Spike Glycoprotein (Stabilized) from SARS Coronavirus, Tor2 with C-Terminal Histidine and *Strep*® II Tags, Recombinant from HEK293 Cells

Catalog No. NR-53590

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Contributor and Manufacturer:

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Product Description:

A recombinant form of the spike (S) glycoprotein from severe acute respiratory syndrome coronavirus (SARS-CoV), Tor2 (GenPept: NP_828851) was produced by transient transfection into human embryonic kidney HEK293 cells and purified by immobilized metal affinity and gel filtration chromatography.[1,2] NR-53590 lacks the signal sequence and contains 1177 residues (ectodomain) of the SARS-CoV S glycoprotein; the recombinant protein was stabilized by KV→PP mutations (residues 968 and 969), and includes a T4 foldon trimerization domain, HRV3C protease cleavage site, and C-terminal octa-histidine and *Strep*® II tags.[1,2] The predicted protein sequence is shown in Figure 1. NR-53590 has a theoretical molecular weight of 137,136 daltons. The crystal structure for trimeric S glycoprotein from SARS-CoV has been solved at 3.30 Å resolution (PDB: 6CRZ).[2]

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.[3]

Material Provided:

Each vial contains approximately 100 µL of NR-53590 in 10 mM HEPES, pH 7, 150 mM NaCl and 2 mM ethylenediamine-tetraacetic acid (EDTA). The concentration, expressed as mg per mL, is shown on the Certificate of Analysis.

Packaging/Storage:

NR-53590 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 Coronavirus, Tor2 with C-Terminal Histidine and *Strep*® II Tags, Recombinant from HEK293 Cells, NR-53590."

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.

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NR-53590 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.

References:

1. Sather, D. N., P. Myler and J. McLellan, Personal Communication.
2. Kirchdoerfer, R. N., et. al. "Stabilized Coronavirus Spikes Are Resistant to Conformational Changes Induced by Receptor Recognition or Proteolysis." Sci. Rep. 8 (2018): 15701. PubMed: 30356097.
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    SDLDRCTTFD DVQAPNYTQH TSSMRGVYYP DEIFRSDTLY LTQDLFLPFY
51   SNVTGFHTIN HTFGNPVIPF KDGIYFAATE KSNVVRGWVF GSTMNNKSQS
101  VIIINNSTNV VIRACNFELC DNPFFAVSKP MGTQTHTMIF DNAFNCTFEY
151  ISDAFSLDVS EKSGNFKHLR EFVFKNKDGF LYVYKGYQPI DVVRDLPSGF
201  NTLKPIFKLP LGINITNFRA ILTAFSPAQD IWGTSAAAYF VGYLKPTTFM
251  LKYDENGTIT DAVDCSQNPL AELKCSVKSF EIDKGIYQTS NFRVVPSGDV
301  VRFPNITNLC PFGEVFNATK FPSVYAWERK KISNCVADYS VLYNSTFFST
351  FKCYGVSATK LNDLCFSNVY ADSFVVKGDD VRQIAPGQTG VIADYNYKLP
401  DDFMGCVLAW NTRNIDATST GNYNYKYRYL RHGKLRPFER DISNVPFSPD
451  GKPCTPPALN CYWPLNDYGF YTTTGIGYQP YRVVVLSFEL LNAPATVCGP
501  KLSTDLIKNQ CVNFNFNGLT GTGVLTPSSK RFQPFQQFGR DVSDFTDSVR
551  DPKTSEILDI SPCAFGGVSV ITPGTNASSE VAVLYQDVNC TDVSTAIHAD
601  QLTPAWRIYS TGNNVFQTQA GCLIGAEHVD TSYECDIPIG AGICASYHTV
651  SLLRSTSQKS IVAYTMSLGA DSSIAYSNNT IAIPTNFSIS ITTEVMPVSM
701  AKTSVDCNMY ICGDSTECAN LLLQYGSFCT QLNRALSGIA AEQDRNTREV
751  FAQVKQMYKT PTLKYFGGFN FSQILPDPLK PTKRSFIEDL LFNKVTLADA
801  GFMKQYGECL GDINARDLIC AQKFNGLTVL PPLLTDDMIA AYTAALVSGT
851  ATAGWTFGAG AALQIPFAMQ MAYRFNGIGV TQNVLYENQK QIANQFNKAI
901  SQIQESLTTT STALGKLQDV VNQNAQALNT LVKQLSSNFG AISSVLNDIL
951  SRLDPPEAEV QIDRLITGRL QSLQTYVTQQ LIRAAEIRAS ANLAATKMSE
1001 CVLGQSKRVD FCGKGYHLMS FPQAAPHGVV FLHVTYVPSQ ERNFTTAPAI
1051 CHEGKAYFPR EGVFVFNGTS WFITQRNFFS PQIITTDNTF VSGNCDVVIG
1101 IINNTVYDPL QPELDSFKEE LDKYFKNHTS PDVDLGDISG INASVVNIQK
1151 EIDRLNEVAK NLNESLIDLQ ELGKYEQGSG YIPEAPRDGQ AYVRKDGEWV
1201 LLSTFLGRSL EVLFQGPGHH HHHHHHSAWS HPQFEK
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Spike ectodomain – **Residues 1 to 1177** (represents WT amino acid residues 14 to 1190)
KV to PP stabilizing mutations – Residues 955 and 956
T4 foldon trimerization domain – Residues 1181 to 1206
HRV3C protease cleavage site – Residues 1210 to 1217
Octa-histidine tag – Residues 1219 to 1226
Strep®-tag II – Residues 1229 to 1236

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