

# Spike Glycoprotein (Stabilized) from SARS-Related Coronavirus 2, B.1.1.529 Lineage (Omicron Variant) with C-Terminal Histidine and Avi Tags, Recombinant from HEK293 Cells

## Catalog No. NR-56447

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### Contributor:

BEI Resources

### Manufacturer:

D. Noah Sather, Associate Professor, Center for Global Infectious Disease Research, Seattle Children's Research Institute, Seattle, Washington, USA

### Product Description:

A recombinant form of the spike (S) glycoprotein from severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2), B.1.1.529 lineage (Omicron variant) was produced in human embryonic kidney HEK293 cells and purified by immobilized metal affinity chromatography.<sup>1,2,3,4</sup> NR-56447 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.<sup>1,2,3</sup> NR-56447 includes A67V, delH69-V70, T95I, G142D, delV143-Y145, delN211, L212I, ins214EPE, G339D, S371L, S373P, S375F, K417N, L440K, G446S, S477N, T478K, E484A, Q493R, G496S, Q498R, N501Y, Y505H, T547K, D614G, H655Y, N679K, P681H, N764K, D796Y, N856K, Q954H, N969K and L981F mutations in the S glycoprotein as compared to the SARS-CoV-2 reference sequence (GenPept: [QHD43416](#)).<sup>1,5</sup> The predicted protein sequence is shown in Figure 1.<sup>1</sup> NR-56447 has a theoretical molecular weight of 139,900 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>6</sup> B.1.1.529 is one of several lineages and sublineages designated Omicron by the World Health Organization (WHO) and was first identified in South Africa, followed by multiple countries in November 2021.<sup>7</sup> This lineage contains multiple mutations in the receptor-binding domain (RBD) that have been identified in other variants, including K417N, N501Y and D614G.<sup>8,9,10</sup> The presence of D614G among variants has been shown to increase

transmissibility, with K417N, Q493R, N501Y and Y505H shown to be important residues mediating virus entry into host cells.<sup>9,11</sup> E484A has been shown to decrease neutralization by post-vaccination sera and some monoclonal antibody treatments.<sup>8,9,10</sup>

### Material Provided:

Each vial contains approximately 100 microliters of NR-56447 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-56447 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, B.1.1.529 Lineage (Omicron Variant) with C-Terminal Histidine and Avi Tags, Recombinant from HEK293 Cells, NR-56447."

### 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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Figure 1: Predicted Protein Sequence

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1  SQCVNLTRT QLPPAYTNSF TRGVYYPDKV FRSSVLHSTQ DLFLPFFSNV
51  TWFHVISGTN GTKRFDNPVL PFNDGVYFAS IEKSNIIRGW IFGTTLDSKT
101 QSLILVNNAT NVVIKVCSEQ FCNDPFLDHK NNKSWMESEF RVYSSANNCT
151 FEYVSQPFLL DLEGKQGNFK NLREFVFKNI DGYFKIYSKH TPIIVREPED
201 LPQGFSALEP LVDLPIGINI TRFQTLLALH RSYLTPGDSS SGWTAGAAAY
251 YVGYLQPRTF LLKYNENGTI TDAVDCALDP LSETKCTLKS FTVEKGIYQT
301 SNFRVQPTES IVREFPNITNL CPFDEVFNAT RFASVYAWNR KRISNCVADY
351 SVLYNLAPFF TFKCYGVSPK KLNDLCFTNV YADSFVIRGD EVRQIAPGQT
401 GNIADYNYKL PDDFTGCVIA WNSNKLDSKV SGNYNLYRL FRKSNLKPFE
451 RDISTEIQQA GNKPCNGVAG FNCYFPLRSY SFRPTYGVGH QPYRVVLSF
501 ELLHAPATVC GPKKSTNLVK NKCYNFNENG LKGTGVLTES NKKFLPFQQF
551 GRDIADTTDA VRDPQTLEIL DITPCSFGGV SVITPGTNTS NQVAVLYQGV
601 NCTEVPVAIH ADQLTPTWRV YSTGSNVFQT RAGCLIGAEY VNNSYECDDP
651 IGAGICASYQ TQTKSHGSAS SVASQSIIAY TMSLGAENSV AYSNNSIAIP
701 TNFTISVTTE ILPVSMTKTS VDCTMYICGD STECSNLLLQ YGSFCTQLKR
751 ALTGIAVEQD KNTQEVFAQV KQIYKTPPIK YFGGFNFSQI LPDPSKPSKR
801 SFIEDLLFNK VTLADAGFIK QYGDCLGDIA ARDLICAQKF KGLTVLPPLL
851 TDEMIAQYTS ALLAGTITSG WTFGAGAALQ IPFAMQMAYR FNGIGVTQNV
901 LYENQKLIAN QFNSAIGKIQ DSLSSTASAL GKLQDVVNHN AQALNTLVKQ
951 LSSKFGAISS VLNDIFSRLD PPEAEVQIDR LITGRLQSLQ TYVTQQLIRA
1001 AEIRASANLA ATKMSECVLG QSKRVDFCGK GYHLSMFPQS APHGCVFLHV
1051 TYVPAQEKNF TTAPAICHDG KAHFPREGVF VSNGTHWFTV QRNFYEPQII
1101 TTDNTFVSGN CDVVIGIVNN TVYDPLQPEL DSFKEELDKY FKNHTSPDVD
1151 LGDISGINAS VVNIQKEIDR LNEVAKNLNE SLIDLQELGK YEQSGGYIPE
1201 APRDGGAYVR KDGEWVLLST FLGRSLEVLV 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

A67V, T95I, G142D, L212I, ins214EPE, G339D, S371L, S373P, S375F, K417N, N440K, G446S, S477N, T478K, E484A, Q493R, G496S, Q498R, N501Y, Y505H, T547K, D614G, H655Y, N679K, P681H, N764K, D796Y, N856K, Q954H, N969K, L981F –

**Residues 55, 81, 128, 194, 197-199, 324, 356, 358, 360, 402, 425, 431,**

**462, 463, 469, 478, 481, 483, 486, 490, 532, 599, 640, 664, 666, 749, 781, 841, 939, 954, 966**

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