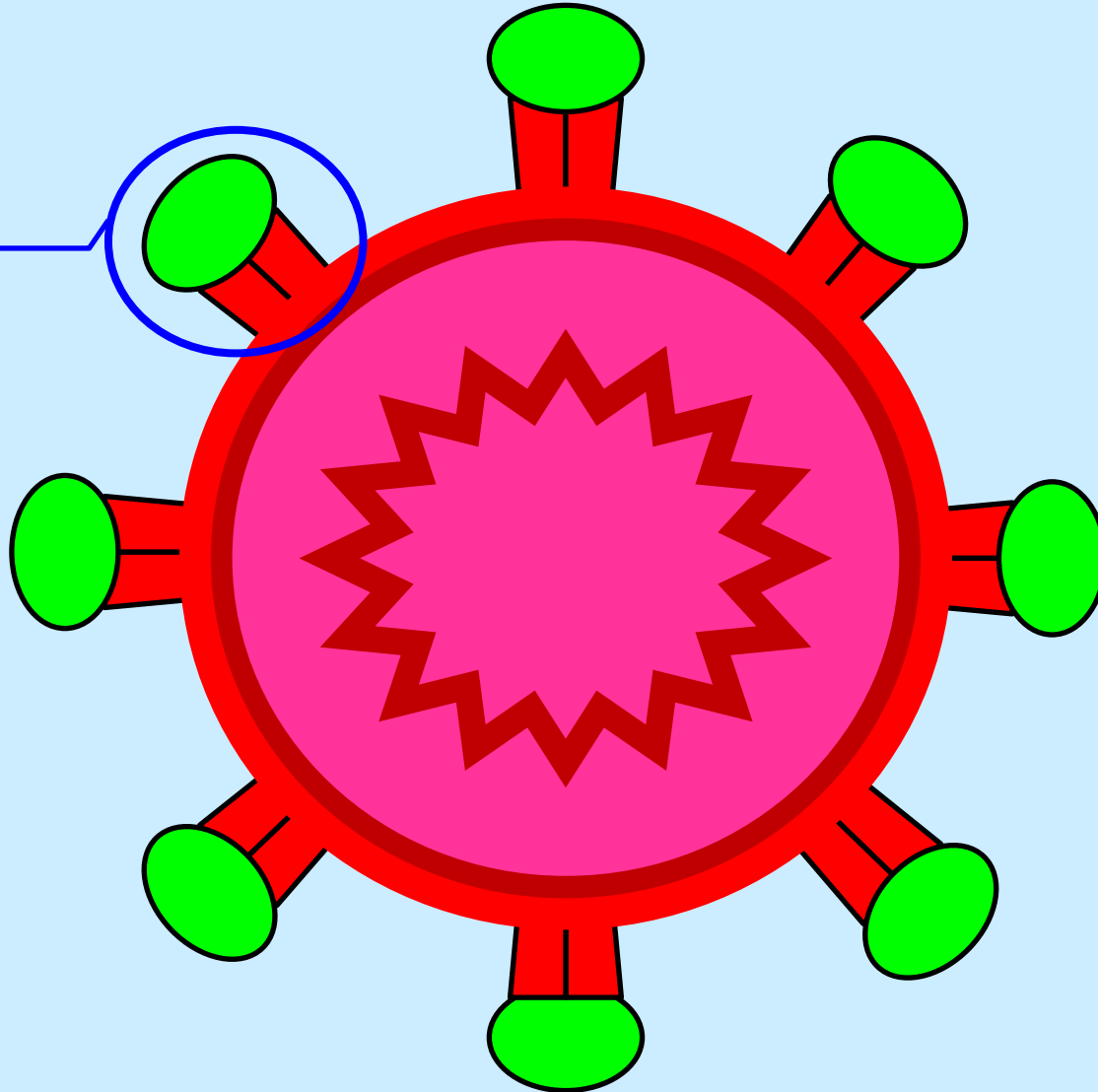


# **MENGAPA VARIAN OMIKRON MENJADI LEBIH MELEMAH ?**

**Moh Indro Cahyono**

