

REFERENCES

- Abdelbary, M.M.H., Basset, P., Blanc, D.S. and Feil, E.J. (2017). The Evolution and Dynamics of Methicillin-Resistant *Staphylococcus aureus*. *Genetics and Evolution of Infectious Diseases*, pp.553–572. doi:10.1016/b978-0-12-799942-5.00024-x.
- Bhatia, S. and Dahiya, R. (2015). Concepts and Techniques of Plant Tissue Culture Science. *Modern Applications of Plant Biotechnology in Pharmaceutical Sciences*, [online] pp.121–156. doi:10.1016/b978-0-12-802221-4.00004-2.
- Cahyani, I., Putro, E.W., Ridwanuloh, A.M., Wibowo, S., Hariyatun, H., Syahputra, G., Akbariani, G., Utomo, A.R., Ilyas, M., Loose, M., Kusharyoto, W. and Susanti, S. (2022). Genome Profiling of SARS-CoV-2 in Indonesia, ASEAN and the Neighbouring East Asian Countries: Features, Challenges and Achievements. *Viruses*, 14(4), p.778. doi:<https://doi.org/10.3390/v14040778>.
- Cao, Y., Wang, J., Jian, F., Xiao, T., Song, W., Yisimayi, A., Huang, W., Li, Q., Wang, P., An, R., Wang, J., Wang, Y., Niu, X., Yang, S., Liang, H., Sun, H., Li, T., Yu, Y., Cui, Q. and Liu, S. (2021). Omicron escapes the majority of existing SARS-CoV-2 neutralizing antibodies. *Nature*, 602(7898), pp.657–663. doi:<https://doi.org/10.1038/s41586-021-04385-3>.
- Carter, L.J., Garner, L.V., Smoot, J.W., Li, Y., Zhou, Q., Saveson, C.J., Sasso, J.M., Gregg, A.C., Soares, D.J., Beskid, T.R., Jervy, S.R. and Liu, C. (2020). Assay Techniques and Test Development for COVID-19 Diagnosis. *ACS Central Science*, 6(5), pp.591–605. doi:10.1021/acscentsci.0c00501.
- CDC. 2020. *Coronavirus Disease 2019 (COVID-19)*. [online] Centers for Disease Control and Prevention. Available at: https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-classifications.html?CDC_AA_refVal=https%3A%2F%2Fwww.cdc.gov%2Fcoronavirus%2F2019-ncov%2Fvariants%2Fvariant-info.html. [Accessed 30 Mar. 2022].
- CDC. 2022. *Whole Genome Sequencing (WGS)*. [online] CDC. Available at: <https://www.cdc.gov/pulsenet/pathogens/wgs.html>.
- CNN Indonesia. (2021). Satgas Ungkap Alasan Tes Covid-19 Rendah di Indonesia. [online] nasional. Available at: <https://www.cnnindonesia.com/nasional/20210720195832-20-670025/satgas-ungkap-alasan-tes-covid-19-rendah-di-indonesia> [Accessed 11 Jun. 2023].
- Collier, D.A., De Marco, A., Ferreira, I.A.T.M., Meng, B., Datir, R., Walls, A.C., Kemp S, S.A., Bassi, J., Pinto, D., Fregni, C.S., Bianchi, S., Tortorici, M.A.,

- Bowen, J., Culap, K., Jaconi, S., Cameroni, E., Snell, G., Pizzuto, M.S., Pellanda, A.F. and Garzoni, C. 2021. Sensitivity of SARS-CoV-2 B.1.1.7 to mRNA vaccine-elicited antibodies. *Nature*: 1–8. Available at: <https://www.nature.com/articles/s41586-021-03412-7> [Accessed 30 Mar. 2022].
- Dyer, O. (2021). Covid-19: Indonesia becomes Asia's new pandemic epicentre as delta variant spreads. *BMJ*, (374), p.n1815. doi:<https://doi.org/10.1136/bmj.n1815>
- Guo, S., Liu, K. and Zheng, J. 2021. The Genetic Variant of SARS-CoV-2: would It Matter for Controlling the Devastating Pandemic? *International Journal of Biological Sciences*, [online] 17(6): 1476–1485. Available at: <https://pubmed.ncbi.nlm.nih.gov/33907511/>. [Accessed 30 Mar. 2022]
- Hadfield, J., Megill, C., Bell, S.M., Huddleston, J., Potter, B., Callender, C., Sagulenko, P., Bedford, T. and Neher, R.A. 2018. Nextstrain: real-time tracking of pathogen evolution. *Bioinformatics*, 34(23): 4121–4123.
- Heather, J.M. and Chain, B. (2016). The Sequence of sequencers: the History of Sequencing DNA. *Genomics*, [online] 107(1), pp.1–8. doi:10.1016/j.ygeno.2015.11.003.
- Hong, Y., Guo, M. and Wang, J. (2021). ENJ algorithm can construct triple phylogenetic trees. *Molecular Therapy - Nucleic Acids*, [online] 23(1), pp.286–293. doi:<https://doi.org/10.1016/j.omtn.2020.11.004>.
- Huang, J., Liu, Y., Zhu, T. and Yang, Z. (2020). The Asymptotic Behavior of Bootstrap Support Values in Molecular Phylogenetics. *Systematic Biology*, 70(4), pp.774–785. doi:<https://doi.org/10.1093/sysbio/syaa100>.
- Itokawa, K., Sekizuka, T., Hashino, M., Tanaka, R. and Kuroda, M. 2020. Disentangling primer interactions improves SARS-CoV-2 genome sequencing by multiplex tiling PCR. *PLOS ONE*, 15(9): e0239403.
- Jawerth, N. (2020). How is the COVID-19 Virus Detected using Real Time RT-PCR? [online] www.iaea.org. Available at: <https://www.iaea.org/newscenter/news/how-is-the-covid-19-virus-detected-using-real-time-rt-pcr>
- Katoh, K. and Standley, D.M. 2016. A simple method to control over-alignment in the MAFFT multiple sequence alignment program. *Bioinformatics*, 32(13): 1933–1942.
- Khan, A., Khan, T., Ali, S., Aftab, S., Wang, Y., Qiankun, W., Khan, M., Suleman, M., Ali, S., Heng, W., Ali, S.S., Wei, D.-Q. and Mohammad, A. 2021. SARS-CoV-2 new variants: Characteristic features and impact on the efficacy of different vaccines. *Biomedicine & Pharmacotherapy*, 143: 112176.

