MRC PPU Reagents and Services

Standard Operating Procedure

Preparation of Spike Protein [1 – 1255] SARS CoV

Enzyme description:-	SARS S Protein [1 - 1255]
Clone number:-	DU 67727
Source:-	Recombinant
Expression system:-	*E. coli*
Tag:-	N-terminal GST
Purification method:-	GSH Agarose

Calculated molecular mass:-

Monoisotopic	165, 875.35	daltons
Average Mass	165, 982.16	daltons

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:-	5.46
Purity:-	50 %

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

Spike Protein [1 – 1255] SARS CoV

Protein SARS S Protein [1 - 1255]

Clone number DU 67727

Accession number AAX16192.1

Tags N-terminal GST

Bacterially expressed protein

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKK
FELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERA
EISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFED
RLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFK
KRIEAIPQIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLEVLF
QGPLGS**MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRG**
VYYPDEIFRSDTLYLTQDLFLPFYSNVTGFHTINHTFDNPVIPFK
DGIYFAATEKSNVVRGWVFGSTMNNKSQSVIIINNSTNVVIRACN
FELCDNPFFAVSKPMGTQTHTMIFDNAFNCTFEYISDAFSLDVSE
KSGNFKHLREFVFKNKDGFLYVYKGYQPIDVVRDLPSGFNTLKPI
FKLPLGINITNFRAILTAFSPAQDTWGTSAAAYFVGYLKPTTFML
KYDENGTITDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVP
SGDVVRFPNITNLCPFGEVFNATKFPSVYAWERKKISNCVADYSV
LYNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAP
GQTGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYKYRYLR
HGKLRPFERDISNVPFSPDGKPCTPPALNCYWPLNDYGFYTTTGI
GYQPYRVVVLSFELLNAPATVCGPKLSTDLIKNQCVNFNFNGLTG
TGVLTPSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDISPCSFG
GVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYST
GNNVFQTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSLLRST
SQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMA
KTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRN
TREVFAQVKQMYKTPTLKDFGGFNFSQILPDPLKPTKRSFIEDLL
FNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTD
DMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVT
QNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQ
ALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQ
SLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGY
HLMSFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEGKAYFPRE
GVFVFNGTSWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNTV
YDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQEE
IDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAI

VMVTILLCCMTSCCSCLKGACSCGSCCKFDEDDSEPVFKGVKLHY
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Native sequence	Amino acids M1 – T1255 (end). Residue M232 of the fusion protein is equivalent to M1 of the native enzyme. The GST tag is located at residues 1 – 220.
Protease cleavage	PreScission (LEVLFQGP) residues 221 – 228