

COVID 19 Spike protein, Delta B.1.617.2 variant Coronavirus Recombinant Protein | COVID-19 recombinant protein

Recombinant SARS-CoV-2 Spike protein, Delta B.1.617.2 variant (Indian variant, T19R, G142D, EF156-157del, R158G, L452R, T478K, D614G, P681R and D950N)

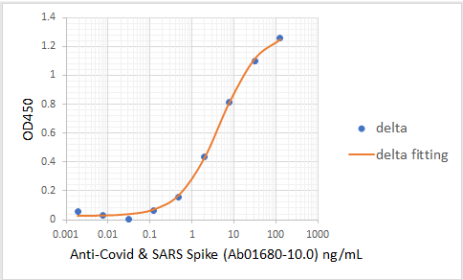
CATALOG # AAA47146	HOST HEK293 Cells	APPLICATIONS IA (Immunoassay)
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PRODUCT SYNONYMS

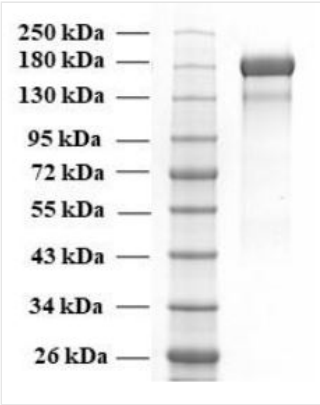
COVID 19 Spike protein; Delta B.1.617.2 variant Coronavirus; Recombinant SARS-CoV-2 Spike protein; Delta B.1.617.2 variant (Indian variant; T19R; G142D; EF156-157del; R158G; L452R; T478K; D614G; P681R and D950N); 2019 Novel Coronavirus; Coronavirus; CoV; COVID-19 virus; HCoV-2; Human Coronavirus 2019; SARS2; SARS-CoV-2; Severe acute respiratory syndrome coronavirus 2; B.1.617.2 Variant of Concern; India mutant; Indian variant; P681R; D950N; Indian mutant Spike glycoprotein; Delta Variant of Concern S protein.; COVID-19 recombinant protein

PRODUCT SPECIFICATIONS

Host	HEK293 Cells
Purity/Purification	Affinity chromatography, >90% as estimated by SDS-PAGE
Form/Format	Liquid; PBS 20% Glycerol
Sequence Positions	16-1211
Sequence	VNLRTRTQLP PAYTNSFTRG VYYPDKVFRS SVLHSTQDLF LPFFSNVTWF HAIHVSGTNG TKRFDNPVLP FNDGVYFAST EKSNIIRGWI FGTTLDSTQ SLLIVNNATN VVIKVECFQF CNDPFLDYH KNNKSWMESG VYSSANNCTF EYVSQPFLMD LEGKQGNFKN LREFVFNID GYFKIYSKHT PINLVRDLPQ GFSALEPLVD LPIGINITRF QTLALHRSY LTPGDSSSGW TAGAAAYYVG YLQPTFLKY NENGITDAV DCALDPLSET KCTLKSFTVE KGIYQTSNFR VQPTESIVRF PNITNLCPFG EVFNATRFAS VYAWNRRKRIS NCVADYSVLY NSASFSTFKC YGVSPTKLND LCFTNVYADS FIRGDEVRFQI APGQTGKIAD YNYKLPDDFT GCVIAWNSNN LDSKVGNGYN YRYRLFRKSN LKPFERDIST EIYQAGSKPC NGVEGFNCYF PLQSYGFQPT NGVGYQPYRV VVLSEFLLHA PATVCGPKST NLVKNKCVNF NFNGLTGTGV LTESNKKFLP FQQFGRDIAD TDAVRDPQT LEILDITPCS FGGVSITPG TNSNQVAVL YQGVNCTEVP VAIHADQLTP TWRVYSTGSN VFQTRAGCLI GAEHVNSYEC DIPIGAGICA SYQTQNSRR GAGSVASQSI IAYTMSLGAE NSVAYSNNNSI AIPTNFTISV TTEILPVSM TKSVDCTMYI CGDSTECSNL LLQYGSFCTQ LNRALTGIIV EQDKNTQEVF AQKQIYKTPP IKDFGGFNFS QILPDPSKPS KRSPIEDLLF NKVTLADAGF IKQYGDCLGD IAARDLCAQ KFNGLTVLPP LLTDEIAQY TSALLAGTIT SGWTFGAGPA LQIPFPMQMA YRFNGIGVTN VLYENQKLI A NQFNSAIGKI QDLSSTPSA LGKLQNVVNQ NAQALNTLVK QLSNFGAIS SVLNDILSRL DPPEAEVQID RLITGRLQSL QTYVTQQLIR AAEIRASANL AATKMSECVL GQSKRVFCGK GYHLSMFPQS APHGVLVHV TYVPAQEKNF TTAPAICHDG KAHFPREGVF VSNHTWVFVT QRNFYEPQII TTDNTFVSGN CDVVIGIVNN TVYDPLQPEL DSFKEELDKY FKNHTSPDVD LGDSGINASV VNIQKEIDRL NEVAKNLNES LIDLQELGKY EQYIKGSGSG YIPEAPRDGQ AYVRKDGWV LLSTFLGSGH HHHHHHHH
Applicable Applications for COVID-19 recombinant protein	IA (Immunoassay)
Species	Severe Acute Respiratory Syndrome Coronavirus 2
Amount Sent	0.27 ml of 0.45 mg/ml by A280 absorbance=120 ug (lot specific)
Tag	8xHis at the C terminus.
Endotoxin	Less than 0.1 ng/ug (1 IEU/ug), as measured by LAL method.
Dry Ice Note	The product may be shipped with dry ice, and an additional fee may be added to your shipping cost.
Preparation and Storage	The protein can be stored at 2-8°C for 1 month. For long term, it should be stored at -20°C to -70°C preferably in small aliquots to avoid repeated freeze-thaw cycles.



