

**Spike Glycoprotein Receptor Binding Domain (RBD) from SARS-Related Coronavirus 2, B.1.1.529 BA.2 Lineage (Omicron Variant) with C-Terminal Histidine and Avi Tags, Recombinant from HEK293F Cells**

**Catalog No. NR-56548**

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**Contributor:**

BEI Resources

**Manufacturer:**

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**Product Description:**

A recombinant form of the spike (S) glycoprotein receptor binding domain (RBD) from severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2), B.1.1.529 BA.2 lineage (Omicron variant) was produced in human embryonic kidney HEK293F cells and purified by immobilized metal affinity and gel filtration chromatography.<sup>1,2,3,4</sup> NR-56548 lacks the signal sequence and contains 223 residues of the SARS-CoV-2 S glycoprotein RBD and features a C-terminal octa-histidine tag fused to an AviTag™ BirA biotinylation acceptor sequence.<sup>1,2,3</sup> NR-56548 includes S371F, S373P, S375F, T376A, D405N, R408S, K417N, N440K, S477N, T478K, E484A, Q493R, Q498R, N501Y and Y505H mutations in the S glycoprotein RBD as compared to the SARS-CoV-2 reference sequence (GenPept: [QHD43416](#)).<sup>1,5</sup> The predicted protein sequence is shown in Figure 1.<sup>1</sup> NR-56548 has a theoretical molecular weight of 139,700 daltons. The crystal structure for trimeric S glycoprotein from SARS-CoV-2 has been solved at 3.46 Å resolution (PDB: [6VSB](#)).<sup>2</sup>

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.<sup>6</sup> B.1.1.529 BA.2 is one of several lineages and sublineages designated Omicron by the World Health Organization (WHO) and was first identified in South Africa, followed by multiple countries in November 2021.<sup>7</sup> This lineage contains multiple mutations in the RBD that have been identified in other variants, including K417N, N501Y and D614G.<sup>8,9,10</sup> The presence of D614G among variants has been shown to increase transmissibility, with K417N, Q493R, N501Y and Y505H shown to be important residues mediating virus entry into host cells.<sup>9,11</sup> E484A has been shown to decrease neutralization by post-vaccination sera and some monoclonal antibody treatments.<sup>8,9,10</sup>

**Material Provided:**

Each vial contains approximately 100 microliters of NR-56548 in 10 mM HEPES, pH 7, 150 mM NaCl and 2 mM ethylenediamine-tetraacetic acid (EDTA). The concentration, expressed as milligrams per milliliter, is shown on the Certificate of Analysis.

**Packaging/Storage:**

NR-56548 was packaged aseptically in cryovials. The product is provided on dry ice and should be stored at -20°C or colder immediately upon arrival. Storage at warmer temperatures is not recommended due to a low bioburden. Freeze-thaw cycles should be avoided.

**Citation:**

Acknowledgment for publications should read "The following reagent was obtained through BEI Resources, NIAID, NIH: Spike Glycoprotein Receptor Binding Domain (RBD) from SARS-Related Coronavirus 2, B.1.1.529 BA.2 Lineage (Omicron Variant) with C-Terminal Histidine and Avi Tags, Recombinant from HEK293F Cells, NR-56548."

**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/bmb15/index.htm](http://www.cdc.gov/biosafety/publications/bmb15/index.htm).

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**References:**

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Figure 1: Predicted Protein Sequence

1 RVQPTESIVR FPNITNLCPE DEVFNATREA SVYAWNRKRI SNCVADYSVL  
 51 YNFAPFFAFK CYGVSPTKLN DLCFTNVYAD SFVIRGNEVS QIAPGQTGNI  
 101 ADYNYKLPDD FTGCVIAWNS NKLDSKVGGN YNYLYRLEFRK SNLKPFFERDI  
 151 STEIYQAGNK PCNGVAGFNC YFPLRSYGFR PTYGVGHQPY RVVVLSFELL  
 201 HAPATVCGPK KSTNLVKNKC VNFSGHHHHH HHHGLNDIFE AQKIEWHE

RBD domain – Residues 1 to 223 (represents WT amino acid residues 319 to 541)  
 S371F, S373P, S375F, T376A, D405N, R408S, K417N, N440K, S477N, T478K, E484A, Q493R, Q498R, N501Y and Y505H  
 mutations –

**Residues 53, 55, 57-58, 87, 90, 99, 122, 159-160,**  
**166, 175, 180, 183 and 187**  
 Octa-histidine tag and AviTag™ – Residues 226 to 248