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SUPPORTING INFECTIOUS DISEASE RESEARCH

# Glycoprotein F (+) Fd THS DS-Cav1 from Respiratory Syncytial Virus (RSV) A2, with C-Terminal Histidine Tag, Recombinant from HEK293F Cells

# Catalog No. NR-59413

This reagent is the tangible property of the U.S. Government.

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

### **Contributor:**

Barney Graham, M.D., Ph.D., Deputy Director and Chief, Vaccine Research Center, National Institutes of Health, Bethesda, Maryland, USA

### Manufacturer:

**BEI Resources** 

### **Product Description:**

NR-59413 was produced from an expression vector (BEI Resources NR-55425), encoding Respiratory Syncytial Virus A2 (RSV A2) recombinant prefusion F glycoprotein variant DS-Cav1.<sup>1</sup> The construct consists of synthesized, mammalian codon-optimized RSV F(+) residues 1 to 513 [containing two sets of mutations: S155C AND S290C (DS) and S190F-V207L (Cav1)], a C-terminal T4 fibritin trimerization motif, thrombin cleavage site, hexa-histidine tag, and Strep-tag®II.<sup>1</sup> The RSV F (+) variant is derived from A2 strain (GenPept: <u>P03420</u>) with three naturally occurring substitutions (P102A, I379V and M447V) for enhanced protein expression.<sup>1</sup> The recombinant protein was expressed in human embryonic kidney HEK293F cells and purified by nickel affinity chromatography. The predicted protein sequence is shown in Figure 1. NR-59413 comprises 568 amino acids with a theoretical molecular weight of 63,146 daltons.

### **Material Provided:**

Each vial contains approximately 96 µg of purified recombinant protein in sterile 18 mM Tris-HCI (pH 7.5), 225 mM NaCI and 10% glycerol. The concentration, expressed as mg/mL, is shown on the Certificate of Analysis.

## Packaging/Storage:

Purified recombinant RSV protein was packaged aseptically, in screw-capped plastic cryovials. This product is provided on dry 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: Glycoprotein F (+) Fd THS DS-Cav1 from Respiratory Syncytial Virus (RSV) A2, with C-Terminal Histidine Tag, Recombinant from HEK293F Cells, NR-59413."

### **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. <u>Biosafety in Microbiological and Biomedical Laboratories (BMBL)</u>. 6th ed. Washington, DC: U.S. Government Printing Office, 2020.

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### **References:**

- McLellan, J. S. et al. "Structure-Based Design of a fusion Glycoprotein vaccine for Respiratory Syncytial Virus." <u>Science</u> 342 (2013): 592-598. PubMed: 24179220.
- McLellan, J. S. et al. "Structure of RSV Fusion Glycoprotein Trimer Bound to a Prefusion-Specific Neutralizing Antibody." <u>Science</u> 340 (2013): 1113-11137. PubMed: 23618766.
- McLellan, J. S., W. C. Ray and M. E. Peeples. "Structure and Function of Respiratory Syncytial Virus Surface Glycoproteins." <u>Curr. Top. Microbiol. Immunol.</u> 372 (2013) 83-104. PubMed: 24362685.

E-mail: <u>contact@beiresources.org</u> Tel: 800-359-7370 Fax: 703-365-2898 **b**|**e**|**i** resources

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Figure 1: Predicted Protein Sequence

1	MELLILKANA	ITTILTAVTF	CFASGQNITE	EFYQSTCSAV	SKGYLSALRT	
51	GWYTSVITIE	LSNIKENKCN	GTDAKVKLIK	QELDKYKNAV	TELQLLMQST	
101	PATNNRARRE	LPRFMNYTLN	NAKKTNVTLS	KKRKRRFLGF	LLGVGSAIAS	
151	GVAV <u>C</u> KVLHL	EGEVNKIKSA	LLSTNKAVVS	LSNGVSVLT <u>F</u>	KVLDLKNYID	
201	KQLLPILNKQ	SCSISNIETV	IEFQQKNNRL	LEITREFSVN	AGVTTPVSTY	
251	MLTNSELLSL	INDMPITNDQ	KKLMSNNVQI	VRQQSYSIMC	IIKEEVLAYV	
301	VQLPLYGVID	TPCWKLHTSP	LCTTNTKEGS	NICLTRTDRG	WYCDNAGSVS	
351	FFPQAETCKV	QSNRVFCDTM	NSLTLPSEVN	LCNVDIFNPK	YDCKIMTSKT	
401	DVSSSVITSL	GAIVSCYGKT	KCTASNKNRG	IIKTFSNGCD	YVSNKG <u>V</u> DTV	
451	SVGNTLYYVN	KQEGKSLYVK	GEPIINFYDP	LVFPSDEFDA	SISQVNEKIN	
501	QSLAFIRKSD	<b>ELL</b> SAIGGYI	PEAPRDGQAY	VRKDGEWVLL	STFLGGLVPR	
551	GS <u>HHHHHH</u> SA	WSHPQFEK				
Glycoprotein F (+) Fd THS DS-Cav1 – <b>Residues 1 to 513</b> [represents amino acid residues 1 to 513 (GenPept: <u>P03420</u> )] Plasmid-derived amino acids – Residues 514 to 517, 545 to 546 and 559 to 560 SS TO CC (DS) mutations – <b>Residues <u>155</u></b> and <u>290</u> S190F and V207L mutations (Cav1) – <b>Residues <u>190</u></b> and <u>207</u> Naturally occurring substitutions (P102A, I379V and M447V) – <b>Residues <u>102</u></b> , <u>379</u> and <u>447</u> Trimerization foldon domain - 518 to 544						

Thrombin cleavage site - Residues 547 to 552

Hexa-histidine tag - <u>Residues 553 to 558</u> Strep-tag®II - Residues 561 to 568