MRC PPU Reagents and Services

Standard Operating Procedure

Preparation of NSP11 NSP12 [1 - 932] SARS CoV2

Enzyme description:-	NSP11 NSP12 [1 - 932] SARS CoV2
Clone number:-	DU 67736
Source:-	Recombinant
Expression system:-	*E. coli*
Tag:-	N-terminal GST
Purification method:-	GSH Agarose

Calculated molecular mass:-

Monoisotopic	133, 397.72 daltons
Average Mass	133, 484.40 daltons

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:-	6.05
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

MRC PPU Reagents and Services

Clone Data Sheet

NSP11 NSP12 [1 – 932] SARS CoV2

Protein	NSP11 NSP12 [1 - 932]
Clone number	DU 67736
Accession number	QHD43415.1
Tags	N-terminal GST
Bacterially expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKK FELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERA EISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFED RLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFK KRIEAIPQIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLEVLF QGPLGS**SADAQSFLNRVCGVSAARLTPCGTGTSTDVVYRAFDIYN** **DKVAGFAKFLKTNCCRFQEKDEDDNLIDSYFVVKRHTFSNYQHEE** **TIYNLLKDCPAVAKHDFFKFRIDGDMVPHISRQRLTKYTMADLVY** **ALRHFDEGNCDTLKEILVTYNCCDDDYFNKKDWYDFVENPDILRV** **YANLGERVRQALLKTVQFCDAMRNAGIVGVLTLDNQDLNGNWYDF** **GDFIQTTPGSGVPVVDSYYSLLMPILTLTRALTAESHVDTDLTKP** **YIKWDLLKYDFTEERLKLFDRYFKYWDQTYHPNCVNCLDDRCILH** **CANFNVLFSTVFPPTSFGPLVRKIFVDGVPFVVSTGYHFRELGVV** **HNQDVNLHSSRLSFKELLVYAADPAMHAASGNLLLDKRTTCFSVA** **ALTNNVAFQTVKPGNFNKDFYDFAVSKGFFKEGSSVELKHFFFAQ** **DGNAAISDYDYYRYNLPTMCDIRQLLFVVEVVDKYFDCYDGGCIN** **ANQVIVNNLDKSAGFPFNKWGKARLYYDSMSYEDQDALFAYTKRN** **VIPTITQMNLKYAISAKNRARTVAGVSICSTMTNRQFHQKLLKSI** **AATRGATVVIGTSKFYGGWHNMLKTVYSDVENPHLMGWDYPKCDR** **AMPNMLRIMASLVLARKHTTCCSLSHRFYRLANECAQVLSEMVMC** **GGSLYVKPGGTSSGDATTAYANSVFNICQAVTANVNALLSTDGNK** **IADKYVRNLQHRLYECLYRNRDVDTDFVNEFYAYLRKHFSMMILS** **DDAVVCFNSTYASQGLVASIKNFKSVLYYQNNVFMSEAKCWTETD** **LTKGPHEFCSQHTMLVKQGDDYVYLPYPDPSRILGAGCFVDDIVK** **TDGTLMIERFVSLAIDAYPLTKHPNQEYADVFHLYLQYIRKLHDE** **LTGHMLDMYSVMLTNDNTSRYWEPEFYEAMYTPHTVLQ**
Native sequence	Amino acids S1 – Q932 (end). Residue S232 of the fusion protein is equivalent to S1 of the native enzyme. The GST tag is located at residues 1 – 220.

Protease cleavage PreScission (LEVLFQGP) residues 221 – 228