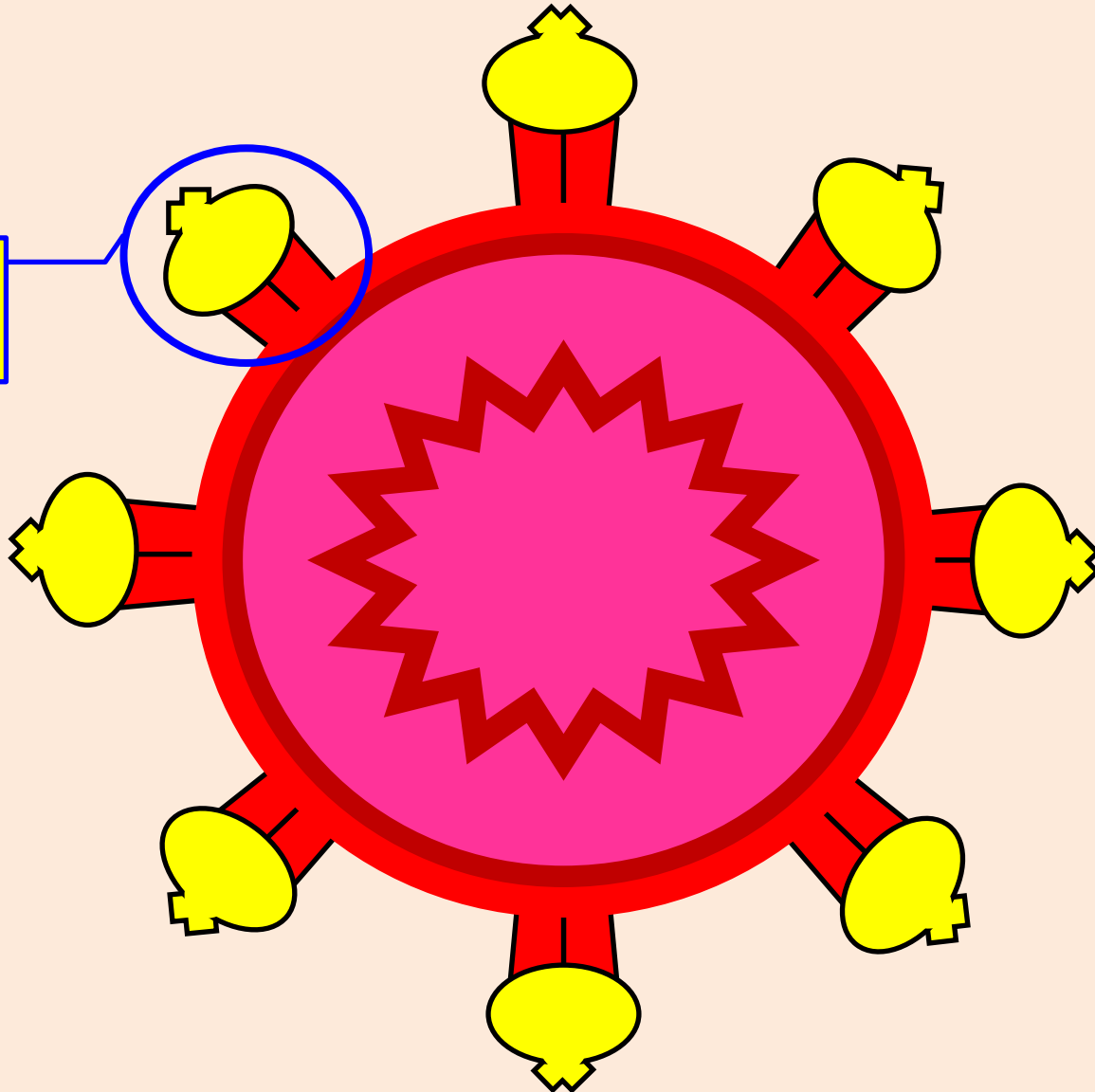
# VIRUS COVID VARIAN WUHAN (AWAL & TANPA PERUBAHAN PROTEIN S / SPIKE )

