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

Catalog No. NR-56517

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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), BA.2 lineage (Omicron variant) was produced in human embryonic kidney HEK293 cells and purified by immobilized metal affinity and gel filtration chromatography.[1,2,3,4] NR-56517 lacks the signal sequence and contains 1193 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-56517 includes T19I, delL24-P26, A27S, G142D, V213G, G339D, S371F, S373P, S375F, T376A, D405N, R408S, K417N, N440K, S477N, T478K, E484A, Q493R, Q498R, N501Y, Y505H, D614G, H655Y, N679K, P681H, N764K, D796Y, Q954H and N969K 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-56517 has a theoretical molecular weight of 139,700 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] BA.2 is one of several lineages and sublineages designated Omicron by the World Health Organization (WHO).[7] BA.2 has been shown to be even more transmissible than BA.1. BA.1 and BA.2 diverge at spike residue 371 (L and F, respectively) and residues 142-145 in the receptor-binding domain (RBD).[8] In BA.2, deletions from amino acid positions 24-26, as well as an A27S substitution are situated in or close to a known N-terminal domain (NTD) antigenic site and are associated with resistance to neutralizing monoclonal antibodies.[8,9]

Material Provided:

Each vial contains approximately 100 microliters of NR-56517 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-56517 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, BA.2 Lineage (Omicron Variant) with C-Terminal Histidine and Avi Tags, Recombinant from HEK293 Cells, NR-56517."

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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9. McCallum, M., et al. "N-terminal Domain Antigenic Mapping Reveals a Site of Vulnerability for SARS-CoV-2." Cell 184 (2021): 2332-2347. PubMed: 33761326.

Support Provided by NIAID

Figure 1: Predicted Protein Sequence

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1    SQCVNLITRT QSYTNSFTRG VYYPDKVFRS SVLHSTQDLF LPFFSNVTWF
51   HAIHVSGTNG TKRFDNPVLP FNDGVYFAST EKSNIIRGWI FGTTLDSKTQ
101  SLLIVNNATN VVIKVCEFQF CNDPFLDVYY HKNNKSWMES EFRVYSSANN
151  CTFEYVSQPF LMDLEGKQGN FKNLREFVFK NIDGYFKIYS KHTPINLGRD
201  LPQGFSALEP LVDLPIGINI TRFQTLLALH RSYLTPGDSS SGWTAGAAAY
251  YVGYLQPRTF LLKYNENGTI TDAVDCALDP LSETKCTLKS FTVEKGIYQT
301  SNFRVQPTES IVRFPNITNL CPFDEVFNAT RFASVYAWNR KRISNCVADY
351  SVLYNFAPFF AFKCYGVSPT KLNDLCFTNV YADSFVIRGN EVSQIAPGQT
401  GNIADYNYKL PDDFTGCVIA WNSNKLDSKV GGNYNYLYRL FRKSNLKPFE
451  RDISTEIYQA GNKPCNGVAG FNCYFPLRSY GFRPTYGVGH QPYRVVVLSF
501  ELLHAPATVC GPKKSTNLVK NKCVNFNFNG LTGTGVLTES NKKFLPFQQF
551  GRDIADTTDA VRDPQTLEIL DITPCSFGGV SVITPGTNTS NQVAVLYQGV
601  NCTEVPVAIH ADQLTPTWRV YSTGSNVFQT RAGCLIGAEY VNNSYECDIP
651  IGAGICASYQ TQTKSHGSAS SVASQSIIAY TMSLGAENSV AYSNNSIAIP
701  TNFTISVTTE ILPVSMTKTS VDCTMYICGD STECSNLLLQ YGSFCTQLKR
751  ALTGIAVEQD KNTQEVFAQV KQIYKTPPIK YFGGFNFSQI LPDPSKPSKR
801  SFIEDLLFNK VTLADAGFIK QYGDCLGDIA ARDLICAQKF NGLTVLPPLL
851  TDEMIAQYTS ALLAGTITSG WTFGAGAALQ IPFAMQMAYR FNGIGVTQNV
901  LYENQKLIAN QFNSAIGKIQ DSLSSTASAL GKLQDVVNHN AQALNTLVKQ
951  LSSKFGAISS VLNDILSRLD PPEAEVQIDR LITGRLQSLQ TYVTQQLIRA
1001 AEIRASANLA ATKMSECVLG QSKRVDFCGK GYHLMSFPQS APHGVVFLHV
1051 TYVPAQEKNF TTAPAICHDG KAHFPREGVF VSNGTHWFVT QRNFYEPQII
1101 TTDNTFVSGN CDVVIGIVNN TVYDPLQPEL DSFKEELDKY FKNHTSPDVD
1151 LGDISGINAS VVNIQKEIDR LNEVAKNLNE SLIDLQELGK YEQGSGYIPE
1201 APRDGQAYVR KDGEWVLLST FLGRSLEVLF QGPGSHHHHH HHHGLNDIFE
1251 AQKIEWHE
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Spike ectodomain – **Residues 1 to 1193** (represents WT amino acid residues 13 to 1208)
RRAR to GSAS substitution of S1/S2 cleavage site – Residues 667 to 670
KV to PP stabilizing mutations – Residues 971 and 972
T19I, A27S, G142D, V213G, G339D, S371F, S373P, S375F, T376A, D405N, R408S, K417N, N440K, S477N, T478K, E484A, Q493R, Q498R, N501Y, Y505H, D614G, H655Y, N679K, P681H, N764K, D796Y, Q954H and N969K mutations – **Residues 7, 16, 127, 198, 324, 356, 358, 360-361, 390, 393, 402, 425, 462-463, 469, 478, 483, 486, 490, 599, 640, 664, 666, 749, 781, 939 and 954**
T4 foldon trimerization domain – Residues 1196 to 1222
HRV3C protease cleavage site – Residues 1226 to 1233
Octa-histidine tag and AviTag™ – Residues 1236 to 1258

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