

MRC PPU Reagents and Services

Standard Operating Procedure

Preparation of NSP5 [1 - 306] SARS CoV2

<u>Enzyme description:-</u>	NSP5 [1- 306]
<u>Clone number:-</u>	DU 67832
<u>Source:-</u>	Recombinant
<u>Expression system:-</u>	<i>E. coli</i>
<u>Tag:-</u>	Both N-terminal GST and C-terminal His6 cleaved
<u>Purification method:-</u>	Cobalt Agarose
<u>Calculated molecular mass:</u>	
Monoisotopic	33, 796.64 daltons [after cleavage of GST and His6 tag]
Average Mass	33, 774.50 daltons [after cleavage of GST and His6 tag] [cysteines reduced, methionines have not been oxidised]
<u>Theoretical pI:-</u>	5.95
<u>Purity:-</u>	90 %
<u>Enzyme storage buffer:-</u>	
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	
<u>Storage temperature:-</u>	-70 °C

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Clone Data Sheet

NSP5 [1 – 306] SARS CoV2

Protein NSP5 [1 - 306]

Clone number DU 67832

Accession number QHD43415.1

Tags N-terminal GST and C-terminal His6 both cleaved

Bacterially expressed protein

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKK
FELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERA
EISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPPEMLKMFED
RLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFK
KRIEAIPOIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLEVL
FQGPLGSSAVLQ**SGFRKMAFPSGKVEGCMVQVTCGTTTTLNGLWLD**
VVYCPRHVICTSEDMLNPNYEDLLIRKSNHNFLVQAGNVQLRVIG
HSMQNCVLKLVDTANPKTPKYKFVRIQPGQTFSVLACYNGSPSG
VYQCAMPNFTTIKGSFLNGSCGSVGFNIDYDCVSFCYMHMELPT
GVHAGTDLEGNFYGPFVDRQTAQAAGTDTTITVNVLAWLYAAVIN
GDRWFLNRFTTTLNDFNLVAMKYNIEPLTQDHVDILGPLSAQTGI
AVLDMCASLKELLQGMNGRTILGSALLEDEFTPFDVVRQCSGVT
FQGPHHHHHH

Native sequence Amino acids S1 – Q306 (end).
Residue S237 of the fusion protein is equivalent to S1 of the native enzyme. The GST tag is located at residues 1 – 220 and the His6 tag is located at residues 545– 550.

Has C-terminal 5' residues of NSP4 (residues 232 – 236) between PreScission site and N-terminus of NSP5 – corresponding to the cleavage site between NSP4 and NSP5 in the polyprotein of the SARS CoV virus to generate an authentic N-terminus during gene expression. The C-terminus encodes for a modified PreScission cleavage site before the His6 tag to generate an authentic C-terminus when cleaved, SGVTFQGP, residues 537 - 544.

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