**PROTEIN S  
VIRUS COVID19  
VARIAN WUHAN  
(AWAL)**

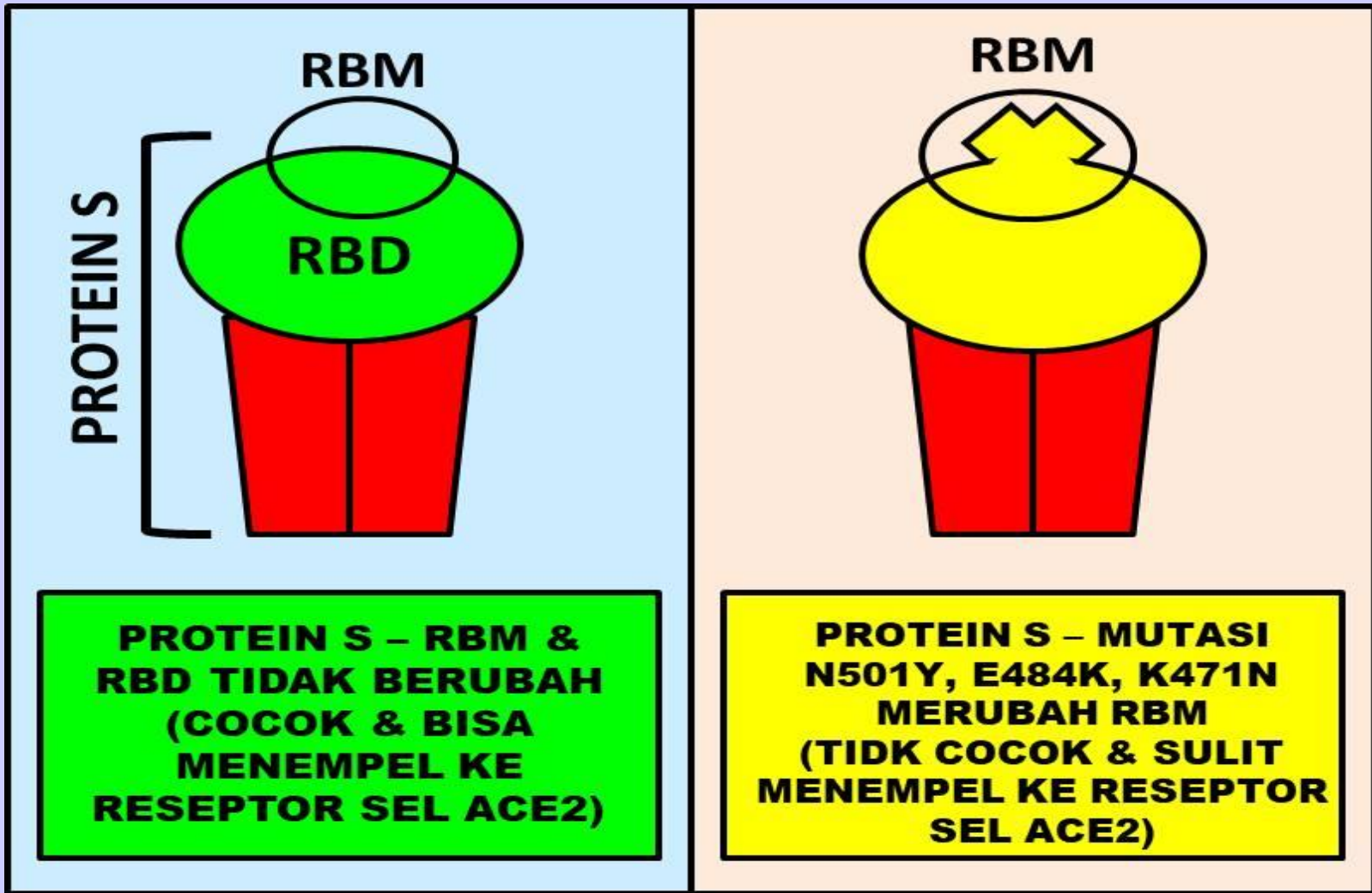


# VIRUS COVID VARIAN OMIKRON (32 MUTASI DI PROTEIN S / SPIKE )

**PROTEIN S  
VIRUS COVID19  
VARIAN OMIKRON**

