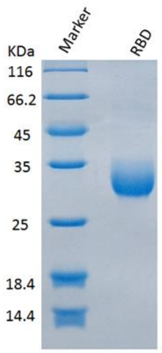
Accelerating Scientific Discovery

Receptor Binding Domain of MERS CoV Spike Protein (aa 358-588)

CATALOG NUMBER: MERS-RBD-005P, 50 µg

Introduction	The Middle East respiratory syndrome coronavirus (MERS-CoV) is a novel positive-sense, single-stranded RNA virus of the genus Betacoronavirus which is distinct from SARS coronavirus and the common-cold coronavirus. Proteins that contribute to the overall structure of all coronaviruses are the spike (S), envelope (E), membrane (M) and nucleocapsid (N). The S glycoprotein consists of a globular S1 domain at the N-terminal region, followed by membrane-proximal S2 domain, a transmembrane domain and an intracellular domain.
Applications	Western blot standard, antibody ELISA, antigen, etc.
Description	Viral protein purified from 293 cell culture
Viral Protein	C-terminal 6x His tagged receptor binding domain of spike (S1) protein (amino acid 358-588) of MERS-CoV (GenBank No. AFS88936.1)
Storage	Store at -20 ^{o}C; Stable for 6-months from the date of shipment when kept at 4 ^{o}C. Non-hazardous, no MSDS required.
Concentration	1 µg/µl in PBS with 0.1% sodium azide
Endotoxin Level	<0.01 EU per 1 µg of the protein by LAL test
Purity	≥ 95% (by SDS PAGE)



SDS-PAGE: purified RBD of (aa 358-588) of MERS-CoV S1 Protein

RBD of S1 (MERS-CoV) SEQ:

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SGVYSVSSFE AKPSGSVVEQ AEGVECDFSP LLSGTPPQVY NFKRLVFTNC NYNLTKLLSL FSVNDFTCSQ ISPAAIASNC
YSSLILDYFS YPLSMKSDLS VSSAGPISQF NYKQSFSNPT CLILATVPHN LTTITKPLKY SYINKCSRLL SDDRTEVPQL
VNANQYSPCV SIVPSTVWED GDYYRKQLSP LEGGGWLVAS GSTVAMTEQL QMGFGITVQY GTDTNSVCPK LHHHHHH
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Reference:

1. Woo, PC., et al. Characterization and complete genome sequence of a novel coronavirus, coronavirus HKU1, from patients with pneumonia. J. Virol., 79: 884-95, 2005.
2. Chen, Y., et al. Crystal structure of the receptor-binding domain from newly emerged Middle East respiratory syndrome coronavirus. J. Virol., 87: 10777-83, 2013.