

MRC PPU Reagents and Services

Standard Operating Procedure

Preparation of NSP2 [1 – 638] SARS CoV2

Enzyme description:- NSP2 [1 – 638]

Clone number:- DU 67715

Source:- Recombinant

Expression system:- *E. coli*

Tag:- N-terminal MBP

Purification method:- Amylose resin

Calculated molecular mass:-

Monoisotopic 114,677.11 daltons

Average Mass 114,750.30 daltons

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 5.43

Purity:- 60 %

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

NSP2 [1 – 638] SARS CoV2

Protein NSP2 [1 – 638]

Clone number DU 67715

Accession number QHD43415.1

Tags N-terminal MBP

**Bacterially
expressed protein**

MKIEEGKLVIIWINGDKGYNGLAEVGGKFEKDTGIKVTVEHPDKLE
EKFPQVAATGDGPDIIFWAHDRFGGYAQSGLLAEITPDKAFQDKL
YFFTWDVAVRYNGKLIAYPIAVEALSLIYNKDLLPNPPKTWEEIPA
LDKELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGYDIK
DVGVDNAGAKAGLTFLVDLIKNKHMNADTDYSIAEAAFNKGETAM
TINGPWAWSNIDTSKVNYGVTVLPTFKGQPSKPFVGVLSAGINAA
SPNKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYYEELVKD
PRIAATMENAQKGEIMPNIPOMSAFWYAVRTAVINAASGRQTVDE
ALKDAQTNSSNNNNNNNNNLGDDDDKVPEFLEVLFGQPLGSAY
TRYVDNNFCGPDGYPLECIKDLLARAGKASCTLSEQLDFIDTKRG
VYCCREHEHEIAWYTERSEKSYELQTPFEIKLAKKFDTFNGECPN
FVFPLNSIIKTIQPRVEKKKLDGFMGRIRSVYPVASPNECNQMCL
STLMKCDHCGETSWQTGDFVKATCEFCGTENLTKEGATTCGYLPQ
NAVVKIYCPACHNSEVGPESHSLAEYHNESGLKTI LRKGGRTIAFG
GCVFSYVVGCHNKCAWVPRASANIGCNHTGVVGESEGLNDNLE
ILQKEKVNINIVGDFKLNEEIAIILASFSASTSAFVETVKGLDYK
AFKQIVESCENFKVTGKAKKGAWNIGEOKSILSPLYAFASEAAR
VVRSIFSRTLETAQNSVRVLQKAAITILDGISQYSLRLIDAMMFT
SDLATNNLVVMAYITGGVVQLTSQWLTNIFGTVEKLPVLDWLE
EKFKEGVEFLRDGWEIVKFI STCACEIVGGQIVTCAKEIKESVQT
FFKLVNKFLALCADSIIIGGAKLKALNLGETFVTHSKGLYRKCVK
SREETGLLMPLKAPKEIIFLEGETLPTEVLTEEVVLKTGDLQPLE
OPTSEAVEAPLVGTPVCINGLMLLEIKDTEKYCALAPNMMVTNNT
FTLKGG

Native sequence Amino acids A1 - G638 (end).
Residue A404 of the fusion protein is equivalent to A1 of the native enzyme. The MBP tag is located at residues 1 – 367.

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

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