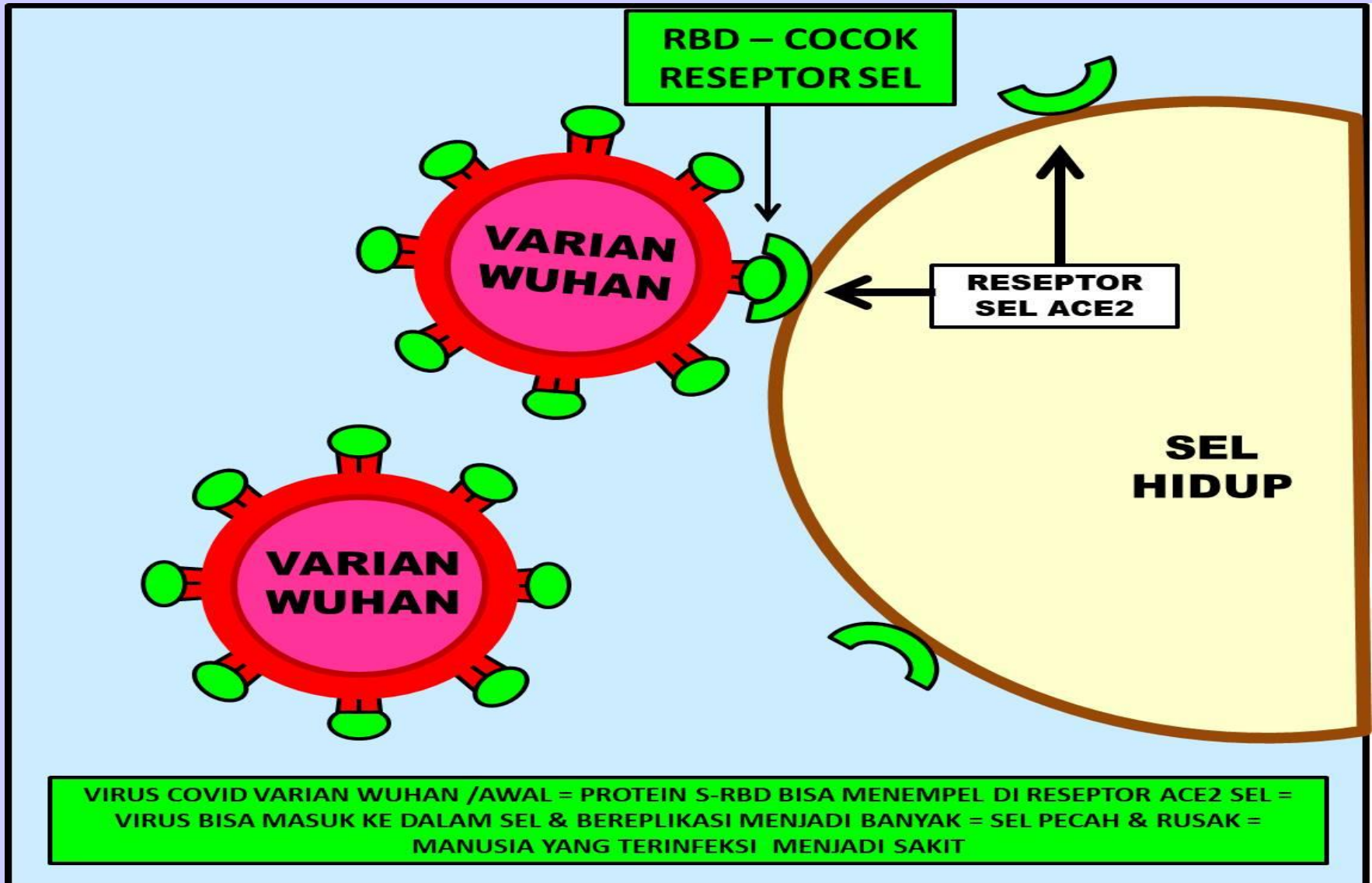


# PERBEDAAN UJUNG RBD PROTEIN S VARIAN WUHAN & VARIAN OMIKRON

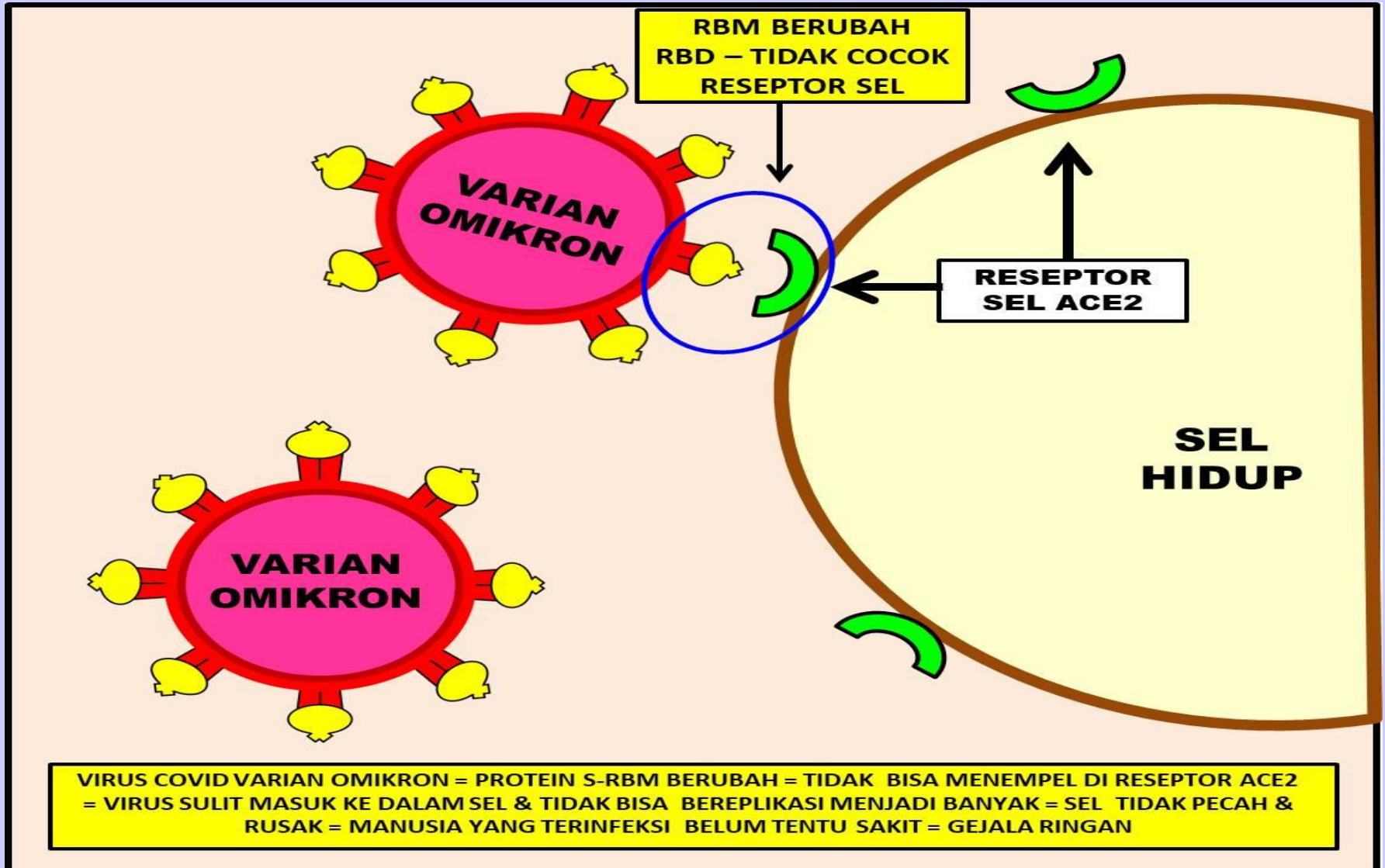


- PROTEIN S = SPIKE / DURI VIRUS COVID 19
- RBD = RECEPTOR BINDING DOMAIN / BAGIAN UJUNG BULAT PROTEIN S YANG MENEMPEL KE RESEPTOR
- RBM = RECEPTOR BINDING MOTIF / BAGIAN PALIN UJUNG RBM
- ACE2 = ANGIOTENSIN CONVERTER ENZYME 2 / BAGIAN RESEPTOR SEL UNTUK TEMPAT TEMPELAN VIRUS COVID19

