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Catalog Number: TEST0003

PRODUCT INFORMATION

Expression system

Baculovirus

Domain

TEST

23-335aa(p40)/23-215aa(p35)

UniProt No.

P43432(p40)/P43431(p35)

NCBI Accession No.

aaaa

Additional Information

as

PRODUCT SPECIFICATION

Molecular Weight

35.7 kDa (p40, 313aa)

22.5 kDa (p35, 199aa)

The heterodimeric II12 has a predicted Molecular weight of 58.3 kDa (512aa).

Molecular weight on SDS-PAGE will appear higher

Concentration

0.5mg/ml (determined by Bradford assay)

Formulation

Liquid in. Phosphate-Buffered Saline (pH 7.4) containing 10% glycerol

Purity

> 95% by SDS-PAGE

Endotoxin level

< 1 EU per 1ug of protein (determined by LAL method)

Tag

His-Tag

Application

SDS-PAGE

Storage Condition

Can be stored at +2C to +8C for 1 week. For long term storage, aliquot and store at -20C to -80C. Avoid repeated freezing and thawing cycles.

BACKGROUND

Description

MERS-CoV, which causes the Middles East Respiratory Syndrome (MERS), belongs to a family of viruses known as



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coronaviruses. MERS-CoV has four structural proteins, known as the S (spike), E (envelope), M (membrane), and N (nucleocapsid) proteins. The spike protein, responsible for allowing the virus to attach to and fuse with the membrane of a host cell and is a large type I transmembrane protein containing two subunits, S1 and S2. S1 mainly contains a receptor binding domain (RBD), which is responsible for recognizing the cell surface receptor. S2 contains basic elements needed for the membrane fusion. The S protein plays key parts in the induction of neutralizing-antibody and T-cell responses, as well as protective immunity. Protein modeling experiments on the spike protein of the virus soon suggested that SARS-CoV-2 has sufficient affinity to the receptor angiotensin converting enzyme 2 (ACE2) on human cells to use them as a mechanism of cell entry.

Amino acid Sequence

IL12B(p40)

MWELEKDVYV VEVDWTPDAP GETVNLTCDT PEEDDITWTS DQRHGVIGSG KTLTITVKEF LDAGQYTCHK GGETLSHSHL LLHKKENGIW STEILKNFKN KTFLKCEAPN YSGRFTCSWL VQRNMDLKFN IKSSSSSPDS RAVTCGMASL SAEKVTLDQR DYEKYSVSCQ EDVTCPTAEE TLPIELALEA RQQNKYENYS TSFFIRDIIK PDPPKNLQMK PLKNSQVEVS WEYPDSWSTP HSYFSLKFFV RIQRKKEKMK ETEEGCNQKG AFLVEKTSTE VQCKGGNVCV QAQDRYYNSS CSKWACVPCR VRS IL12A(p35)

RVIPVSGPAR CLSQSRNLLK TTDDMVKTAR EKLKHYSCTA EDIDHEDITR DQTSTLKTCL PLELHKNESC LATRETSSTT RGSCLPPQKT SLMMTLCLGS IYEDLKMYQT EFQAINAALQ NHNHQQIILD KGMLVAIDEL MQSLNHNGET LRQKPPVGEA DPYRVKMKLC ILLHAFSTRV VTINRVMGYL SSA<HHHHHHH>

General References

Junghyun Goo., et al. (2020) Virus Res. 278:197863. Yan-Hua Li., et al. (2019) Engineering. 5:940-947. Lingshu Wang., et al. (2018) J Virol. 92:e02002-2017. Nicolas Papageorgiou., et al. (2016) Acta Crystallogr D Struct Biol. 72:192-202. Xiao-Yan Che., et al. (2004) J Clin Microbiol. 42:2629-2635.

DATA

SDS-PAGE

