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SARS-CoV-2 Spike (trimeric) (16-1208) Recombinant Protein (8xHis-Tag)

100 µg



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Applications: SEC	MW (kDa): 136 (reduced and non-reduced)	UniProt ID: #P0DTC2	Entrez-Gene Id: 43740568	
Description		SARS-CoV-2 Spike (trimeric) (16-1208) Recombinant Protein (8xHis-Tag) is derived from a recombinant expression construct designed to generate a trimeric, cleavage-resistant variant of the SARS-CoV-2 spike protein ectodomain. The S1/S2 polybasic cleavage site (R685/S686) has been removed by substituting RRAR (R682-R685) with the non-cleavable sequence GSAS. An additional mutation (K986P/V987P) was introduced by site-directed mutagenesis, designed to constrain the coronavirus spike proteins to a pre-fusion configuration (10). Additional sequence corresponding to the foldon domain of bacteriophage T4 fibritin was introduced to the carboxy terminal region to promote trimerization of the expressed protein. The expressed protein also contains an 8xHis-Tag at its carboxy terminus.		
Formulation		Expression Host: Hamste Supplied in a PBS solutio	er (ExpiCHO cells) on (pH 7.2).	
Storage	:	Stable at -80°C for 3 years after receipt. Avoid repeated freeze-thaw cycles.		
Purity	:	>/=94%, determined by SDS-PAGE.		
Background		The cause of the COVID-19 pandemic is a novel and highly pathogenic coronavirus, termed SARS-CoV-2 (severe acute respiratory syndrome coronavirus-2). SARS-CoV-2 is a member of the Coronaviridae family of viruses (1). The genome of SARS-CoV-2 is similar to other coronaviruses, and is comprised of four key structural proteins: S, the spike protein, E, the envelope protein, M, the membrane protein, and N, the nucleocapsid protein (2). Coronavirus spike proteins are class I fusion proteins and harbor an ectodomain, a transmembrane domain, and an intracellular tail (3,4). The highly glycosylated ectodomain projects from the viral envelope surface and facilitates attachment and fusion with the host cell plasma membrane. The ectodomain can be further subdivided into host receptor-binding domain (RBD) (S1) and membrane-fusion (S2) subunits, which are produced upon proteolysis by host proteases at S1/S2 and S2' sites. S1 and S2 subunits remain associated after cleavage and assemble into crown-like homotrimers (2,4). In humans, both SARS-CoV and SARS-CoV-2 spike proteins utilize the angiotensin-converting enzyme 2 (ACE2) protein as a receptor for cellular entry (5-7). Spike protein subunits represent a key antigenic feature of coronavirus virions, and therefore represent an important target of vaccines, novel therapeutic antibodies, and small-molecule inhibitors (8,9).		
Background Re	ferences	1. Zhou, P. et al. (2020) A 2. Tortorici, M.A. and Vee 3. Li, F. et al. (2006) <i>J Virc</i> 4. Li, F. (2016) <i>Annu Rev</i> 5. Shang, J. et al. (2020) <i>J</i> 6. Wrapp, D. et al. (2020) 7. Yan, R. et al. (2020) <i>Sc</i> 8. Yuan, Y. et al. (2017) A 9. Amanat, F. and Kramn 10. Pallesen, J. et al. (201	Vature 579, 270-3. esler, D. (2019) Adv Virus Res 105, 93-116. b/ 80, 6794-800. Virol 3, 237-61. Nature 581, 221-4. o Science 367, 1260-3. ience 367, 1444-8. Vat Commun 8, 15092. mer, F. (2020) Immunity 52, 583-9.	
Applications Ke	ey :	SEC: SEC		
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