# HUBUNGAN RBD VARIAN WUHAN-RESEPTOR ACE2 SPESIFIK (IKATAN KUNCI & GEMBOK)



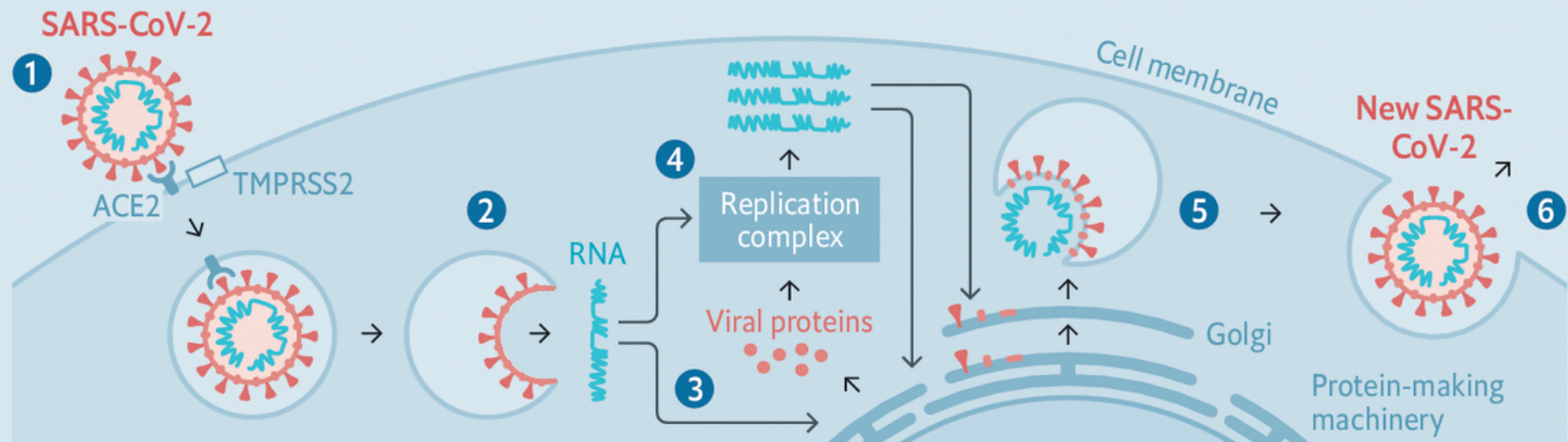
# HUBUNGAN RBD VARIAN OMIKRON-RESEPTOR ACE2 BERUBAH (KUNCI BERUBAH & SULIT COCOK DENGAN GEMBOK)



# PRINSIP UTAMA REPLIKASI VIRUS COVID19 DI DALAM SEL

## Hijack

How SARS-CoV-2 replicates itself in the cells of those infected



**1** Spike protein on the virion binds to ACE2, a cell-surface protein. TMPRSS2, an enzyme, helps the virion enter **2** The virion releases its RNA **3** Some RNA is translated into proteins by the cell's machinery **4** Some of these proteins form a replication complex to make more RNA **5** Proteins and RNA are assembled into a new virion in the Golgi and **6** released

Sources: Song et al., *Viruses*, 2019; Jiang et al., *Emerging Microbes and Infections*, 2012; *The Economist*

