Spike S1(D614G) Protein (SARS-CoV-2/COVID-19)

CATALOG NUMBER: SCV2-S1-614G, 50 µg

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Introduction	The novel coronavirus (SARS-CoV-2), previously called 2019-nCoV, is a newly identified coronavirus causing the ongoing outbreak of atypical pneumonia in Wuhan China from late 2019.
	The genome of SARS-CoV-2 has 89% nucleotide identity with bat SARS-like-CoVZXC21 and 82% with that of human SARS-CoV. The phylogenetic trees of their orf1a/b, Spike, Envelope, Membrane and Nucleocapsid protein also clustered closely with those of the bat, civet and human SARS coronaviruses. However, the external subdomain of Spike's receptor binding domain (RBD) of SARS-CoV-2 shares only 40% amino acid identity with other SARS-related coronaviruses.
Applications	Western blot standard, antibody ELISA, antigen, etc.
Description	Recombinant spike S1(D614G) protein of SARS-CoV-2 purified from 293 cells
Viral Protein	S1(D614G) protein (amino acid 16-685) of human SARS-CoV-2 (GenBank Accession No. YP_009724390.1) with a C-terminal poly his-tag
Storage	Store at -20 ºC; Stable for 6-months from the date of shipment when kept at 4 ºC. Non-hazardous, no MSDS required.
Concentration	50 µg in PBS, pH7.4
Endotoxin Level	<0.01 EU per 1 µg of the protein by LAL test
Purity	≥ 95% (by SDS PAGE)
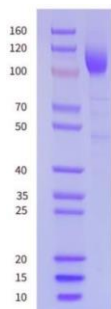
SDS-PAGE: purified spike S1 (D614G) protein (SARS-CoV-2/COVID-19)

S1 (D614G) Protein (aa 16-685)(SARS-CoV-2/COVID-19) SEQ:

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VNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKT
QSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLV
RDLPQGFSALEPLVDLPIGINITRFQTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGI
YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVRQIA
PGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRV
VVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVA
VLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRAR*HHHHHHH*
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