

SUPPORTING INFECTIOUS DISEASE RESEARCH

# **Product Information Sheet for NR-19240**

H1 Hemagglutinin (HA) Protein with C-Terminal Histidine Tag from Influenza Virus, A/Puerto Rico/8/1934 (H1N1), Recombinant from Baculovirus

Catalog No. NR-19240

For research use only. Not for use in humans.

### **Contributor and Manufacturer:**

**BEI Resources** 

### **Product Description:**

A recombinant form of the H1 hemagglutinin (HA) protein from influenza A virus, A/Puerto Rico/8/1934 (H1N1) containing a C-terminal histidine tag was produced in Sf9 insect cells using a baculovirus expression vector system and was purified by nickel affinity chromatography. The HA protein includes a C-terminal peptide containing a thrombin cleavage site, trimerizing (foldon) domain and octa-histidine tag, as described for the 1918 pandemic virus. The full-length HA precursor protein is 562 residues (GenPept: AEX92873). The predicted protein sequence of NR-19240 is shown in Figure 1. NR-19240 has a theoretical molecular weight of approximately 63.4 kilodaltons. The crystal structure of the 1918 human H1 HA precursor has been solved at 3.00 Å resolution (PDB: 1RD8).

### **Material Provided:**

Each vial contains approximately 50 to 100  $\mu g$  of purified recombinant HA protein in PBS (pH 7.4) with 50% glycerol. The concentration, expressed as mg per mL, is shown on the Certificate of Analysis.

### Packaging/Storage:

NR-19240 was packaged aseptically in cryovials. The product is provided on blue ice and should be stored at -20°C immediately upon arrival.

#### Citation:

Acknowledgment for publications should read "The following reagent was obtained through BEI Resources, NIAID, NIH: H1 Hemagglutinin (HA) Protein with C-Terminal Histidine Tag from Influenza Virus, A/Puerto Rico/8/1934 (H1N1), Recombinant from Baculovirus, NR-19240."

### 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:

- Stevens, J., et al. "Structure and Receptor Specificity of the Hemagglutinin from an H5N1 Influenza Virus." Science 312 (2006): 404-410. PubMed: 16543414.
- Stevens, J., et al. "Structure of the Uncleaved Human H1
  Hemagglutinin from the Extinct 1918 Influenza Virus."
  Science 303 (2004): 1866-1870. PubMed: 14764887.
- Kadam, R. U., et al. "Potent Peptidic Fusion Inhibitors of Influenza Virus." <u>Science</u> 358 (2017): 496-502. PubMed: 28971971.
- Anderson, C. S., et al. "Implementing Sequence-Based Antigenic Distance Calculation into Immunological Shape Space Model." <u>BMC Bioinformatics</u> 21 (2020): 256. PubMed: 32560624.
- Yao, Y., et al. "An Influenza A Hemagglutinin Small-Molecular Fusion Inhibitor Identified by a New High-Throughput Fluorescence Polarization Screen." <u>Proc. Natl. Acad. Sci. USA</u> 117 (2020): 18431-18438. PubMed: 32690700.

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BEI Resources www.beiresources.org E-mail: contact@beiresources.org

Tel: 800-359-7370 Fax: 703-365-2898



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### Figure 1: Predicted Protein Sequence

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1 ADPGYLLEDT ICIGYHANNS TDTVDTVLEK NVTVTHSVNL LEDSHNGKLC
51 RLKGIAPLQL GKCNIAGWLL GNPECDPLLP VRSWSYIVET PNSENGICYP
101 GDFIDYEELR EQLSSVSSFE RFEIFPKESS WPNHNTNGVT AACSHEGKSS
151 FYRNLLWLTE KEGSYPKLKN SYVNKKGKEV LVLWGIHHPP NSKEQQNLYQ
201 NENAYVSVVT SNYNRRFTPE IAERPKVRDQ AGRMNYYWTL LKPGDTIIFE
251 ANGNLIAPMY AFALSRGFGS GIITSNASMH ECNTKCQTPL GAINSSLPYQ
301 NIHPVTIGEC PKYVRSAKLR MVTGLRNIPS IQSRGLFGAI AGFIEGGWTG
351 MIDGWYGYHH QNEQGSGYAA DQKSTQNAIN GITNKVNTVI EKMNIQFTAV
401 GKEFNKLEKR MENLNKKVDD GFLDIWTYNA ELLVLLENER TLDFHDSNVK
451 NLYEKVKSQL KNNAKEIGNG CFEFYHKCDN ECMESVRNGT YDYPKYSEES
501 KLNREKVDGV RCRSSGRLVP RGSPGSGYIP EAPRDGQAYV RKDGEWVLLS
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Plasmid-derived amino acids – Residues 1 to 8, 511 to 517, 524, 554 **HA protein – Residues 9 to 510** (represents amino acid residues 18 to 519)

Thrombin cleavage sequence – Residues 518 to 523

T4 foldon trimerization domain – Residues 525 to 553

Octa-histidine tag – Residues 555 to 562

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Tel: 800-359-7370 Fax: 703-365-2898