## The Economist

- 1. VIRUS HARUS MASUK KE DALAM SEL DENGAN RESEPTOR ACE2 DI PARU-PARU (BUKAN DI HIDUNG)**
- 2. RBD VIRUS COVID HARUS COCOK DENGAN RESPTOR ACE2 AGAR BISA MENMPEL**
- 3. SETELAH VIRUS COVID 19 MENEMPEL BARU BISA MASUK KE DALAM SEL & BERTAMBAH BANYAK / REPLIKASI**
- 4. TEMPELAN RBD-ACE2 COCOK = VIRUS MASUK KE SEL = SEL RUSAK & ORANG SAKIT**
- 5. TEMPELAN TIDAK COCOK = VIRUS SULIT MASUK = SEL SULIT RUSAK & GEJALA RINGAN**

# GEJALA VARIAN OMIKRON LEBIH RINGAN 32 MUTASI VARIAN MENYEBABKAN VIRUS COVID MELEMAH

THREAT ASSESSMENT BRIEF

## Implications of the further emergence and spread of the SARS-CoV-2 B.1.1.529 variant of concern (Omicron) for the EU/EEA – first update

2 December 2021

### Summary

The number of countries reporting SARS-CoV-2 Omicron variant of concern (VOC) cases continues to increase globally, with a total of 352 confirmed cases reported by 27 countries as of 16.00 on 1 December 2021, including 70 confirmed cases reported by 13 European Union and European Economic Area (EU/EEA) countries. The majority of confirmed cases have a history of travel to southern African countries, with some having taken connecting flights ~~at other destinations between Africa and Europe. Several European countries have already reported subsequent community or household transmission.~~ All cases for which there is available information on severity were either asymptomatic or mild. To date, there have been no severe cases and no deaths reported among these cases.

~~Current evidence on transmissibility, severity, and immune escape is highly uncertain for the Omicron VOC.~~ However, preliminary data from South Africa suggest that it may have a substantial growth advantage over the Delta VOC. If this is the case, mathematical modelling indicates that the Omicron VOC is expected to cause over half of all SARS-CoV-2 infections in the EU/EEA within the next few months. The greater Omicron's growth advantage over the Delta VOC and the greater its circulation in the EU/EEA, the shorter the expected time until the Omicron VOC causes the majority of all SARS-CoV-2 infections.

The presence of multiple mutations in the spike protein of the Omicron VOC indicates a high likelihood of reduction of neutralising activity by antibodies induced by infection or vaccination. Preliminary data suggest that the Omicron VOC may be associated with increased risk of reinfection in South Africa. However, the full extent to which the Omicron VOC evades or erodes existing vaccine- or infection-derived immunity remains uncertain in the absence of in vitro neutralisation data, vaccine effectiveness data, and further data on reinfection in populations exposed to different SARS-CoV-2 variants during previous pandemic waves.

### Risk assessed

#### What is the risk associated with the further introduction and spread of the SARS-CoV-2 variant Omicron in the EU/EEA?

The evidence from the initial cases of this new variant that has been collated from around the world is limited, but suggests that the Omicron VOC may be associated with higher transmissibility than the Delta VOC, although robust evidence is still lacking. There remains considerable uncertainty related to vaccine effectiveness, risk for

Suggested citation: European Centre for Disease Prevention and Control. Implications of the spread of the SARS-CoV-2 B.1.1.529 variant of concern (Omicron) for the EU/EEA – first update. 2 December 2021. ECDC: Stockholm; 2021.

© European Centre for Disease Prevention and Control, Stockholm, 2021

Europe Union “Severity were either **ASYMPTOMATIC or MILD**. To date there have been **NO SEVERE CASES AND NO DEATHS** reported among these cases”

