

DAFTAR PUSTAKA

- Amit Roy, S. R. (2014). Molecular Markers in Phylogenetic Studies-A Review. *Journal of Phylogenetics & Evolutionary Biology*, 02(02). <https://doi.org/10.4172/2329-9002.1000131>
- Bernasconi, A., Canakoglu, A., Masseroli, M., Pinoli, P., & Ceri, S. (2020). A review on viral data sources and integration methods for COVID-19 mitigation. August, 1–10. <https://doi.org/10.20944/preprints202008.0133.v1>
- Chatzou, M., Magis, C., Chang, J. M., Kemeny, C., Bussotti, G., Erb, I., & Notredame, C. (2016). Multiple sequence alignment modeling: Methods and applications. *Briefings in Bioinformatics*, 17(6), 1009–1023. <https://doi.org/10.1093/BIB/BBV099>
- Chowdhury, B., & Garai, G. (2017). A review on multiple sequence alignment from the perspective of genetic algorithm. *Genomics*, 109(5–6), 419–431. <https://doi.org/10.1016/j.ygeno.2017.06.007>
- Colijn, C., & Gardy, J. (2014). Phylogenetic tree shapes resolve disease transmission patterns. *Evolution, Medicine and Public Health*, 2014(1), 96–108. <https://doi.org/10.1093/emph/eou018>
- Cui, J., Li, F., & Shi, Z. L. (2019). Origin and evolution of pathogenic coronaviruses. *Nature Reviews Microbiology*, 17(3), 181–192. <https://doi.org/10.1038/s41579-018-0118-9>
- Fehr, A. R., & Perlman, S. (2015). Coronaviruses: an overview of their replication and pathogenesis. *Methods in Molecular Biology (Clifton, N.J.)*, 1282, 1–23. https://doi.org/10.1007/978-1-4939-2438-7_1
- Gorbalenya, A. E., Baker, S. C., Baric, R. S., de Groot, R. J., Drosten, C., Gulyaeva, A. A., Haagmans, B. L., Lauber, C., Leontovich, A. M., Neuman, B. W., Penzar, D., Perlman, S., Poon, L. L. M., Samborskiy, D. V., Sidorov, I. A., Sola, I., & Ziebuhr, J. (2020). The species Severe acute respiratory syndrome-related coronavirus: classifying 2019-nCoV and naming it SARS-CoV-2. *Nature Microbiology*, 5(4), 536–544. <https://doi.org/10.1038/s41564-020-0695-z>
- Grubaugh, N. D., Petrone, M. E., & Holmes, E. C. (2020). We shouldn't worry when a virus mutates during disease outbreaks. *Nature Microbiology*, 5(4), 529–530. <https://doi.org/10.1038/s41564-020-0690-4>
- Gunadi, Wibawa, H., Marcellus, Hakim, M. S., Daniwijaya, E. W., Rizki, L. P., Supriyati, E., Nugrahaningsih, D. A. A., Afiahayati, Siswanto, Iskandar, K., Anggorowati, N., Kalim, A. S., Puspitarani, D. A., Athollah, K., Arguni, E., Nuryastuti, T., & Wibawa, T. (2020). Full-length genome characterization and phylogenetic analysis of SARS-CoV-2 virus strains from Yogyakarta and Central Java, Indonesia. *PeerJ*, 8, 1–15. <https://doi.org/10.7717/peerj.10575>
- Harapan, H., Itoh, N., Yufika, A., Winardi, W., Keam, S., Te, H., Megawati, D., Hayati, Z., Wagner, A. L., & Mudatsir, M. (2020). Coronavirus disease 2019 (COVID-19): A literature review. *Journal of Infection and Public Health*, 13(5), 667–673. <https://doi.org/10.1016/j.jiph.2020.03.019>