- Kim, Y.C. and Reyes-Sandoval, A. 2022. Viral-vectored vaccines against SARS-CoV-2. *Biomedical Innovations to Combat COVID-19*: 115–127.
- KOMPAS (2021). Angka Testing Covid-19 Indonesia Disorot, Pemerintah Tak Mampu atau Tak Mau? Halaman all. [online] KOMPAS.com. Available at: <https://www.kompas.com/tren/read/2021/06/28/200000765/angka-testing-covid-19-indonesia-disorot-pemerintah-tak-mampu-atau-tak-mau?page=all> [Accessed 11 Jun. 2023].
- Krawczyk, B. and Kur, J. 2018. Molecular Identification and Genotyping of Staphylococci: Genus, Species, Strains, Clones, Lineages, and Interspecies Exchanges. *Pet-To-Man Travelling Staphylococci*:199–223.
- Langthorp, S. (2021). Five things you need to know about: the Delta variant | Research and Innovation. [online] ec.europa.eu. Available at: <https://ec.europa.eu/research-and-innovation/en/horizon-magazine/five-things-you-need-know-about-delta-variant>.
- Li, H. 2011. A statistical framework for SNP calling, mutation discovery, association mapping and population genetical parameter estimation from sequencing data. *Bioinformatics*, 27(21): 2987–2993.
- McCallum, M., Bassi, J., Marco, A.D., Chen, A., Walls, A.C., Iulio, J.D., Tortorici, M.A., Navarro, M.-J., Silacci-Fregni, C., Saliba, C., Sprouse, K.R., Agostini, M., Pinto, D., Culap, K., Bianchi, S., Jaconi, S., Cameroni, E., Bowen, J.E., Tilles, S.W. and Pizzuto, M.S. 2021. SARS-CoV-2 immune evasion by the B.1.427/B.1.429 variant of concern. *Science*. [online] Available at: <https://science.sciencemag.org/content/early/2021/06/30/science.abi7994> [Accessed 30 Mar. 2022].
- Mitsias, P.D., Aboul Nour, H., Mohamud, A., Vourakis, G., Chebl, A.A. and Alsroutji, O.K. 2021. *COVID-19 and Cerebrovascular Diseases. Neurological Care and the COVID-19 Pandemic*: 57–72.
- Muik, A., Wallisch, A.-K., Sanger, B., Swanson, K.A., Muhl, J., Chen, W., Cai, H., Maurus, D., Sarkar, R., Tureci, .., Dormitzer, P.R. and ahin, U. 2021. Neutralization of SARS-CoV-2 lineage B.1.1.7 pseudovirus by BNT162b2 vaccine–elicited human sera. *Science*. [online] Available at: <https://science.sciencemag.org/content/early/2021/01/28/science.abg6105>. [Accessed 30 Mar. 2022].
- Nguyen, L.-T., Schmidt, H.A., von Haeseler, A. and Minh, B.Q. 2014. IQ-TREE: A Fast and Effective Stochastic Algorithm for Estimating Maximum-Likelihood Phylogenies. *Molecular Biology and Evolution*, [online] 32(1), pp.268–274. Available at: <https://academic.oup.com/mbe/article/32/1/268/2925592>. The Visual and Data Journalism Team. 2022. Covid map: Coronavirus cases, deaths,

vaccinations by country. *BBC News*. [online] 29 Mar. Available at: <https://www.bbc.com/news/world-51235105> [Accessed 30 Mar. 2022].

