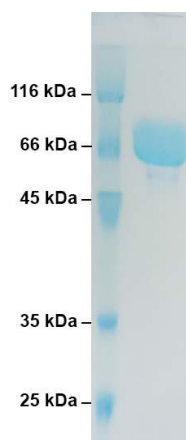


## HA (A/Guangdong-Maonan/SWL1536/2019)(H1N1)-pdm09-like virus

CATALOG NUMBER: IA-H1-GM19WP, 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 purified from 293 cell culture
<b>Viral Protein</b>	C-terminal 6xHis tagged HA (amino acid 18-530) (H1N1)(A/Guangdong-Maonan/SWL1536/2019)-pdm09-like virus protein (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 (A/Guangdong-Maonan/SWL1536/2019)(H1N1) protein

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

DTLTCIGYHANNSTDVDTVLEKNVTVTHSVNLLLEDKHNGKLCCKLRGVAPLHLGKCNIAGWILGNPECESLSTARSWSYIVETSNSDNGTCYPGDFINYE  
ELREQLSSVSSFERFEIIFPKTSSWPNHSDSKGVTAACPHAGAKSFYKNLIWLVKKNSYPKLNQTYINDKGKEVLVLWGIHHPPTIAAQESLYQNADAY  
VFGVTSRYSKFKPEIATRPKVRDQEGRMNYYWTLVEPGDKITFEATGNLVVPRYAFTMERDAGSGIIISDTPVHDCNTTCQTPEGAINNTSLPFQNVHP  
ITIGKCPKYVKSTKLRRLATGLRNVPSIQSRGLFGAIAAGFIEGGWTGMVDGWYGYHHQNEQGSYAADLKSTQNAIDKITNKVNSVIEKMNTQFTAVGKE  
FNHLEKRIENLNKKVDDGFLDIWTYNAELLVLENERTLDYHDSNVKNLYEKVRNQLKNNAKEIGNGCFEFYHKCDNTCMESVKNGTYDYPKYSEEAKL  
NREKIDGVKLESTRIYQIHSHHHH