- Laha, S., Chakraborty, J., Das, S., Manna, S. K., Biswas, S., & Chatterjee, R. (2020). Characterizations of SARS-CoV-2 mutational profile, spike protein stability and viral transmission. *Infection, Genetics and Evolution*, 85(May), 104445. <https://doi.org/10.1016/j.meegid.2020.104445>
- Lim, W. S., Liang, C. K., Assantachai, P., Auyueung, T. W., Kang, L., Lee, W. J., Lim, J. Y., Sugimoto, K., Akishita, M., Chia, S. L., Chou, M. Y., Ding, Y. Y., Iijima, K., Jang, H. C., Kawashima, S., Kim, M., Kojima, T., Kuzuya, M., Lee, J., ... Arai, H. (2020). COVID-19 and older people in Asia: Asian Working Group for Sarcopenia calls to actions. *Geriatrics and Gerontology International*, 20(6), 547–558. <https://doi.org/10.1111/ggi.13939>
- Lucianus, J. (2003). Introduksi Genetika Molekular Virus. *Jurnal Kedokteran Maranatha*, 3(1), 1–5.
- Ogawa, J., Zhu, W., Tonnu, N., Singer, O., Hunter, T., Ryan, A. L., & Pao, G. M. (2020). The D614G mutation in the SARS-CoV2 Spike protein increases infectivity in an ACE2 receptor dependent manner. *BioRxiv*, 2020.07.21.214932. <https://doi.org/10.1101/2020.07.21.214932>
- Peck, K. M., & Lauring, A. S. (2018). Complexities of Viral Mutation Rates. *Journal of Virology*, 92(14), e01031-17. <https://doi.org/10.1128/JVI.01031-17>
- Prastyowati, A. (2020). Mengenal Karakteristik Virus SARS-CoV-2 Penyebab Penyakit COVID-19 Sebagai Dasar Upaya Untuk Pengembangan Obat Antivirus Dan Vaksin. *BioTrends*, 11(1), 1–10.
- Puenpa, J., Suwannakarn, K., Chansaenroj, J., Nilyanimit, P., Yorsaeng, R., Auphimai, C., Kitphati, R., Mungaomklang, A., Kongklieng, A., Chirathaworn, C., Wanlapakorn, N., & Poovorawan, Y. (2020). Molecular epidemiology of the first wave of severe acute respiratory syndrome coronavirus 2 infection in Thailand in 2020. *Scientific Reports*, 10(1), 1–8. <https://doi.org/10.1038/s41598-020-73554-7>
- Rahman, M. S., Islam, M. R., Hoque, M. N., Alam, A. S. M. R. U., Akther, M., Puspo, J. A., Akter, S., Anwar, A., Sultana, M., & Hossain, M. A. (2020). Comprehensive annotations of the mutational spectra of SARS-CoV-2 spike protein: a fast and accurate pipeline. *BioRxiv*, 2020.06.29.177238. <https://doi.org/10.1101/2020.06.29.177238>
- Sanjuán, R., Nebot, M. R., Chirico, N., Mansky, L. M., & Belshaw, R. (2010). Viral Mutation Rates. *Journal of Virology*, 84(19), 9733. <https://doi.org/10.1128/JVI.00694-10>
- Shereen, M. A., Khan, S., Kazmi, A., Bashir, N., & Siddique, R. (2020). COVID-19 infection: Origin, transmission, and characteristics of human coronaviruses. *Journal of Advanced Research*, 24, 91–98. <https://doi.org/10.1016/j.jare.2020.03.005>
- Walls, A. C., Park, Y.-J., Tortorici, M. A., Wall, A., McGuire, A. T., & Veesler, D. (2020). Structure, Function, and Antigenicity of the SARS-CoV-2 Spike Glycoprotein. *Cell*. <https://doi.org/10.1016/j.cell.2020.02.058>
- Wang, Z., Qiang, W., & Ke, H. (2020). A Handbook of 2019-nCoV Pneumonia Control and Prevention. *Hubei Science and Technology Press*, 1–108.
- Woo, P. C. Y., Huang, Y., Lau, S. K. P., & Yuen, K. Y. (2010). Coronavirus genomics and

bioinformatics analysis. *Viruses*, 2(8), 1805–1820. <https://doi.org/10.3390/v2081803>

