

SARS-CoV-2 Spike S1 protein

Receptor binding domain (RBD) (Omicron Variant B.1.1.529 BA.1)

Cat. no. P2020-061

Product Information

Protein:	SARS-CoV-2 S1 (RBD) (Omicron Variant B.1.1.529 BA.1), GFP/His-tag (cleavable) (~ 54.0 kDa)
Uniprot#:	PODTC2
Sequence:	MRVQPTESIVRFPNITNLCPF <u>D</u> EVFNATRFASVYAWNRKRISNVCVADYSVLYNL <u>A</u> PFETF KCYGVSPTKLNLDLCFTNYYADSFVIRGDEVQRQIAPGQTG <u>N</u> IADYNYKLPDDFTGCVIAWN SN <u>K</u> LDSKVS <u>G</u> NYNYLYRFLFRKSNLKPFERDISTEIQAG <u>N</u> KPCNGV <u>A</u> GFCYFPLRSY <u>S</u> F <u>R</u> PT <u>Y</u> GVG <u>H</u> QPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
	Methionine at pos. 1 present due to cloning constraints, C-terminal His-tag and GFP-fusion not shown in sequence. <u>X</u> indicates mutation sites.
Source:	Recombinantly expressed in HEK293 cells.
Tag(s):	GFP/His-tag, C-terminal
Purification:	Purified by affinity chromatography and subsequent buffer exchange.
Formulation:	PBS; pH 7.4 Liquid, stored and shipped at -80 °C.
Purity:	> 75 % (will be determined by densitometry of Coomassie stained gel, example next page)
Concentration:	Will be determined by BCA-Assay.
Long-term storage:	No recommendations.
Comment:	Protein migrates at higher molecular weight during SDS-PAGE due to posttranslational modifications.

Background Information:

The spike (S) glycoprotein of coronaviruses is essential for binding of the virus to the host cell at the beginning of the infection process. During the actual COVID-19 pandemic, several variants of the virus evolved and some of them are continuously spreading all over the world.

This SARS-CoV-2 variant assigned as "Omicron" by the World Health Organization (WHO) is belonging to Pango lineage B.1.1.529. It is characterised by 30 changes, three small deletions and one small insertion in the spike protein, of these, 15 are in the receptor binding domain. Since the Omicron variant is the most divergent variant that has been detected in significant numbers during the pandemic so far, many concerns raised that it may be associated with increased transmissibility, significant reduction in vaccine effectiveness and increased risk for reinfections.



Structural model of the receptor binding domain (RBD) of the spike protein. The location of the mutations is indicated by the green parts.

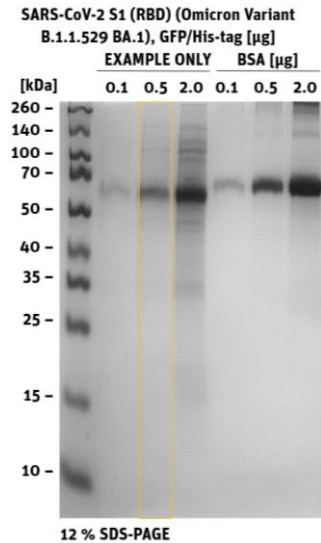
SARS-CoV-2 Spike S1 protein

Receptor binding domain (RBD) (Omicron Variant B.1.1.529 BA.1)

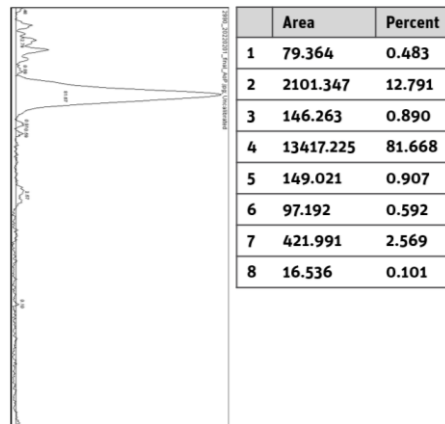
Cat. no. P2020-061

Product Information

Quality Information (provided for each lot):



SDS-PAGE/Coll.Coomassie



Histogram (of marked lane in gel picture)