

Product Information Sheet for NR-56134

Spike Glycoprotein (Stabilized) from Human Coronavirus NL63, with C-Terminal Histidine and Twin-Strep® Tags, Recombinant from HEK293 Cells

Catalog No. NR-56134

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:

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 NL63, (HCoV-NL63; GenPept: AFV53148) was produced by transient transfection into human embryonic kidney HEK293 cells and purified by immobilized metal affinity chromatography. 1,2,3 NR-56134 lacks the signal sequence and contains 1273 residues (ectodomain) of the HCoV-NL63 spike glycoprotein; the recombinant protein was stabilized by SI->PP mutations (residues 1034 and 1035), 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-56134 has a theoretical molecular weight of 149.0 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 μ L of NR-56134 in phosphate buffered saline (PBS). The concentration, expressed as milligrams per milliliter, is shown on the Certificate of Analysis.

Packaging/Storage:

NR-56134 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 Human Coronavirus NL63, with C-Terminal Histidine and Twin-Strep® Tags, Recombinant from HEK293 Cells, NR-56134."

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.

Disclaimers:

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References:

- 1. Tompkins, S. M., Personal Communication.
- van der Hoek, L., et al. "Identification of a New Human Coronavirus." <u>Nat. Med.</u> 10 (2004): 368-373. PubMed: 15034574.

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- Gallagher, T. M. and M. J. Buchmeier. "Coronavirus Spike Proteins in Viral Entry and Pathogenesis." <u>Virology</u> 279 (2001): 371-374. PubMed: 11162792.
- Hulswit, R. J. G., C. A. M. de Haan and B.-J. Bosch. "Coronavirus Spike Protein and Tropism Changes." <u>Adv.</u> Virus Res. 96 (2016): 29-57. PubMed: 27712627.

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Figure 1: Predicted Protein Sequence

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1
   CNSNANLSML QLGVPDNSST IVTGLLPTHW FCANQSTSVY SANGFFYIDV
   GNHRSAFALH TGYYDANOYY IYVTNEIGLN ASVTLKICKF SRNTTFDFLS
101 NASSSFDCIV NLLFTEOLGA PLGITISGET VRLHLYNVTR TFYVPAAYKL
151 TKLSVKCYFN YSCVFSVVNA TVTVNVTTHN GRVVNYTVCD DCNGYTDNIF
201 SVQQDGRIPN GFPFNNWFLL TNGSTLVDGV SRLYQPLRLT CLWPVPGLKS
251 STGFVYFNAT GSDVNCNGYO HNSVVDVMRY NLNFSANSLD NLKSGVIVFK
301 TLQYDVLFYC SNSSSGVLDT TIPFGPSSQP YYCFINSTIN TTHVSTFVGI
351 LPPTVREIVV ARTGQFYING FKYFDLGFIE AVNFNVTTAS ATDFWTVAFA
401 TFVDVLVNVS ATNIQNLLYC DSPFEKLQCE HLQFGLQDGF YSANFLDDNV
451 LPETYVALPI YYQHTDINFT ATASFGGSCY VCKPHQVNIS LNGNTSVCVR
501 TSHFSIRYIY NRVKSGSPGD SSWHIYLKSG TCPFSFSKLN NFQKFKTICF
551 STVEVPGSCN FPLEATWHYT SYTIVGALYV TWSEGNSITG VPYPVSGIRE
601 FSNLVLNNCT KYNIYDYVGT GIIRSSNOSL AGGITYVSNS GNLLGFKNVS
651 TGNIFIVTPC NOPDOVAVYO OSIIGAMTAV NESRYGLONL LOLPNFYYVS
701 NGGNNCTTAV MTYSNFGICA DGSLIPVRPR NSSDNGISAI ITANLSIPSN
751 WTTSVQVEYL QITSTPIVVD CATYVCNGNP RCKNLLKQYT SACKTIEDAL
801 RLSAHLETND VSSMLTFDSN AFSLANVTSF GDYNLSSVLP QRNIRSSRIA
851 GRSALEDLLF SKVVTSGLGT VDVDYKSCTK GLSIADLACA QYYNGIMVLP
901 GVADAERMAM YTGSLIGGMV LGGLTSAAAI PFSLALQARL NYVALQTDVL
951 QENQKILAAS FNKAINNIVA SFSSVNDAIT QTAEAIHTVT IALNKIQDVV
1001 NQQGSALNHL TSQLRHNFQA ISNSIQAIYD RLDPPQADQQ VDRLITGRLA
1051 ALNAFVSQVL NKYTEVRGSR RLAQQKINEC VKSQSNRYGF CGNGTHIFSI
1101 VNSAPDGLLF LHTVLLPTDY KNVKAWSGIC VDGIYGYVLR QPNLVLYSDN
1151 GVFRVTSRIM FOPRLPVLSD FVOIYNCNVT FVNISRVELH TVIPDYVDVN
1201 KTLQEFAQNL PKYVKPNFDL TPFNLTYLNL SSELKQLEAK TASLFQTTVE
1251 LQGLIDQINS TYVDLKLLNR FENGSGYIPE APRDGQAYVR KDGEWVLLST
1301 FLGRSLEVLF QGPGHHHHHH HHSAWSHPQF EKGGGSGGGG SGGSAWSHPQ
1351 FEK
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Spike ectodomain – **Residues 1 to 1273** (representing WT residues 19 to 1291)

SI to PP stabilizing mutations – Residues 1034 and 1035

T4 foldon trimerization domain – Residues 1276 to 1302

HRV3C Protease cleavage site – Residues 1306 to 1313

Octa-histidine tag– Residues 1315 to 1322

Twin-Strep® tag – Residues 1325 to 1353

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