Functional Data
Binding curve of anti-Cov-19&SARS S glycoprotein antibody IgG CR3022 to the trimeric Spike B.1.617.2, Delta variant.



SDS-PAGE
>90% as estimated by SDS-PAGE stained with Instant Blue Stain (Abcam).

ADDITIONAL INFORMATION

Related Product Information for COVID-19 recombinant protein	Full-length soluble with foldon trimerization motif, mutated Furin recognition site and 6 stabilising mutations (F817P, A892P, A899P, A942P, K986P and V987P), based on/modified from Amanat et al, 2020 and Hsieh et al, 2020. The first reports of atypical pneumonia in China were announced at the very end of 2019, in the city of Wuhan, Hubei province. Its cause was identified in January 2020 as a novel ?-CoV (1), named SARS-CoV-2, which started spreading very quickly causing a global pandemic COVID-19. Spike protein attaches the virion to the cell membrane by interacting with host receptor, initiating the infection. Binding to human ACE2 receptor and internalization of the virus into the endosomes of the host cell induces conformational changes in the Spike glycoprotein (2, 3). The protein forms a trimer in vivo mediating receptor binding and membrane fusion (4). It has been demonstrated by Florian Krammer's group that certain mutations and the inclusion of trimerization motif can stabilize recombinant Spike protein (5, 6). The original Wuhan strain of the virus has become quickly replaced by its more transmissible variant, mainly determined by a single amino acid point mutation D614G (7). A novel SARS-CoV-2 variant, B.1.617, known as Indian variant, originated in India and quickly became dominant (8,9).
References	1. Zhu N., Zhang D., Wang W., et al. China Novel Coronavirus Investigating and Research Team. A novel coronavirus from patients with pneumonia in China, 2019. N Engl J Med., 2020;382:727–733. 2. Hoffmann M., Kleine-Weber H., Schroeder S., et al. SARS-CoV-2 Cell Entry Depends on ACE2 and TMPRSS2 and Is Blocked by a Clinically Proven Protease Inhibitor. Cell, 2020;181(2):271-280. 3. Wrapp D., Wang N., Corbett KS., et al. Cryo-EM structure of the 2019-nCoV spike in the prefusion conformation. Science, 2020;367(6483):1260-1263. 4. Yin HS., Wen X., Paterson RG., Lamb RA., Jardetzky TS. Structure of the parainfluenza virus 5 F protein in its metastable, prefusion conformation. Nature, 2006;439(7072):38-44. 5. Amanat, F., Stadlbauer, D., Strohmeier, S., et al. A serological assay to detect SARS-CoV-2 seroconversion in humans. Nat Med., 2020;26:1033–1036. 6. Stadlbauer, D., Amanat, F., Chromikova, V., et al. SARS-CoV-2 seroconversion in humans: A detailed protocol for a serological assay, antigen production, and test setup. Current Protocols in Microbiology, 2020;57, e100. 7. Korber, B., Fischer, W., Gnanakaran, S., et al. Tracking Changes in SARS-CoV-2 Spike: Evidence that D614G Increases Infectivity of the COVID-19 Virus. Cell, 2020;182:1-16. 8. Tegally, H., Wilkinson, E., Giovanetti, M., et al. Emergence and rapid spread of a new severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2) lineage with multiple Spike mutations in South Africa. MedRxiv, 21.12.2020;182:1-16.

NCBI AND UNIPROT INFORMATION

UniProt Accession #	P0DTC2
Molecular Weight	Predicted Molecular Weight: 137 kDa Estimated Molecular Weight, SDS-PAGE: ≈190 kDa

For Research Use Only. Not for use in diagnostic or therapeutic procedures. Small volumes of product may become entrapped in the seal of the vial during shipment and storage; if necessary, briefly centrifuge the vial on a tabletop centrifuge to dislodge any liquid in the cap.

