

# *MRC PPU Reagents and Services*

## **Standard Operating Procedure**

### **Preparation of Nucleocapsid Protein [1 - 389] Human CoV 229E**

**Enzyme description:-** Human CoV 229E N Protein [1 - 389]

**Clone number:-** DU 67739

**Source:-** Recombinant

**Expression system:-** *E. coli*

**Tag:-** N-terminal MBP

**Purification method:-** Amylose Resin

**Calculated molecular mass:-**

Monoisotopic 87,651.64 daltons

Average Mass 87,705.68 daltons

[cysteines reduced, methionines have not been oxidised]

**Theoretical pI:-** 7.67

**Purity:-** 85 %

**Enzyme storage buffer:-**

50 mM Tris-HCl pH 7.5, 270 mM Sucrose, 150 mM NaCl, 0.1 mM EGTA,  
0.1 % 2-mercaptoethanol, 0.03 % Brij-35

**Storage temperature:-** -70 °C

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## Clone Data Sheet

### Nucleocapsid Protein [1 - 389] Human CoV 229E

**Protein** Human CoV 229E N Protein [1 – 389]

**Clone number** DU 67739

**Accession number** NP\_073556.1

**Tags** N-terminal MBP

**Bacterially  
expressed protein**

MKIEEGKLVIIWINGDKGYNGLAEVGGKFEKDTGIKVTVEHPDKLE  
EKFPQVAATGDGPDIIFWAHDRFGGYAQSGLLAEITPDKAFQDKL  
YPFTWDAVRYNGKLIAYPIAVEALSLIYNKDLLPNPPKTWEEIPA  
LDKELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGGYDIK  
DVGVDNAGAKAGLTFVLVDLIKKNHMNADTDYSIAEAAFNKGETAM  
TINGPWAWSNIDTSKVNYGVTVLPTFKGQPSKPFVGVLSAGINAA  
SPNKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYYEELVKD  
PRIAATMENAQKGEIMPNIPOMSAFWYAVRTAVINAASGRQTVDE  
ALKDAQTNSSNNNNNNNNNNLGDGDDDKVPEFLEVLVLFQGPLGSM  
**TVKWADASEPQRGRQGRIPYSLYSPLLVDSEQPWKVIPRNLPIN**  
**KKDKNKLIQYWNVQKRFRTRKGGKRVDLSPKLHFYYLGTGPHKDAK**  
**FREVEGVVWVAVDGAKTEPTGYGVRKRNSEPEIPHFNQKLPNGV**  
**TVVEEPDSRAPRSQRSRSQSRGRGESKPSRNPSSDRNHNSQDDI**  
**MKAVAAALKSLGFDKPQEKDKKSAKTGTPKPSRNQSPASSQTSK**  
**SLARSQSSETKEQKHEMQKPRWKRQPNDDVTSNVTQCFGPRDLDH**  
**NFGSAGVVANGVKAKGYPQFAELVPSTAAMLFDSHIVSKESGNTV**  
**VLTFTRVTVPKDHPHGLGKFLLELNAFTREMQQHPLLNP SALEFN**  
**PSQTS PATAEPVRDEVSIETDIIDEVN**

**Native sequence** Amino acids M1 – N389 (end).  
Residue M404 of the fusion protein is equivalent to M1 of the native enzyme. The MBP tag is located at residues 1 – 367.

**Protease cleavage** Enterokinase (DDDDK) residues 384 – 388  
PreScission (LEVLVLFQGP) residues 393 – 400