

DAFTAR PUSTAKA

- Abduljalil, J. M., & Abduljalil, B. M. (2020). *Epidemiology, genome, and clinical features of the pandemic SARS-CoV-2: a recent view*. *New Microbes and New Infections*, 100672. doi:10.1016/j_nmni.2020.100672
- Andersen, K. G., Rambaut, A., Lipkin, W. I., Holmes, E. C., and Garry, R. F. (2020). The proximal origin of SARS-CoV-2. *Nat. Med.* 26, 450–452. doi: 10.1038/s41591-020-0820-9
- Brufsky, A. (2020). Distinct viral clades of SARS-CoV-2: implications for modeling of viral spread. *J. Med. Virol.* doi: 10.1002/jmv.25902. doi:10.1002/jmv.25902
- Butarbutar, V. M. D., Setiawan, A., Mahatma, T. (2020). ANALISIS DATA SNP (SINGLE NUCLEOTIDE POLYMORPHISM) DENGAN METODE CHI-SQUARE. Universitas Muhammadiyah Purworejo : Seminar Nasional Matematika dan Pendidikan Matematika (Sendika) 2020. Prosiding Sendika Vol. 6, No. 1, 2020 ISSN. 2459-962X
- Chen, J., Wang, R., Wang, M., & Wei, G.-W. (2020). *Mutations Strengthened SARS-CoV-2 Infectivity*. *Journal of Molecular Biology*. doi:10.1016/j.jmb.2020.07.009
- Cosma, E. (2019). Pivot Table: A Tool to Calculate, Summarize, and Analyze Data. “Ovidius” University Annals, Economic Sciences Series Volume XIX, Issue 1 /2019
- Coutard, B., Valle, C., de Lamballerie, X., Canard, B., Seidah, N.G., Decroly, E. (2020). The spike glycoprotein of the new coronavirus 2019-nCoV contains a furin-like cleavage site absent in CoV of the same clade. *Antiviral Research* 176 (2020) 104742 0166-3542 [doi:10.1016/j.antiviral.2020.104742](https://doi.org/10.1016/j.antiviral.2020.104742)
- Dharmayanti, N.L.P. I. (2011). Molecular Phylogenetic: Organism Taxonomy Method Based on Evolution History. WARTAZOA. Indonesian Bulletin of Animal and Veterinary Sciences; Vol 21, No 1 (2011): MARCH 2011 <http://medpub.litbang.pertanian.go.id/index.php/wartazoa/article/view/948/957>
- Elbe, S., & Buckland-Merrett, G. (2017). *Data, disease and diplomacy: GISAID's*

- innovative contribution to global health. Global Challenges, 1(1), 33–46.* doi:10.1002/gch2.1018
- Hijikata, A., Shionyu-Mitsuyama, C., Nakae, S., Shionyu, M., Ota, M., Kanaya, S., & Shirai, T. (2020). *Knowledge-based structural models of SARS-CoV-2 proteins and their complexes with potential drugs. FEBS Letters.* doi:10.1002/1873-3468.13806
- <https://www.worldometers.info/coronavirus/>
- Koyama, T., Platt, D., & Parida, L. (2020). Variant analysis of SARS-CoV-2 genomes. *Bulletin of the World Health Organization, 98(7), 495–504.*
<https://doi.org/10.2471/BLT.20.253591>
- Lusiastuti, A. M., Seeger, H., Sugiani, D., Mufidah, T., & Novita, H. (2015). Deteksi Polymorfisme dengan Substitusi Nukleotida Tunggal pada Streptococcus Agalactiae Isolat Lokal Indonesia. *Ejournal-Balitbang.Kkp.Go.Id, 10(2)*, Media Akuakultur Vol. 10 No. 2 Tahun 2015: 91–95. <http://ejournal-balitbang.kkp.go.id/index.php/ma/article/view/961>
- Mercatelli, Daniele; Giorgi, Federico M. (2020). Geographic and Genomic Distribution of SARS-CoV-2 Mutations. *Frontiers in Microbiology, 11()*, 1800–. doi:10.3389/fmicb.2020.01800
- Modrow, S., Falke, D., Truyen, U., & Schätzl, H. (2013). *Viruses: Definition, Structure, Classification. Molecular Virology, 17–30.* doi:10.1007/978-3-642-20718-1_2
- Mulyono, A., Ristiyanto, Handayani, F. D., Putro, D. B. W., Joharina, A. S. (2016). Karakteristik Molekuler Segmen L Virus Seoul (SEOV) dari Rattus Norvegicus Asal Semarang, Jawa Tengah. Salatiga : Buletin Penelitian Kesehatan, Vol. 44, No. 1, Maret 2016 : 69-76
- Parikesit AA, D Anurogo & RA Putranto (2017). The utilization of bioinformatics in the field of agriculture and health. *E-Journal Menara Perkebunan, 85(2), 106-115.*
- Park, J.-E., Kim, K., Jung, Y., Kim, J.-H., & Nam, J.-M. (2016). Metal Nanoparticles for Virus Detection. *ChemNanoMat, 2(10), 927–936.* doi:10.1002/cnma.201600165
- Peck, K. M., & Lauring, A. S. (2018). *Complexities of Viral Mutation Rates.*

