Spike Glycoprotein (Stabilized) from MERS Coronavirus, England 1 with C-Terminal Histidine and Twin-Strep® Tags, Recombinant from HEK293 Cells

Catalog No. NR-53591

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For research use only. Not for human use.

Contributor and Manufacturer:

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Product Description:

A recombinant form of the spike (S) glycoprotein from the England 1 strain (UK/H123990006/2012 isolate) of Middle East respiratory syndrome coronavirus (MERS-CoV; GenPept: YP_007188579) was produced by transient transfection into human embryonic kidney HEK293 cells and purified by immobilized metal affinity and gel filtration chromatography.[1,2] NR-53591 lacks the signal sequence and contains 1274 residues (ectodomain) of the MERS-CoV S glycoprotein; the recombinant protein was stabilized by substitution at the furin S1/S2 cleavage site (RSVR→ASVG; residues 748 to 751) and VL→PP mutations (residues 1060 and 1061), and includes a T4 foldon trimerization domain, HRV3C protease cleavage site, and C-terminal octa-histidine and Twin-Strep® tags.[1,2] The predicted protein sequence is shown in Figure 1. NR-53591 has a theoretical molecular weight of 148,650 daltons. The crystal structure for trimeric S glycoprotein from MERS-CoV has been solved at 4.00 Å resolution (PDB: 5W9P).[2]

The S glycoprotein mediates viral binding to the host dipeptidyl peptidase 4 (DPP4). 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.[3]

Material Provided:

Each vial contains approximately 100 µL of NR-53591 in 10 mM HEPES, pH 7, 150 mM NaCl and 2 mM ethylenediaminetetraacetic acid (EDTA). The concentration, expressed as mg per mL, is shown on the Certificate of Analysis.

Packaging/Storage:

NR-53591 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 MERS Coronavirus, England 1 with C-Terminal Histidine and Twin-Strep® Tags, Recombinant from HEK293 Cells, NR-53591."

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. 5th ed. Washington, DC: U.S. Government Printing Office, 2009; see www.cdc.gov/biosafety/publications/bmbl5/index.htm.

Disclaimers:

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NR-53591 is claimed in U.S. Provisional Patent Application number 16/344,774 and the continuations, continuations-in-part, re-issues and foreign counterparts thereof. The University of Texas-Austin, The Scripps Research Institute, Dartmouth College and the National Institutes of Health all have rights to this material.

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References:

1. Sather, D. N., P. Myler and J. McLellan, Personal Communication.
2. Pallesen, J., et al. "Immunogenicity and Structures of a Rationally Designed Prefusion MERS-CoV Spike Antigen." Proc. Natl. Acad. Sci. USA 114 (2017): E7348-E7357. PubMed: 28807998.
3. 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    YVDVGPDSVK SACIEVDIQQ TFFDKTWPRP IDVSKADGII YPQGRTYSNI
51   TITYQGLFPY QGDHGDMYVY SAGHATGTTP QKLFVANYSQ DVKQFANGFV
101  VRIGAAANST GTVIISPSTS ATIRKIYPAF MLGSSVGNFS DGKMGRFFNH
151  TLVLLPDGCG TLLRAFYCIL EPRSGNHCPA GNSYTSFATY HTPATDCSDG
201  NYNRNASLNS FKEYFNLRNC TFMYTYNITE DEILEWFGIT QTAQGVHLFS
251  SRYVDLYGGN MFQFATLPVY DTIKYYSIIP HSIRSIQSDR KAWAAFYVYK
301  LQPLTFLLDF SVDGYIRRAI DCGFNDLSQL HCSYESFDVE SGVYSVSSFE
351  AKPSGSVVEQ AEGVECDFSP LLSGTPPQVY NFKRLVFTNC NYNLTKLLSL
401  FSVNDFTCSQ ISPAAIASNC YSSLILDYFS YPLSMKSDLS VSSAGPISQF
451  NYKQSFSNPT CLILATVPHN LTTITKPLKY SYINKCSRFL SDDRTEVPQL
501  VNANQYSPCV SIVPSTVWED GDYYRKQLSP LEGGGWLVAS GSTVAMTEQL
551  QMGFGITVQY GTDTNSVCPK LEFANDTKIA SQLGNCVEYS LYGVSGRGVF
601  QNCTAVGVRQ QRFVYDAYQN LVGYYSDDGN YYCLRACVSV PVSVIYDKET
651  KTHATLFGSV ACEHISSTMS QYSRSTRSML KRRDSTYGPL QTPVGCVLGL
701  VNSSLFVEDC KLPLGQSLCA LPDTPSTLTP ASVGSVPGEM RLASIAFNHP
751  IQVDQLNSSY FKLSIPTNFS FGVTQEYIQT TIQKVTVDCK QYVCNGFQKC
801  EQLLREYGQF CSKINQALHG ANLRQDDSVR NLFASVKSSQ SSPIIPGFGG
851  DFNLTLLEPV SISTGSRSAR SAIEDLLFDK VTIADPGYMQ GYDDCMQQGP
901  ASARDLICAQ YVAGYKVLPP LMDVNMEAAY TSSLLGSIAG VGWTAGLSSF
951  AAIPFAQSIF YRLNGVGITQ QVLSENQKLI ANKFNQALGA MQTGFTTTNE
1001 AFHKVQDAVN NNAQALSKLA SELSNTFGAI SASIGDIIQR LDPPEQDAQI
1051 DRLINGRLTT LNAFVAQQLV RSESAALSAQ LAKDKVNECV KAQSKRSGFC
1101 GQGTHIVSFV VNAPNGLYFM HVGYYPSNHI EVVSAYGLCD AANPTNCIAP
1151 VNGYFIKTNN TRIVDEWSYT GSSFYAPEPI TSLNTKYVAP QVTYQNISTN
1201 LPPPLLGNST GIDFQDELDE FFKNVSTSIP NFGSLTQINT TLLDLTYEML
1251 SLQQVVKALN ESYIDLKELG NYTYGSGYIP EAPRDGQAYV RKDGEWVLLS
1301 TFLGRSLEVL FQGPGHHHHH HHHSAWSHPQ FEKGGGSGGG GSGGSAWSHP
1351 QFEK
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Spike ectodomain – **Residues 1 to 1274** (represents WT amino acid residues 18 to 1291)
RSVR to ASVG substitution of S1/S2 cleavage site – Residues 731 to 735
VL to PP stabilizing mutations – Residues 1043 and 1044
T4 foldon trimerization domain – Residues 1278 to 1303
HRV3C protease cleavage site – Residues 1307 to 1314
Octa-histidine tag – Residues 1316 to 1323
Twin-Strep® tag – Residues 1326 to 1354

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