Spike Glycoprotein (Stabilized) from SARS-Related Coronavirus 2, (Lineage AY.4.2; Delta Variant) with C-Terminal Histidine and Avi Tags, Recombinant from HEK293 Cells

Catalog No. NR-56448

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For research use only. Not for use in humans.

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), lineage AY.4.2 (Delta variant) was produced in human embryonic kidney HEK293 cells and purified by immobilized metal affinity and gel filtration chromatography.[1] NR-56448 lacks the signal sequence and contains 1194 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] NR-56448 includes T19R, T95I, G142D, Y145H, E156G, delF157-R158, A222V, L452R, T478K, D614G, P681R and D950N mutations in the S glycoprotein as compared to the SARS-CoV-2 reference sequence (GenPept: QHD43416).[1,2] The predicted protein sequence is shown in Figure 1. NR-56448 has a theoretical molecular weight of 139,550 daltons. The crystal structure for trimeric S glycoprotein from SARS-CoV-2 has been solved at 3.46 Å resolution (PDB: 6VSB).[3]

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.[4,5] AY.4.2 is one of the several lineages of SARS-CoV2 Delta variant.[6,7] The AY.4.2 spike displays three additional mutations (T95I, Y145H and A222V) in the N-terminal domain when compared to the original Delta variant (B.1.617.2).[6,7]

Material Provided:

Each vial contains approximately 100 µL of NR-56448 in 10 mM HEPES, pH 7, 150 mM NaCl and 2 mM ethylenediamine-tetraacetic acid (EDTA). The concentration, expressed as mg/mL, is shown on the Certificate of Analysis.

Packaging/Storage:

NR-56448 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, (Lineage AY.4.2; Delta Variant) with C-Terminal Histidine and Avi Tags, Recombinant from HEK293 Cells, NR-56448."

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 (BMBL). 6th ed. Washington, DC: U.S. Government Printing Office, 2020.

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References:

1. Sather, D. N., Personal Communication.
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Figure 1: Predicted Protein Sequence

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   1 SQCVNLRTRT QLPPAYTNSF TRGVYYPDKV FRSSVLHSTQ DLFLPFFSNV
  51 TWFHAIHVSG TNGTKRFDNP VLPFNDGVYF ASIEKSNIIR GWIFGTTLDS
 101 KTQSLLIVNN ATNVVIKVCE FQFCNDPFLD VYHHKNNKSW MESGVYSSAN
 151 NCTFEYVSQP FLMDLEGKQG NFKNLREFVF KNIDGYFKIY SKHTPINLVR
 201 DLPQGFSVLE PLVDLPIGIN ITRFQTLLAL HRSYLTPGDS SSGWTAGAAA
 251 YYVGYLQPRT FLLKYNENGT ITDAVDCALD PLSETKCTLK SFTVEKGIYQ
 301 TSNFRVQPTE SIVRFPNITN LCPFGEVFNA TRFASVYAWN RKRISNCVAD
 351 YSVLYNSASF STFKCYGVSP TKLNDLCFTN VYADSFVIRG DEVRQIAPGQ
 401 TGKIADYNYK LPDDFTGCVI AWNSNNLDSK VGGNYNYRYR LFRKSNLKPF
 451 ERDISTEIYQ AGSKPCNGVE GFNCYFPLQS YGFQPTNGVG YQPYRVVVLS
 501 FELLHAPATV CGPKKSTNLV KNKCVNFNFN GLTGTGVLTE SNKKFLPFQQ
 551 FGRDIADTTD AVRDPQTLEI LDITPCSFGG VSVITPGTNT SNQVAVLYQG
 601 VNCTEVPVAI HADQLTPTWR VYSTGSNVFQ TRAGCLIGAE HVNNSYECDI
 651 PIGAGICASY QTQTNSRGSA SSVASQSIIA YTMSLGAENS VAYSNNSIAI
 701 PTNFTISVTT EILPVSMTKT SVDCTMYICG DSTECSNLLL QYGSFCTQLN
 751 RALTGIAVEQ DKNTQEVFAQ VKQIYKTPPI KDFGGFNFSQ ILPDPSKPSK
 801 RSFIEDLLFN KVTLADAGFI KQYGDCLGDI AARDLICAQK FNGLTVLPPL
 851 LTDEMIAQYT SALLAGTITS GWTFGAGAAL QIPFAMQMAY RFNGIGVTQN
 901 VLYENQKLIA NQFNSAIGKI QDSLSSTASA LGKLQNVVNQ NAQALNTLVK
 951 QLSSNFGAIS SVLNDILSRL DPPEAEVQID RLITGRLQSL QTYVTQQLIR
1001 AAEIRASANL AATKMSECVL GQSKRVDFCG KGYHLMSFPQ SAPHGVVFLH
1051 VTYVPAQEKN FTTAPAICHD GKAHFPREGV FVSNGTHWFV TQRNFYEPQI
1101 ITTDNTFVSG NCDVVIGIVN NTVYDPLQPE LDSFKEELDK YFKNHTSPDV
1151 DLGDISGINA SVVNIQKEID RLNEVAKNLN ESLIDLQELG KYEQGSGYIP
1201 EAPRDGQAYV RKDGEWVLLS TFLGRSLEVL FQGPGSHHHH HHHHGLNDIF
1251 EAQKIEWHE
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Spike ectodomain – **Residues 1 to 1194** [represents amino acid residues 13 to 1208 of the native S protein (GenPept: QHD43416)]
RRAR to GSAS substitution of S1/S2 cleavage site – Residues 668 to 671
KV to PP stabilizing mutations – Residues 972 and 973
T19R, T95I, G142D, Y145H, E156G, A222V, L452R, T478K, D614G, P681R and D950N mutations–
Residues 7, 83, 130, 133, 144, 208, 438, 464, 600, 667, 936
T4 foldon trimerization domain – Residues 1197 to 1223
HRV3C protease cleavage site – Residues 1227 to 1234
Octa-histidine tag and AviTag™ – Residues 1237 to 1259

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