Store at -80°C

Human ACE2 (multimeric) (18-652) Recombinant Protein

#85054

20 µg

Cell Signaling TECHNOLOGY®

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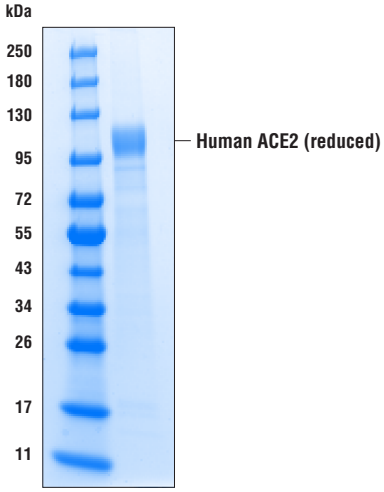
Entrez-Gene ID #59272
UniProt ID #Q9BYF1

For Research Use Only. Not for Use in Diagnostic Procedures.

Description: Human ACE2 (multimeric) (18-652) Recombinant Protein is a fusion protein containing an exogenous oligomerization domain, enabling expression of Human ACE2 as a multimer. The multimeric form provides increased binding avidity (relative to monomeric ACE2 protein) to recombinant protein corresponding to the SARS-CoV-2 receptor binding domain (RBD). Human ACE2 (multimeric) (18-652) Recombinant Protein may be biotinylated using the Avitag™ system.

Background: ACE2 is a carboxypeptidase that catalyses the conversion of angiotensin I to angiotensin 1-9, or of angiotensin II to the vasodilator angiotensin 1-7 (1). ACE2 is a critical component in the renin-angiotensin system (RAS). ACE2 is predominantly expressed in vascular endothelial cells of the heart and kidney and Leydig and Sertoli cells of the testis (2,3). The unique expression pattern of ACE2 determines its essential role in the regulation of cardiovascular and kidney functions, as well as fertility. ACE2 protein is localized mainly in the extracellular space with its carboxy terminal end attached to the membrane via its transmembrane domain. Active ACE2 enzyme is secreted by cleavage at the amino terminus. Research studies have shown that ACE2 expression is elevated in human failing heart (4). ACE2 has also been identified as the receptor for SARS and SARS-CoV-2 coronaviruses (5-7).



The purity of Human ACE2 (multimeric) (18-652) Recombinant Protein was determined by densitometry after SDS-PAGE (in reducing conditions) of 2 µg of protein followed by staining with Coomassie Blue.

Molecular Weight: 96 kDa (reduced)

Formulation:

Expression Host: Human (HEK293-EBNA cells)
Supplied in a PBS solution.

Purity: 93%, determined by SDS-PAGE.

Storage: Stable at -80°C for 3 years after receipt. Avoid repeated freeze-thaw cycles.

Background References:

(1) Schmidt, B.L. et al. (2000) *J Clin Microbiol* 38, 1279-82.

(2) Boehm, M. and Nabel, E.G. (2002) *N Engl J Med* 347, 1795-7.

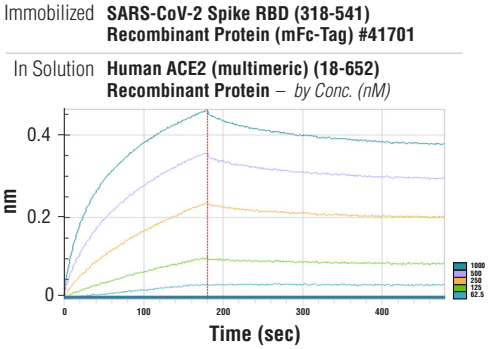
(3) Douglas, G.C. et al. (2004) *Endocrinology* 145, 4703-11.

(4) Goulter, A.B. et al. (2004) *BMC Med* 2, 19.

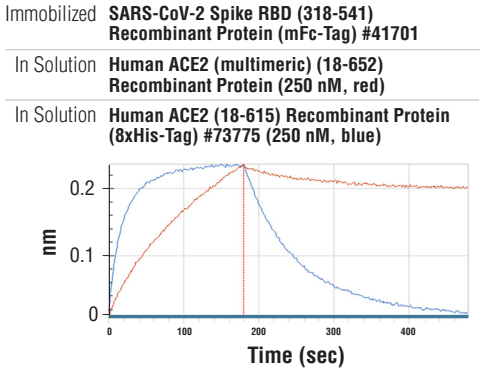
(5) Li, W. et al. (2005) *EMBO J* 24, 1634-43.

(6) Hoffmann, M. et al. (2020) *Cell* 181, 271-280.e8.

(7) Lan, J. et al. (2020) *Nature* 581, 215-20.



Binding kinetics between SARS-CoV-2 Spike RBD (318-541) Recombinant Protein (mFc-Tag) #41701 (immobilized) and Human ACE2 (multimeric) (18-652) Recombinant Protein (in solution, at indicated concentrations). The vertical red line (180 sec) indicates addition of PBS to induce dissociation. Binding was detected with an anti-mouse Fc biosensor. Values on y-axis indicate binding response signals recorded for 5 different concentrations of Human ACE2 (multimeric) (18-652) Recombinant Protein (62.5, 125, 250, 500 and 1000 nM).



Binding kinetics between SARS-CoV-2 Spike RBD (318-541) Recombinant Protein (mFc-Tag) #41701 (immobilized) and Human ACE2 (multimeric) (18-652) Recombinant Protein (in solution, 250 nM, red), or Human ACE2 (18-615) Recombinant Protein (8xHis-Tag) #73775 (in solution, 250 nM, blue). The vertical red line (180 sec) indicates addition of PBS to induce dissociation. Binding was detected with an anti-mouse Fc biosensor. Values on y-axis indicate binding response signals (nm) recorded over time.

Applications: **W**—Western **IP**—Immunoprecipitation **IHC**—Immunohistochemistry **ChIP**—Chromatin Immunoprecipitation **IF**—Immunofluorescence **F**—Flow cytometry **FC-FP**— Flow cytometry-Fixed/Permeabilized **FC-L**— Flow cytometry-Live **E-P**—ELISA-Peptide
Species Cross-Reactivity: **H**—human **M**—mouse **R**—rat **Hm**—hamster **Mk**—monkey **Mi**—mink **C**—chicken **Dm**—D. melanogaster **X**—Xenopus **Z**—zebrafish **B**—bovine **Dg**—dog **Pg**—pig **Sc**—S. cerevisiae **Ce**—C. elegans **Hr**—Horse
All—all species expected Species enclosed in parentheses are predicted to react based on 100% homology.