Datasheet

Cat. No. P1602

Recombinant SARS-CoV-2 Spike RBD Fc Chimera, Insect Cells Derived

Information

Gene ID	
Accession #	
Alternate Names	
Source	Insect Cell
M.Wt	Approximately 52.3 kDa as predicted, containing 465 amino acids. On SDS-PAGE, 54 kDa under reducing conditions, and 101.5 kDa as homodimer under non-reducing conditions.
AA Sequence	AGMGRVQPTE SIVRFPNITN LCPFGEVFNA TRFASVYAWN RKRISNCVAD YSVLYNSASF STFKCYGVSP TKLNDLCFTN VYADSFVIRG DEVRQIAPGQ TGKIADYNYK LPDDFTGCVI AWNSNNLDSK VGGNYNYLYR LFRKSNLKPF ERDISTEIYQ AGSTPCNGVE GFNCYFPLQS YGFQPTNGVG YQPYRVVVLS FELLHAPATV CGPKKSTNLV KNKCVNFIEG RMDEPKSSDK THTCPPCPAP EFEGAPSVFL FPPKPKDTLM ISRTPEVTCV VVDVSHEDPE VKFNWYVDGV EVHNAKTKPR EEQYNSTYRV VSVLTVLHQD WLNGKEYKCK VSNKALPTPI EKTISKAKGQ PREPQVYTLP PSRDELTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG SFFLYSKLTV DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS LSPGK
Appearance	White lyophilized (freeze-dried) powder.
Stability & Storage	Use a manual defrost freezer and avoid repeated freeze-thaw cycles - 12 months from date of receipt, -20 to -70 °C as supplied - 1 month, 2 to 8 °C under sterile conditions after reconstitution - 3 months, -20 to -70 °C under sterile conditions after reconstitution
Formulation	Lyophilized from a 0.2 μm filtered concentrated solution in PBS, pH 7.0, 5 % Trehalose.
Reconstitution	We recommend that this vial is briefly centrifuged prior to opening to bring the contents to the bottom. Reconstitute in PBS to a concentration of 0.1-1.0 mg/mL. Stock solutions should be apportioned into working aliquots and stored at ⩽ -20 °C. Further dilutions should be made in appropriate buffered solutions.
Biological Activity	Testing in progress.
Shipping Condition	Gel pack.
Handling	Centrifuge the vial prior to opening.
Usage	For Research Use Only! Not to be used in humans.

Components and Storage

	100μg

Components	
Recombinant SARS-CoV-2 Spike RBD Fc Chimera, Insect Cells Derived	100μg
Use a manual defrost freezer and avoid repeated freeze-thaw cycles - 12 months from date of receipt, -20 to -70 °C as supplied - 1 month, 2 to 8 °C under sterile conditions after reconstitution - 3 months, -20 to -70 °C under sterile conditions after reconstitution	

Quality Control

Purity	> 90% by SDS-PAGE.
Endotoxin	Less than 0.1 EU/μg of rSARS-CoV-2 Spike RBD-Fc as determined by LAL method.

Description

SARS-CoV-2, which causes the global pandemic coronavirus disease 2019 (Covid-19), belongs to a family of viruses known as coronaviruses that are commonly comprised of four structural proteins: Spike protein(S), Envelope protein (E), Membrane protein (M), and Nucleocapsid protein (N). SARS-CoV-2 Spike Protein (S Protein) is a glycoprotein that mediates membrane fusion and viral entry. The S protein is homotrimeric, with each ~180-kDa monomer consisting of two subunits, S1 and S2. In SARS-CoV-2, as with most coronaviruses, proteolytic cleavage of the S protein into two distinct peptides, S1 and S2 subunits, is required for activation. The S1 subunit is focused on attachment of the protein to the host receptor while the S2 subunit is involved with cell fusion. Based on structural biology studies, the receptor binding domain (RBD), located in the C-terminal region of S1, can be oriented either in the up/standing or down/lying state. The standing state is associated with higher pathogenicity and both SARS-CoV-1 and MERS can access this state due to the flexibility in their respective RBDs. A similar two-state structure and flexibility is found in the SARS-CoV-2 RBD. Based on amino acid (aa) sequence homology, the SARS-CoV-2 S1 subunit RBD has 73% identity with the RBD of the SARS-CoV-1 S1 RBD, but only 22% homology with the MERS S1 RBD. The low aa sequence homology is consistent with the finding that SARS and MERS bind different cellular receptors. The S Protein of the SARS-CoV-2 virus, like the SARS-CoV-1 counterpart, binds Angiotensin-Converting Enzyme 2 (ACE2), but with much higher affinity and faster binding kinetics. Before binding to the ACE2 receptor, structural analysis of the S1 trimer shows that only one of the three RBD domains in the trimeric structure is in the "up" conformation. This is an unstable and transient state that passes between trimeric subunits but is nevertheless an exposed state to be targeted for neutralizing antibody therapy. Polyclonal antibodies to the RBD of the SARS-CoV-2 protein have been shown to inhibit interaction with the ACE2 receptor, confirming RBD as an attractive target for vaccinations or antiviral therapy. There is also promising work showing that the RBD may be used to detect presence of neutralizing antibodies present in a patient's bloodstream, consistent with developed immunity after exposure to the SARS-CoV-2 virus. Lastly, it has been demonstrated the S Protein can invade host cells through the CD147/EMMPRIN receptor and mediate membrane fusion.

Reference

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