Spike Glycoprotein (Stabilized) from Human Coronavirus 229E with C-Terminal Histidine and Twin-Strep® Tags, Recombinant from HEK293 Cells

Catalog No. NR-55701

This reagent is the tangible property of the U.S. Government.

For research use only. Not for use in humans.

Contributor:

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Manufacturer:

Emory-UGA Center of Excellence of Influenza Research and Surveillance (Emory-UGA CEIRS) and 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 human coronavirus (HCoV), 229E (GenPept: AOG74783) was produced in human embryonic kidney (HEK293) cells and purified by immobilized metal affinity chromatography.[1,2] NR-55701 lacks the signal sequence and contains 1093 residues (ectodomain) of the HCoV spike glycoprotein; the recombinant protein was stabilized by a pair of mutations (I854P and I855P, wild-type numbering), 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-55701 has a theoretical molecular weight of 128,100 daltons. The crystal structure for trimeric S glycoprotein from HCoV, 229E has been solved at 3.10 Å resolution (PDB: 6U7H).[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. The S protein is a target for neutralizing antibodies.[4]

Material Provided:

Each vial contains approximately 100 µL of NR-55701 in phosphate buffered saline (PBS). The concentration, expressed as milligrams per milliliter, is shown on the Certificate of Analysis.

Packaging/Storage:

NR-55701 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 produced under HHSN272201400004C and obtained through BEI Resources, NIAID, NIH: Spike Glycoprotein (Stabilized) from Human Coronavirus 229E with C-Terminal Histidine and Twin-Strep® Tags, Recombinant from HEK293 Cells, NR-55701."

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.

Disclaimers:

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References:

1. Tompkins, S. M., Personal Communication.
2. Corman, W. M., et al. "Link of a Ubiquitous Human Coronavirus to Dromedary Camels." Proc. Natl. Acad. Sci. USA 113 (2016): 9864-9869. PubMed: 27528677.

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3. Li, Z., et al. "The Human Coronavirus HCoV-229E S-Protein Structure and Receiptor Binding." eLIFE 8 (2019): e51230. PubMed: 31650956.
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.

Support Provided by NIAID

Figure 1: Predicted Protein Sequence

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1    CQTTNGTNTS HSVCNGCVGH SENVFAVESG GYIPSNFAFN NWFLLTNTSS
51   VVDGVVRSFQ PLLLNCLWSV SGSQFTTGFV YFNGTGRGAC KGFYSNASSD
101  VIRYNINFEE NLRRGTILFK TSYGAVVFYC TNNTLVSGDA HIPSGTVLGN
151  FYCFVNTTIG NETTSAFVGA LPKTVREFVI SRTGHFYING YRYFSLGDVE
201  AVNFNVTNAA TTVCTVALAS YADVLVNVSQ TAIANIIYCN SVINRLRCDQ
251  LSFDVPDGFY STSPIQPVEL PVSIVSLPVY HKHTFIVLYV NFEHRRGPGK
301  CYNCRPAVIN ITLANFNETK GPLCVDTSHF TTQFVDNVKL ARWSASINTG
351  NCPFSFGKVN NFVKFGSVCF SLKDIPGGCA MPIMANLVNS KSHNIGSLYV
401  SWSDGDVITG VPKPVEGVSS FMNVTLNKCT KYNIYDVSGV GVIRISNDTF
451  LNGITYTSTS GNLLGFKDVT NGTIYSITPC NPPDQLVVYQ QAVVGAMLSE
501  NFTSYGFSNV VEMPKFFYAS NGTYNCTDAV LTYSSFGVCA DGSIIAVQPR
551  NVSYDSVSAI VTANLSIPFN WTTSVQVEYL QITSTPIVVD CSTYVCNGNV
601  RCVELLKQYT SACKTIEDAL RNSAMLESAD VSEMLTFDKK AFTLANVSSF
651  GDYNLSSVIP SLPRSGSRVA GRSAIEDILF SKLVTSGLGT VDADYKKCTK
701  GLSIADLACA QYYNGIMVLP GVADAERMAM YTGSLIGGIA LGGLTSAASI
751  PFSLAIQSRL NYVALQTDVL QENQRILAAS FNKAMTNIVD AFTGVNDAIT
801  QTSQALQTVA TALNKIQDVV NQQGNSLNHL TSQLRQNFQA ISSSIQAIYD
851  RLDPPQADQQ VDRLITGRLA ALNVFVSHTL TKYTEVRASR QLAQQKVNEC
901  VKSQSKRYGF CGNGTHIFSL VNAAPEGLVF LHTVLLPTQY KDVEAWSGLC
951  VDGINGYVLR QPNLALYKEG NYYRITSRIM FEPRIPTIAD FVQIENCNVT
1001 FVNISRSELQ TIVPEYIDVN KTLQELSYKL PNYTVPDLVV EQYNQTILNL
1051 TSEISTLENK SAELNYTVQK LQTLIDNINS TLVDLKWLNR VETGSGYIPE
1101 APRDGQAYVR KDGEWVLLST FLGRSLEVLF QGPGHHHHHH HHSAWSHPQF
1151 EKGGGSGGGG SGGSAWSHPQ FEK
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Spike ectodomain – Residues 1 to 1093 [represents amino acids17 to 519 of the native HA protein (GenPept: AOG74783)]
II to PP stabilizing mutations – Residues 854 and 855
T4 foldon trimerization domain – Residues 1096 to 1122
HRV3C protease cleavage site – Residues 1126 to 1133
Octa-histidine tag – Residues 1135 to 1342
Twin-Strep® tag – Residues 1145 to 1173

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