[1,2,3] NR-55615 includes G75V, T76I, del246-252 (RSYLTPG), D253N, L452Q, F490S, D614G and T859N mutations in the S glycoprotein as compared to the SARS-CoV-2 reference sequence (GenPept: QHD43416).[1,5] The predicted protein sequence is shown in Figure 1.[1] NR-55615 has a theoretical molecular weight of 138,900 daltons. The crystal structure for trimeric S glycoprotein from SARS-CoV-2 has been solved at 3.46 Å resolution (PDB: 6VSB).[2]

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.[6] The B.1.1.1 lineage includes the sublineage C.37, designated Lambda by the World Health Organization (WHO) and first identified in Peru.[7,8] The B.1.1.1 lineage is characterized by a novel deletion (del246-252) and mutations including L452Q and F490S in the S glycoprotein Receptor Binding Domain (RBD).[7] These deletions and mutations may contribute to increased transmissibility.[8,9,10]

Material Provided:

Each vial contains approximately 100 µL of NR-55615 in 10 mM HEPES, pH 7, 150 mM NaCl and 2 mM ethylenediamine-tetraacetic acid (EDTA). The concentration, expressed as mg per mL, is shown on the Certificate of Analysis.

Packaging/Storage:

NR-55615 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, B.1.1.1 Lineage with C-Terminal Histidine and Avi Tags, Recombinant from HEK293 Cells, NR-55615."

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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Support Provided by NIAID

Figure 1: Predicted Protein Sequence

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1    SQCVNLTTRT QLPPAYTNSF TRGVYYPDKV FRSSVLHSTQ DLFLPFFSNV
51   TWFHAIHVSG TNVIKRFDNP VLPFNDGVYF ASTEKSNIIR GWIFGTTLDS
101  KTQSLLIVNN ATNVVIKVCE FQFCNDPFLG VYYHKNNKSW MESEFRVYSS
151  ANNCTFEYVS QPFLMDLEGK QGNFKNLREF VFKNIDGYFK IYSKHTPINL
201  VRDLPQGFSA LEPLVDLPIG INITRFQTLL ALHNSSSGWT AGAAAYYVGY
251  LQPRTFLLKY NENGTITDAV DCALDPLSET KCTLKSFTVE KGIYQTSNFR
301  VQPTESIVRF PNITNLCPFG EVFNATRFAS VYAWNRKRIS NCVADYSVLY
351  NSASFSTFKC YGVSPTKLND LCFTNVYADS FVIRGDEVRQ IAPGQTGKIA
401  DYNYKLPDDF TGCVIAWNSN NLDSKVGGNY NYQYRLFRKS NLKPFERDIS
451  TEIYQAGSTP CNGVEGFNCY SPLQSYGFQP TNGVGYQPYR VVVLSFELLH
501  APATVCGPKK STNLVKNKCV NFNFNGLTGT GVLTESNKKF LPFQQFGRDI
551  ADTTDAVRDP QTLEILDITP CSFGGVSVIT PGTNTSNQVA VLYQGVNCTE
601  VPVAIHADQL TPTWRVYSTG SNVFQTRAGC LIGAEHVNNS YECDIPIGAG
651  ICASYQTQTN SPGSASSVAS QSIIAYTMSL GAENSVAYSN NSIAIPTNFT
701  ISVTTEILPV SMTKTSVDCT MYICGDSTEC SNLLLQYGSF CTQLNRALTG
751  IAVEQDKNTQ EVFAQVKQIY KTPPIKDFGG FNFSQILPDP SKPSKRSFIE
801  DLLFNKVTLA DAGFIKQYGD CLGDIAARDL ICAQKFNGLN VLPPLLTDEM
851  IAQYTSALLA GTITSGWTFG AGAALQIPFA MQMAYRFNGI GVTQNVLYEN
901  QKLIANQFNS AIGKIQDSLS STASALGKLQ DVVNQNAQAL NTLVKQLSSN
951  FGAISSVLND ILSRLDPPEA EVQIDRLITG RLQSLQTYVT QQLIRAAEIR
1001 ASANLAATKM SECVLGQSKR VDFCGKGYHL MSFPQSAPHG VVFLHVTYVP
1051 AQEKNFTTAP AICHDGKAHF PREGVFVSNG THWFVTQRNF YEPQIITTDN
1101 TFVSGNCDVV IGIVNNTVYD PLQPELDSFK EELDKYFKNH TSPDVDLGDI
1151 SGINASVVNI QKEIDRLNEV AKNLNESLID LQELGKYEQG SGYIPEAPRD
1201 GQAYVRKDGE WVLLSTFLGR SLEVLFQGPG SHHHHHHHHG LNDIFEAQKI
1251 EWHE
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Spike ectodomain – **Residues 1 to 1189** (represents WT amino acid residues 13 to 1208)
RRAR to GSAS substitution of S1/S2 cleavage site – Residues 663 to 666
KV to PP stabilizing mutations – Residues 967 and 968
G75V, T76I, D253N, L452Q, F490S, D614G and T859N mutations –
Residues 63, 64, 234, 433, 471, 595 and 840
T4 foldon trimerization domain – Residues 1192 to 1218
HRV3C protease cleavage site – Residues 1222 to 1229
Octa-histidine tag and AviTag™ – Residues 1232 to 1254

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