

Resource Summary Report

Generated by [NIF](#) on Jul 30, 2026

pcDNA3-sACE2v2.4(732)-IgG1

RRID:Addgene_154106

Type: Plasmid

Proper Citation

RRID:Addgene_154106

Plasmid Information

URL: <http://www.addgene.org/154106>

Proper Citation: RRID:Addgene_154106

Insert Name: Angiotensin-converting enzyme 2

Organism: Homo sapiens

Bacterial Resistance: Ampicillin

Defining Citation: [PMID:32753553](#)

Vector Backbone Description: Backbone Marker:Invitrogen; Backbone Size:5332; Vector Backbone:pcDNA3.1(+); Vector Types:Mammalian Expression; Bacterial Resistance:Ampicillin

Comments: Please visit <https://www.biorxiv.org/content/10.1101/2020.03.16.994236v1> for BioRxiv preprint.

Plasmid Name: pcDNA3-sACE2v2.4(732)-IgG1

Relevant Mutation: Extracellular, soluble protease and neck domains (a.a. M1-G732) with mutations T27Y, L79T, N330Y

Record Creation Time: 20220422T221844+0000

Record Last Update: 20260725T074034+0000

Ratings and Alerts

No rating or validation information has been found for pcDNA3-sACE2v2.4(732)-IgG1.

No alerts have been found for pcDNA3-sACE2v2.4(732)-IgG1.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Skeeters S, et al. (2024) Modulation of the pharmacokinetics of soluble ACE2 decoy receptors through glycosylation. Molecular therapy. Methods & clinical development, 32(3), 101301.

Zhang L, et al. (2022) An engineered ACE2 decoy receptor can be administered by inhalation and potently targets the BA.1 and BA.2 omicron variants of SARS-CoV-2. bioRxiv : the preprint server for biology.

Wang Q, et al. (2021) Functional differences among the spike glycoproteins of multiple emerging severe acute respiratory syndrome coronavirus 2 variants of concern. iScience, 24(11), 103393.

Havranek B, et al. (2021) Computationally Designed ACE2 Decoy Receptor Binds SARS-CoV-2 Spike (S) Protein with Tight Nanomolar Affinity. Journal of chemical information and modeling, 61(9), 4656.