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# 32-190040: Recombinant ACE2 SARS-CoV2 Binding Domain

**Application :** ELISA
**Uniprot ID :** Q9BYF1

## Description

The sequence below is that of our recombinant construct of the ACE2 extracellular domain which includes the entire region which interacts with both SARS-CoV1 and SARS-CoV2. The specific binding of both SARS viruses to ACE2 is essential for viral internalization and infection. We designed this construct based on amino acids 1-500 in the S-protein sequence in BAB40370.1. This is a defined globular domain recently shown to include all of the amino acids necessary for ACE2 binding (4). Human ACE2 is 805 amino acids long so this construct is missing the C-terminal 305 amino acids, which at 741-763, includes a membrane spanning domain. The construct lacks this region as inclusion would likely have made the molecule difficult to express. The construct was expressed in and purified from E. coli and includes an N-terminal His-tag and other vector derived sequence shown underlined below. Amino acids printed in bold below are those which have been shown to interact with the SARS-CoV2 binding domain.

## Product Info

**Amount :** 25µg / 50 µg
**Content :** Supplied as 1mg/mL in 6M urea, 10mM phosphate buffer pH=7.5
**Storage condition :** Stable at 4°C for several months. For longer term store at -20°C, minimize freeze/thaw cycles
**Amino Acid :**
MHHHHHHSSG LVPRGSGMKE TAAAKFERQH MDSPDLGTDD DDKAMADIGS EFMSSSSWLL 60
LSLVAVTAAQ STIEEQAKTF LDKFNHEAED LFYQSSLASW NYNTNITEEN VQNMNNAGDK 120
WSAFLKEQST LAQMYPLQEI QNLTVKLQLQ ALQQNGSSVL SEDKSKRLNT ILNTMSTIYS 180
TGKVCNPDNP QECLLLEPGL NEIMANSLDY NERLWAWESW RSEVGKQLRP LYEEYVVLKN 240
EMARANHYED YGDYWRGDYE VNGVDGYDYS RGQLIEDVEH TFEEIKPLYE HLHAYVRAKL 300
MNAYPSYISP IGCLPAHLLG DMWGRFWTNL YSLTVPFGQK PNIDVTDAMV DQAWDAQRIF 360
KEAEKFFVSV GLPNMTQGFW ENSMLTDPGN VQKAVCHPTA WDLGKGDFRI LMCTKVTMDD 420
FLTAHHEMGH IQYDMAYAAQ PFLLRNGANE GFHEAVGEIM SLSAATPKHL KSIGLLSPDF 480
QEDNETEINF LLKQALTIVG TLPFTYMLEK WRWMVFKGEI PKDQWMKKWW EMKREIVGVV 540
EPVPHDETYC DP 552

## Application Note

ELISA

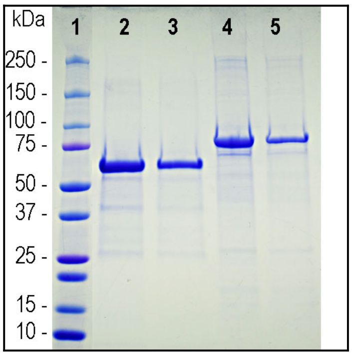

Figure-1: SDS-PAGE gel of recombinant human ACE2 virus binding region. Lane 1 shows protein molecular weight standards of apparent size indicated in kiloDaltons. Lanes 2 and 3 are 5.6Î¼g and 2.8Î¼g BSA and 4 and 5 are the ACE2 construct running at an apparent molecular weight about 70kDa, somewhat higher than the 63kDa predicted from the amino acid sequence. This discrepancy is likely due to the highly acidic nature of the protein. The protein was expressed in E. coli and extracted from inclusion bodies using 6M urea.