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Lieferung & Zahlungsart

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Zuschläge

- Mindermengenzuschlag
- Trockeneiszuschlag
- Gefahrgutzuschlag
- Expressversand

SZABO-SCANDIC HandelsgmbH

Quellenstraße 110, A-1100 Wien

T. +43(0)1 489 3961-0

F. +43(0)1 489 3961-7

mail@szabo-scandic.com

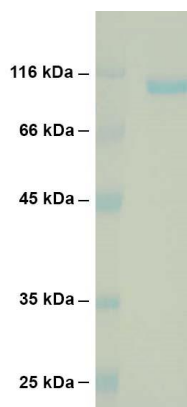
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Spike S1 Protein (SARS-CoV-2/COVID-19)

CATALOG NUMBER: SCV2-S1-150P, 50 µg, 1 mg

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 (RCB) 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 protein of SARS-CoV-2 purified from 293 cells
Viral Protein	S1 protein (amino acid 19-676) of human SARS-CoV-2 (GenBank Accession No. MN908947) with a C-terminal poly his-tag
Storage	Store at -20 °C; Stable for 6-months from the date of shipment when kept at 4 °C. Non-hazardous, no MSDS required.
Concentration	1 µg/µl 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 protein (SARS-CoV-2/COVID-19)

S1 Protein (aa 19-676)(SARS-CoV-2/COVID-19) SEQ:

TTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSL
LIVNNATNVVIKVCEFFQFCNDPFLGVYHKNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDL
PQGFSALEPLVDLPIGINITRFQTLALLHRSYLT PGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGIYQT
SNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFKCYGVSPTKLNLDLCTNVYADSFVIRGDEVRQIAPGQ
TGKIADYNYKLPDDFTGCVIAWNSNLDKSKVGGNYNYLYRFRKSNLKPFERDISTEYIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVVL
SFELHAPATVCGPKKSTNLVKNKCVNFNENGLTGTGVLTESNKKFLPFQQFGRDIADTPTDAVRDPQTLLEILDITPCSFGGVSVITPGTNTSNQVAVLY
QDVNCTEVPVAIHADQLTPTWRVYSTGNSVNFQTRAGCLIGAEHVNNSEYCDIPIGAGICASYQT **HHHHHH**