Spike Glycoprotein (Stabilized) from SARS-Related Coronavirus 2, with C-Terminal Histidine and Twin-Strep® Tags, Recombinant from HEK293F Cells

Catalog No. NR-56132

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For research use only. Not for use in humans.

Contributor:

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Manufacturer:

UGA Bioexpression and Fermentation Facility

Product Description:

Note: The Strep tag designation on the label is incorrect; the correct Strep tag is a Twin-Strep® tag.

A recombinant form of the spike (S) glycoprotein from severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2; GenPept: QIZ14569.1) was produced by transient transfection into human embryonic kidney HEK293F cells and purified by immobilized metal affinity chromatography.[1,2,3] NR-56132 lacks the signal sequence and contains 1196 residues (ectodomain) of the SARS-CoV-2 spike glycoprotein; the recombinant protein was stabilized by substitution at the furin S1/S2 cleavage site (RRAR→GSAS; residues 670 to 673) and KV→PP mutations (residues 974 and 975), and includes a HRV3C protease cleavage site, T4 foldon trimerization domain, and C-terminal octa-histidine and Twin-Strep® tags. The predicted protein sequence is shown in Figure 1.[1] NR-56132 has a theoretical molecular weight of 140.9 kilodaltons.

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.[4]

Material Provided:

Each vial contains approximately 100 µL of NR-56132 in phosphate buffered saline (PBS). The concentration, expressed as milligrams per milliliter, is shown on the Certificate of Analysis.

Packaging/Storage:

NR-56132 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, with C-Terminal Histidine and Twin-Strep® Tags, Recombinant from HEK293F Cells, NR-56132."

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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References:

1. Tompkins, S. M., 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.

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3. Amanat, F., et al. "A Serological Assay to Detect SARS-CoV-2 Seroconversion in Humans." Nat. Med. 26 (2020): 1033-1036. PubMed: 32398876.
4. 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    SQCVNLTTRT QLPPAYTNSF TRGVYYPDKV FRSSVLHSTQ DLFLPFFSNV
51   TWFHAIHVSG TNGTKRFDNP VLPFNDGVYF ASTEKSNIIR GWIFGTTLDS
101  KTQSLLIVNN ATNVVIKVCE FQFCNDPFLG VYYHKNNKSW MESEFRVYSS
151  ANNCTFEYVS QPFLMDLEGK QGNFKNLREF VFKNIDGYFK IYSKHTPINL
201  VRDLPQGFSA LEPLVDLPIG INITRFQTLL ALHRSYLTPG DSSSGWTAGA
251  AAYYVGYLQP RTFLLKYNEN GTITDAVDCA LDPLSETKCT LKSFTVEKGI
301  YQTSNFRVQP TESIVRFPNI TNLCPFGEVF NATRFASVYA WNRKRISNCV
351  ADYSVLYNSA SFSTFKCYGV SPTKLNDLCF TNVYADSFVI RGDEVRQIAP
401  GQTGKIADYN YKLPDDFTGC VIAWNSNNLD SKVGGNYNYL YRLFRKSNLK
451  PFERDISTEI YQAGSTPCNG VEGFNCYFPL QSYGFQPTNG VGYQPYRVVV
501  LSFELLHAPA TVCGPKKSTN LVKNKCVNFN FNGLTGTGVL TESNKKFLPF
551  QQFGRDIADT TDAVRDPQTL EILDITPCSF GGVSVITPGT NTSNQVAVLY
601  QDVNCTEVPV AIHADQLTPT WRVYSTGSNV FQTRAGCLIG AEHVNNSYEC
651  DIPIGAGICA SYQTQTNSPG SASSVASQSI IAYTMSLGAE NSVAYSNNSI
701  AIPTNFTISV TTEILPVSMT KTSVDCTMYI CGDSTECSNL LLQYGSFCTQ
751  LNRALTGIAV EQDKNTQEVF AQVKQIYKTP PIKDFGGFNF SQILPDPSKP
801  SKRSFIEDLL FNKVTLADAG FIKQYGDCLG DIAARDLICA QKFNGLTVLP
851  PLLTDEMIAQ YTSALLAGTI TSGWTFGAGA ALQIPFAMQM AYRFNGIGVT
901  QNVLYENQKL IANQFNSAIG KIQDSLSSTA SALGKLQDVV NQNAQALNTL
951  VKQLSSNFGA ISSVLNDILS RLDPPEAEVQ IDRLITGRLQ SLQTYVTQQL
1001 IRAAEIRASA NLAATKMSEC VLGQSKRVDF CGKGYHLMSF PQSAPHGVVF
1051 LHVTYVPAQE KNFTTAPAIC HDGKAHFPRE GVFVSNGTHW FVTQRNFYEP
1101 QIITTDNTFV SGNCDVVIGI VNNTVYDPLQ PELDSFKEEL DKYFKNHTSP
1151 DVDLGDISGI NASVVNIQKE IDRLNEVAKN LNESLIDLQE LGKYEQGSGY
1201 IPEAPRDGQA YVRKDGEWVL LSTFLGRSLE VLFQGPGHHH HHHHHSAWSH
1251 PQFEKGGGSG GGGSGGSAWS HPQFEK
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Spike ectodomain **– Residues 1 to 1196** (representing WT residues 13 to 1208)
RRAR to GSAS substitution of S1/S2 cleavage site – Residues 670 to 673
KV to PP stabilizing mutations – Residues 974 and 975
T4 foldon trimerization domain – Residues 1199 to 1225
HRV3C Protease cleavage site – Residues 1229 to 1236
Octa-histidine tag– Residues 1237 to 1244
Twin-Strep® tag – Residues 1248 to 1276

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