Office of Assistant to Deputy Cabinet Secretary for State Document & Translation (2021). Indonesia Reports First Case of Omicron Variant. [online] Sekretariat Kabinet Republik Indonesia. Available at: <https://setkab.go.id/en/indonesia-reports-first-case-of-omicron-variant/#:~:text=The%20Indonesian%20Government%20has%20reported> [Accessed 16 Apr. 2023].

Ojha, K.K., Mishra, S. and Singh, V.K. (2022). Computational molecular phylogeny: concepts and applications. *Bioinformatics*, 1(1), pp.67–89. doi:<https://doi.org/10.1016/b978-0-323-89775-4.00025-0>.

O'Toole, Á., Scher, E., Underwood, A., Jackson, B., Hill, V., McCrone, J.T., Colquhoun, R., Ruis, C., Abu-Dahab, K., Taylor, B., Yeats, C., Du Plessis, L., Maloney, D., Medd, N., Attwood, S.W., Aanensen, D.M., Holmes, E.C., Pybus, O.G. and Rambaut, A. 2021. Assignment of Epidemiological Lineages in an Emerging Pandemic Using the Pangolin Tool. *Virus Evolution* 7(2): veab064.

O'Toole A, Scher E, Rambaut A, Van Heus P, McCrone JT, Poon A, Colquhoun R, Underwood A, Maguire F, Hinrichs A, Watson M, Taylor B, Kruczkiewicz P, Nguyen SH, Roemer C, Hill V, Innes MJ, Jackson B, Maricato V, Sjödin A, Grüning B, Fairley D, Menzel P, Hoeven E. 2020. Software package for assigning SARSCoV-2 genome sequences to global lineages. Available at <https://github.com/covlineages/pangolin>. [Accessed 30 Mar. 2022].

Peyambari, M., Guan, S. and Roossinck, M.J. (2021). RdRp or RT, That is the Question. *Molecular Biology and Evolution*, 38(11), pp.5082–5091. doi:10.1093/molbev/msab235.

Sah, R., Mohammed Amir Rais, Mohanty, A., Chopra, H., Chandran, D., Talha Bin Emran and Kuldeep Dhama (2023). Omicron (B.1.1.529) variant and its subvariants and lineages may lead to ANOTHER COVID-19 wave in the world? -An OVERVIEW of current EVIDENCE and counteracting strategies. *International Journal of Surgery Open*, 55, pp.100625–100625. doi:<https://doi.org/10.1016/j.ijso.2023.100625>.

Sun, Y.-S., Xu, F., An, Q., Chen, C., Yang, Z.-N., Lu, H.-J., Chen, J.-C., Yao, P.-P., Jiang, J.-M. and Zhu, H.-P. (2020). A SARS-CoV-2 variant with the 12-bp deletion at E gene. *Emerging Microbes & Infections*, 9(1), pp.2361–2367. doi:10.1080/22221751.2020.1837017.

Taslem Mourosi, J., Anwar, S. and Hosen, M.J. (2022). The sex and gender dimensions of COVID-19: A narrative review of the potential underlying factors. *Infection, Genetics and Evolution*, [online] 103, p.105338. doi:<https://doi.org/10.1016/j.meegid.2022.105338>.

- Velarosdela, R.N. (2021). Kilas Balik Kronologi Munculnya Kasus Pertama Covid-19 di Indonesia Halaman all. [online] KOMPAS.com. Available at: <https://megapolitan.kompas.com/read/2021/03/02/05300081/kilas-balik-kronologi-munculnya-kasus-pertama-covid-19-di-indonesia?page=all> [Accessed 15 Feb. 2023].
- WHO. 2022. *Tracking SARS-CoV-2 variants*. [online] www.who.int. Available at: <https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/> . [Accessed 30 Mar. 2022].
- Zhang, J., Xiao, T., Cai, Y., Lavine, C.L., Peng, H., Zhu, H., Anand, K., Tong, P., Gautam, A., Mayer, M.L., Walsh, R.M., Jr., Rits-Volloch, S., Wesemann, D.R., Yang, W., Seaman, M.S., Lu, J. and Chen, B. (2021). Membrane fusion and immune evasion by the spike protein of SARS-CoV-2 Delta variant. *Science*, 374(6573), pp.1353–1360. doi:<https://doi.org/10.1126/science.abl9463>.
- Zhou, B., Thao, T.T.N., Hoffmann, D., Taddeo, A., Ebert, N., Labroussaa, F., Pohlmann, A., King, J., Steiner, S., Kelly, J.N., Portmann, J., Halwe, N.J., Ulrich, L., Trüeb, B.S., Fan, X., Hoffmann, B., Wang, L., Thomann, L., Lin, X. and Stalder, H. 2021. SARS-CoV-2 spike D614G change enhances replication and transmission. *Nature*, [online] 592(7852): 122–127. Available at: <https://www.nature.com/articles/s41586-021-03361-1> [Accessed 30 Mar. 2022].