# GEJALA VARIAN OMIKRON LEBIH RINGAN 32 MUTASI VARIAN MENYEBABKAN VIRUS COVID MELEMAH



Early Release / Vol. 70

Morbidity and Mortality Weekly Report

December 10, 2021

## SARS-CoV-2 B.1.1.529 (Omicron) Variant — United States, December 1–8, 2021

CDC COVID-19 Response Team

A new variant of SARS-CoV-2 (the virus that causes COVID-19), B.1.1.529 (Omicron) (1), was first reported to the World Health Organization (WHO) by South Africa on November 24, 2021. Omicron has numerous mutations with potential to increase transmissibility, confer resistance to therapeutics, or partially escape infection- or vaccine-induced immunity (2). On November 26, WHO designated B.1.1.529 as a variant of concern (3), as did the U.S. SARS-CoV-2 Interagency Group (SIG)\* on November 30. On December 1, the first case of COVID-19 attributed to the Omicron variant was reported in the United States. As of December 8, a total of 22 states had identified at least one Omicron variant case, including some that indicate community transmission. Among 43 cases with initial follow-up, one hospitalization and no deaths were reported. This report summarizes U.S. surveillance for SARS-CoV-2 variants, characteristics of the initial persons investigated with COVID-19 attributed to the Omicron variant and public health measures implemented to slow the spread of Omicron in the United States. Implementation of concurrent prevention strategies, including vaccination, masking, increasing ventilation, testing, quarantine, and isolation, are recommended to slow transmission of SARS-CoV-2, including variants such as Omicron, and to protect against severe illness and death from COVID-19.

### Surveillance for SARS-CoV-2 Variants and Initial Detection of Omicron in the United States

CDC has a multifaceted surveillance system for analyzing SARS-CoV-2 variants circulating in the United States. This

\* SIG includes representatives from CDC, the National Institutes of Health (NIH), the Food and Drug Administration (FDA), the Biomedical Advanced Research and Development Authority (BARDA), the U.S. Department of Defense (DoD), the U.S. Department of Agriculture (USDA), and the U.S. Department of Health and Human Services (HHS). This interagency group focuses on the rapid characterization of emerging variants and actively monitors their potential impact on critical SARS-CoV-2 countermeasures, including vaccines, therapeutics, and diagnostics.

system obtains genomic surveillance data from 1) National SARS-CoV-2 Strain Surveillance, 2) CDC-supported contracts with several commercial diagnostic laboratories, and 3) public repositories (the Global Initiative on Sharing Avian Influenza Data [GISAID]<sup>†</sup> and the National Center for Biotechnology Information [NCBI]<sup>‡</sup>) of randomly sampled viruses with metadata tagging of sequences by various partners. Genomic surveillance is implemented in partnership with state and local public health laboratories, the Association of Public Health Laboratories, and other academic and government partners.<sup>¶</sup> As of the week ending December 4, the SARS-CoV-2 B.1.617.2 (Delta) variant was estimated to account for 99.9% of SARS-CoV-2 circulating in the United States.\*\* Based on CDC analysis of the sequences currently available, and accounting for clustering, CDC estimates a 95% chance of detecting the Omicron variant if it accounted for  $\geq 0.03\%$  of circulating SARS-CoV-2 lineages during the week ending November 13 and for  $\geq 0.05\%$  of circulating lineages during the week ending November 20 (4).

To accelerate detection of COVID-19 cases attributed to the Omicron variant until they are common enough to be reliably measured by routine genomic surveillance, enhanced surveillance was initiated through National SARS-CoV-2 Strain Surveillance on November 28. The method is based on rapid screening for S-gene target failures (SGTFs) by polymerase chain reaction (PCR)-based diagnostic assays to flag potential cases of Omicron variant infection for confirmation by genomic sequencing (5). Specimens that display SGTFs have a higher likelihood to be Omicron (although SGTFs are not unique to Omicron) based on a mutation (69–70 deletion) that reduces S-gene target amplification in some PCR assays.

<sup>†</sup> <https://www.gisaid.org>

<sup>‡</sup> <https://www.ncbi.nlm.nih.gov/sars-cov-2>

<sup>¶</sup> <https://www.cdc.gov/coronavirus/2019-ncov/variants/spheres.html>

\*\* <https://covid.cdc.gov/covid-data-tracker/#variant-proportion>

United States “Among 43 cases with initial follow up, one hospitalization and **NO DEATHS** were reported”

**“Logika mengalahkan kepanikan,  
Pengetahuan mengalahkan  
ketakutan”**

**- Moh Indro Cahyono, 2020**

**SELALU BELAJAR & SELAMAT MERAYAKAN NATAL & TAHUN  
BARU 2022 DENGAN BERLOGIKA & BERGEMBIRA**