MRC PPU Reagents and Services

Standard Operating Procedure

Preparation of Spike Protein [1 – 1353] MERS CoV

Enzyme description:-	MERS S Protein [1 - 1353]
Clone number:-	DU 67745
Source:-	Recombinant
Expression system:-	*E. coli*
Tag:-	N-terminal GST
Purification method:-	GSH Agarose

Calculated molecular mass:-

Monoisotopic	176, 107.10 daltons
Average Mass	176, 220.26 daltons

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:-	5.75
Purity:-	65 %

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

Spike Protein [1 – 1353] MERS CoV

Protein MERS S Protein [1 - 1353]

Clone number DU 67745

Accession number AHI48572.1

Tags N-terminal GST

Bacterially expressed protein

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKK
FELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERA
EISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFED
RLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFK
KRIEAIPQIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLEVLF
QGPLGS**MIHSVFLLMFLLTPTESYVDVGPDSVKSACIEVDIQQTF**
FDKTWPRPIDVSKADGIIYPQGRTYSNITITYQGLFPYQGDHGDM
YVYSAGHATGTTPQKLFVANYSQDVKQFANGFVVRIGAAANSTGT
VIISPSTSATIRKIYPAFMLGSSVGNFSDGKMGRFFNHTLVLLPD
GCGTLLRAFYCILEPRSGNHCPAGNSYTSFATYHTPATDCSDGNY
NRNASLNSFKEYFNLRNCTFMYTYNITEDEILEWFGITQTAQGVH
LFSSRYVDLYGGNMFQFATLPVYDTIKYYSIIPHSIRSIQSDRKA
WAAFYVYKLQPLTFLLDFSVDGYIRRAIDCGFNDLSQLHCSYESF
DVESGVYSVSSFEAKPSGSVVEQAEGVECDFSPLLSGTPPQVYNF
KRLVFTNCNYNLTKLLSLFSVNDFTCSQISPAAIASNCYSSLILD
YFSYPLSMKSDLSVSSAGPISQFNYKQSFSNPTCLILATVPHNLT
TITKPLKYSYINKCSRLLSDDRTEVPQLVNANQYSPCVSIVPSTV
WEDGDYYRKQLSPLEGGGWLVASGSTVAMTEQLQMGFGITVQYGT
DTNSVCPKLEFANDTKIASQLGNCVEYSLYGVSGRGVFQNCTAVG
VRQQRFVYDAYQNLVGYYSDDGNYYCLRACVSVPVSVIYDKETKT
HATLFGSVACEHISSTMSQYSRSTRSMLKRRDSTYGPLQTPVGCV
LGLVNSSLFVEDCKLPLGQSLCALPDTPSTLTPRSVRSVPGEMRL
ASIAFNHPIQVDQLNSSYFKLSIPTNFSFGVTQEYIQTTIQKVTV
DCKQYVCNGFQKCEQLLREYGQFCSKINQALHGANLRQDDSVRNL
FASVKSSQSSPIIPGFGGDFNLTLLEPVSISTGSRSARSAIEDLL
FDKVTIADPGYMQGYDDCMQQGPASARDLICAQYVAGYKVLPPLM
DVNMEAAYTSSLLGSIAGVGWTAGLSSFAAIPFAQSIFYRLNGVG
ITQQVLSENQKLIANKFNQALGAMQTGFTTTNEAFRKVQDAVNNN
AQALSKLASELSNTFGAISASIGDIIQRLDVLEQDAQIDRLINGR
LTTLNAFVAQQLVRSESAALSAQLAKDKVNECVKAQSKRSGFCGQ
GTHIVSFVVNAPNGLYFMHVGYYPSNHIEVVSAYGLCDAANPTNC
IAPVNGYFIKTNNTRIVDEWSYTGSSFYAPEPITSLNTKYVAPQV

TYQNISTNLPPPLLGNSTGIDFQDELDEFFKNVSTSIPNFGSLTQ
INTTLLDLTYEMLSLQQVVKALNESYIDLKELGNYTYYNKWPWYI
WLGFIAGLVALALCVFFILCCTGCGTNCMGKLKCNRCCDRYEEYD
LEPHKVHVH

Native sequence	Amino acids M1 – H1353 (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