# Spike S1+S2 Trimer Protein (Extracellular Domain) from SARS-Related Coronavirus 2, B.1.1.529 (Omicron) with C-Terminal Histidine Tag, Recombinant from HEK293 Cells

## Catalog No. NR-56479
## Sino Biological Catalog No. 40589-V08H26

**For research use only. Not for use in humans.**

### Contributor and Manufacturer:
Sino Biological, Wayne, Pennsylvania, USA

### Product Description:
A recombinant form of the spike glycoprotein S1+S2 from severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2), B.1.1.529 (Omicron) which originated in South Africa was produced by transfection in human embryonic kidney HEK293 cells and purified.[1] NR-56479 lacks the signal sequence, contains 1192 residues of the SARS-CoV-2 spike glycoprotein (amino acid residues V16 to 1208 according to the numbering of GenPept: YP_009724390), contains mutations A67V, HV69-70 deletion, T95I, G142D, VYY143-145 deletion, N211 deletion, L212I, ins214EPE, G339D, S371L, S373P, S375F, K417N, N440K, G446S, S477N, T478K, E484A, Q493R, G496S, Q498R, N501Y, Y505H, T547K, D614G, H655Y, N679K, P681H, N764K, D796Y, F817P, N856K, A892P, A899P, A942P, Q954H, N969K, L981F, K986P, V987P and furin cleavage site mutations. NR-56479 features a bacteriophage T4 fibritin foldon domain and a C-terminal poly-histidine tag.[1] The predicted amino acid sequence is shown in Figure 1. NR-56479 has a theoretical molecular weight of 136.67 kilodaltons.[1] As a result of glycosylation, NR-56479 migrates at a higher molecular weight in SDS-PAGE under reducing conditions.

### Material Provided:
Each vial contains approximately 50 µg of purified recombinant protein in 25 mM sodium citrate, 200 mM NaCl, 0.02% tween 80, (pH 6.0). Note: NR-56479 was not lyophilized. The concentration, expressed as mg/mL, is shown on the Certificate of Analysis.

### Packaging/Storage:
NR-56479 was packaged aseptically in cryovials. The product is provided on dry ice and should be stored under sterile conditions at -20°C to -80°C immediately upon arrival. It is recommended that the protein be aliquoted for optimal storage. Freeze-thaw cycles should be avoided.

### Functional Activity:
The biological activity of NR-56479 was measured by its binding ability in a functional ELISA.[1]

### Citation:
Acknowledgment for publications should read "The following reagent was obtained through BEI Resources, NIAID, NIH: Spike S1+S2 Trimer Protein (Extracellular Domain) from SARS-Related Coronavirus 2, B.1.1.529 (Omicron) with C-Terminal Histidine Tag, Recombinant from HEK293 Cells, NR-56479."

### 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.

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### References:
1. Lu, Z., Personal Communication.

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**Figure 1 – Predicted Protein Sequence**

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1     VNLTTRTQLP PAYTNSFTRG VYYPDKVFRS SVLHSTQDLF LPFFSNVTWF
51    HVISGTNGTK RFDNPVLPFN DGVYFASIEK SNIIRGWIFG TTLDSKTQSL
101   LIVNNATNVV IKVCEFQFCN DPFLDHKNNK SWMESEFRVY SSANNCTFEY
151   VSQPFLMDLE GKQGNFKNLR EFVFKNIDGY FKIYSKHTPI IVREPEDLPQ
201   GFSALEPLVD LPIGINITRF QTLLALHRSY LTPGDSSSGW TAGAAAYYVG
251   YLQPRTFLLK YNENGTITDA VDCALDPLSE TKCTLKSFTV EKGIYQTSNF
301   RVQPTESIVR FPNITNLCPF DEVFNATRFA SVYAWNRKRI SNCVADYSVL
351   YNLAPFFTFK CYGVSPTKLN DLCFTNVYAD SFVIRGDEVR QIAPGQTGNI
401   ADYNYKLPDD FTGCVIAWNS NKLDSKVSGN YNYLYRLFRK SNLKPFERDI
451   STEIYQAGNK PCNGVAGFNC YFPLRSYSFR PTYGVGHQPY RVVVLSFELL
501   HAPATVCGPK KSTNLVKNKC VNFNFNGLKG TGVLTESNKK FLPFQQFGRD
551   IADTTDAVRD PQTLEILDIT PCSFGGVSVI TPGTNTSNQV AVLYQGVNCT
601   EVPVAIHADQ LTPTWRVYST GSNVFQTRAG CLIGAEYVNN SYECDIPIGA
651   GICASYQTQT KSHGSASSVA SQSIIAYTMS LGAENSVAYS NNSIAIPTNF
701   TISVTTEILP VSMTKTSVDC TMYICGDSTE CSNLLLQYGS FCTQLKRALT
751   GIAVEQDKNT QEVFAQVKQI YKTPPIKYFG GFNFSQILPD PSKPSKRSPI
801   EDLLFNKVTL ADAGFIKQYG DCLGDIAARD LICAQKFKGL TVLPPLLTDE
851   MIAQYTSALL AGTITSGWTF GAGPALQIPF PMQMAYRFNG IGVTQNVLYE
901   NQKLIANQFN SAIGKIQDSL SSTPSALGKL QDVVNHNAQA LNTLVKQLSS
951   KFGAISSVLN DIFSRLDPPE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI
1001  RASANLAATK MSECVLGQSK RVDFCGKGYH LMSFPQSAPH GVVFLHVTYV
1051  PAQEKNFTTA PAICHDGKAH FPREGVFVSN GTHWFVTQRN FYEPQIITTD
1101  NTFVSGNCDV VIGIVNNTVY DPLQPELDSF KEELDKYFKN HTSPDVDLGD
1151  ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ GYIPEAPRDG
1201  QAYVRKDGEW VLLSTFLAHH HHHHHHHH
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**Residues 1 to 1190** [represents amino acid residues 16 to 1208 of the native S protein (GenPept: YP_009724390)]
RRAR to GSAS substitution of S1/S2 cleavage site – Residues **664 to 667**
KV to PP stabilizing mutations – Residues **968 and 969**
T4 Foldon domain: Residues 1191 to 1217; Poly-histidine tag – Residues 1219 to 1218
Mutations are underlined. Gaps indicate deletions. EPE (underlined) is an insertion.
The mutations shown are A67V, HV69-70 deletion, T95I, G142D, VYY143-145 deletion, N211 deletion, L212I, ins214EPE, G339D, S371L, S373P, S375F, K417N, N440K, G446S, S477N, T478K, E484A, Q493R, G496S, Q498R, N501Y, Y505H, T547K, D614G, H655Y, N679K, P681H, N764K, D796Y, F817P, N856K, A892P, A899P, A942P, Q954H, N969K, L981F, K986P, V987P
(numbering according to GenPept: YP_009724390).
**Residues 52, 78, 125, 191, 194-196, 321, 353, 355, 357, 398, 422, 428, 459, 460, 466, 475, 478, 480, 483, 487, 529, 599, 637, 661, 663, 746, 778, 799, 838, 875, 881, 924, 936, 951, 963, 968, 969**

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