- Journal of Virology*, 92(14). doi: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
- Pruesse, E., Peplies, J., & Glöckner, F. O. (2012). *SINA: Accurate high-throughput multiple sequence alignment of ribosomal RNA genes*. *Bioinformatics*, 28(14), 1823–1829. doi:10.1093/bioinformatics/bts252
- Putranto R-A, C Duan, Kuswanhadi, T Chaidamsari, M Rio, P Piyatrakul, E Herlinawati, J Pirrello, F Dessailly, J Leclercq, F Bonnot, C Tang, S Hu & P Montoro (2015). Ethylene Response Factors are controlled by multiple harvesting stresses in *Hevea brasiliensis*. *PLoS ONE*, 10(4), e0123618.
- Putri, A. & Wathon, S. (2018). Aplikasi Single Nucleotide Polymorphism (SNP) Dalam Studi Farmakogenomik Untuk Pengembangan Obat. Universitas Jember : BioTrends Vol.9 No.2 Tahun 2018
- Romano, M., Ruggiero, A., Squeglia, F., Maga, G., & Berisio, R. (2020). *A Structural View of SARS-CoV-2 RNA Replication Machinery: RNA Synthesis, Proofreading and Final Capping*. *Cells*, 9(5), 1267. doi:10.3390/cells9051267
- Sanjuan, R., Nebot, M. R., Chirico, N., Mansky, L. M., & Belshaw, R. (2010). *Viral Mutation Rates*. *Journal of Virology*, 84(19), 9733–9748. doi:10.1128/jvi.00694-10
- Shi, J., Wen, Z., Zhong, G., Yang, H., Wang, C., Huang, B., ... Bu, Z. (2020). *Susceptibility of ferrets, cats, dogs, and other domesticated animals to SARS-coronavirus 2*. *Science*, eabb7015. doi:10.1126/science.abb7015
- Shu, Y., & McCauley, J. (2017). *GISAID: Global initiative on sharing all influenza data – from vision to reality*. *Eurosurveillance*, 22(13). doi:10.2807/1560-7917.es.2017.22.13.30494
- Sunarto, A. A. (2015). Perbandingan Program Sequence Alignment. Sukabumi: JURNAL REKAYASA NUSAPUTRA Vol 1 No. 1 2015
- Zhang, Y.-Z., & Holmes, E. C. (2020). *A Genomic Perspective on the Origin and Emergence of SARS-CoV-2*. *Cell*. doi:10.1016/j.cell.2020.03.035

Zhou, P., Yang, X.-L., Wang, X.-G., Hu, B., Zhang, L., Zhang, W., ... Shi, Z.-L. (2020). *A pneumonia outbreak associated with a new coronavirus of probable bat origin*. *Nature*. doi:10.1038/s41586-020-2012-7