

## HA (Y98F)(A/Guangdong-Maonan/SWL1536/2019)(H1N1)

CATALOG NUMBER: IA-H1-GM19WPm, 50 µg, 1 mg

<b>Introduction</b>	Influenza hemagglutinin (HA) is a type of hemagglutinin found on the surface of the influenza viruses. HA is an antigenic glycoprotein, like all other hemagglutinins, it causes red blood cells to agglutinate. HA is responsible for binding the virus to the cell that is being infected. HA proteins bind to cells with sialic acid on the membranes, such as cells in the upper respiratory tract or erythrocytes.  HA is a homotrimeric integral membrane glycoprotein. HA monomer is synthesized as a single polypeptide that is subsequently cleaved into two smaller polypeptides, the HA1 and HA2 subunits. Each HA monomer consists of a long, helical chain anchored in the membrane by HA2 and topped by a large HA1 globule.
<b>Description</b>	Recombinant hemagglutinin protein expressed and purified from 293 cell culture
<b>Viral Protein</b>	Recombinant hemagglutinin (aa 18-530)(A/Guangdong-Maonan/SWL1536/2019/H1N1)-pdm09-like produced in human 293 cells is a glycosylated polypeptide chain with amino acid change of Y98F, and having a C-terminal 6x his tag and an N-terminal c-Myc tag (GISAID accession#: EPI1542570)
<b>Applications</b>	Western blot standard, antibody ELISA, antigen, etc.
<b>Storage</b>	Store at -20 °C; Stable for 6-months from the date of shipment when kept at 4 °C. Non-hazardous. No MSDS required.
<b>Concentration</b>	1 µg/µl in PBS
<b>Endotoxin Level</b>	<0.01 EU per 1 µg of the protein by LAL test
<b>Purity</b>	>95% pure by 12% SDS PAGE gel



**SDS-PAGE:** purified HA (Y98F)(aa 18-530)(A/Guangdong-Maonan/SWL1536/2019/H1N1)

### HA (Y98F)(aa 18-530)(A/Guangdong-Maonan/SWL1536/2019/H1N1) Seq:

[EQKLISEEDL](#)DTLCLIGYHANNSTDTVDTVLEKNVTVTHSVNLLLEDKHNGKLCCKLRGVAPLHLGKCNITAGWILGNPECESLSTARSWSYIVETSNSDNGT  
CYPGDFINFEELREQLSSVSSFERFEIFPKTSSWPNHSDKGVTAACPHAGAKSFYKNLIWLVKKGNSTYPKLNQTYINDKKGKVLVLWGIHHPPTIAAQ  
ESLYQNADAYVFGTSRYSKKFKPEIATRPKVRDQEGRMNYYWTLVEPGDKITFEATGNLVVPRYAFTMERDAGSGIIISDTPVHDCNTTCQTPEGAIN  
TSLPFQNVHPITIGKCPKYVKSTKLRLATGLRNVPSIQSRGLFGAIAAGFIEGGWTGMVDGWYGYHHQNEQGSYAADLKSTQNAIDKITNKVNSVIEKM  
NTQFTAVGKEFNHLEKRIENLNKKVDDGFLDIWTYNAELLVLENERLTDYHDSNVKNLYEKVRNQLKNNAKEIGNGCFEFYHKCDNTCMESVKNGTYD  
YPKYSEEAKLNREKIDGVKLESTRIYQIHSHHHHH