

REFERENCES

- Acuti Martellucci, C., Flacco, M. E., Cappadona, R., Bravi, F., Mantovani, L., & Manzoli, L. (2020). SARS-CoV-2 pandemic: An overview. *Advances in Biological Regulation*, 77, 100736. <https://doi.org/10.1016/J.JBIOR.2020.100736>
- Adhikari, S. P., Meng, S., Wu, Y. J., Mao, Y. P., Ye, R. X., Wang, Q. Z., Sun, C., Sylvia, S., Rozelle, S., Raat, H., & Zhou, H. (2020). Epidemiology, causes, clinical manifestation and diagnosis, prevention and control of coronavirus disease (COVID-19) during the early outbreak period: a scoping review. *Infectious Diseases of Poverty*, 9(1). <https://doi.org/10.1186/S40249-020-00646-X>
- Agerer, B., Koblischke, M., Gudipati, V., Montaño-Gutierrez, L. F., Smyth, M., Popa, A., Genger, J. W., Endler, L., Florian, D. M., Mühlgrabner, V., Graninger, M., Aberle, S. W., Husa, A. M., Shaw, L. E., Lercher, A., Gattinger, P., Torralba-Gombau, R., Trapin, D., Penz, T., ... Bergthaler, A. (2021). SARS-CoV-2 mutations in MHC-I-restricted epitopes evade CD8+ T cell responses. *Science Immunology*, 6(57), 6461.
- Aleem, A., Akbar Samad, A. B., & Slenker, A. K. (2021). Emerging Variants of SARS-CoV-2 And Novel Therapeutics Against Coronavirus (COVID-19). In *StatPearls*. StatPearls Publishing.
- Astuti, I., & Ysrafil. (2020). Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2): An overview of viral structure and host response. *Diabetes & Metabolic Syndrome*, 14(4), 407. <https://doi.org/10.1016/J.DSX.2020.04.020>
- Atzrodt, C. L., Maknojia, I., McCarthy, R. D. P., Oldfield, T. M., Po, J., Ta, K. T. L., Stepp, H. E., & Clements, T. P. (2020). A Guide to COVID-19: a global pandemic caused by the novel coronavirus SARS-CoV-2. *The FEBS Journal*, 287(17), 3633–3650. <https://doi.org/10.1111/FEBS.15375>
- Barba, M., Czosnek, H., & Hadidi, A. (2014). Historical perspective, development and applications of next-generation sequencing in plant virology. *Viruses*, 6(1), 106–136. <https://doi.org/10.3390/v6010106>
- Bettini, E., & Locci, M. (2021). SARS-CoV-2 mRNA Vaccines: Immunological Mechanism and Beyond. *Vaccines*, 9(2), 1–20. <https://doi.org/10.3390/VACCINES9020147>
- Borcard, L., Gempeler, S., Miani, M. A. T., Baumann, C., Grädel, C., Dijkman, R., ... & Ramette, A. (2022). Investigating the extent of primer dropout in SARS-CoV-2 genome sequences during the early circulation of Delta variants. *Frontiers in Virology*, 28.
- Brejová, B., Boršová, K., Hodorová, V., Čabanová, V., Gafurov, A., Fričová, D., Neboháčová, M., Vinař, T., Klempa, B., & Nosek, J. (2021). Nanopore Sequencing of SARS-CoV-2: Comparison of Short and Long PCR-tiling Amplicon Protocols. *MedRxiv*, 2021.05.12.21256693. <https://doi.org/10.1101/2021.05.12.21256693>

- Bull, R. A., Adikari, T. N., Ferguson, J. M., Hammond, J. M., Stevanovski, I., Beukers, A. G., Naing, Z., Yeang, M., Verich, A., Gamaarachchi, H., Kim, K. W., Luciani, F., Stelzer-Braid, S., Eden, J. S., Rawlinson, W. D., van Hal, S. J., & Deveson, I. W. (2020). Analytical validity of nanopore sequencing for rapid SARS-CoV-2 genome analysis. *Nature Communications* 2020 11:1, 11(1), 1–8. <https://doi.org/10.1038/s41467-020-20075-6>
- Calis, J. J., Maybeno, M., Greenbaum, J. A., Weiskopf, D., De Silva, A. D., Sette, A., Keşmir, C., & Peters, B. (2013). Properties of MHC class I presented peptides that enhance immunogenicity. *PLoS computational biology*, 9(10), e1003266. <https://doi.org/10.1371/journal.pcbi.1003266>
- Cascella, M., Rajnik, M., Aleem, A., Dulebohn, S. C., & Di Napoli, R. (2021). Features, Evaluation, and Treatment of Coronavirus (COVID-19). In *StatPearls*. StatPearls Publishing.
- Chiara, M., D'Erchia, A. M., Gissi, C., Manzari, C., Parisi, A., Resta, N., Zambelli, F., Picardi, E., Pavesi, G., Horner, D. S., & Pesole, G. (2021). Next generation sequencing of SARS-CoV-2 genomes: challenges, applications and opportunities. *Briefings in Bioinformatics*, 22(2), 616–630. <https://doi.org/10.1093/BIB/BBA297>
- Ciotti, M., Ciccozzi, M., Terrinoni, A., Jiang, W. C., Wang, C. bin, & Bernardini, S. (2020). The COVID-19 pandemic. <Https://Doi.Org/10.1080/10408363.2020.1783198>, 57(6), 365–388. <https://doi.org/10.1080/10408363.2020.1783198>
- 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, 104742. <https://doi.org/10.1016/J.ANTIVIRAL.2020.104742>
- Davis, J. J., Long, S. W., Christensen, P. A., Olsen, R. J., Olson, R., Shukla, M., ... & Musser, J. M. (2021). Analysis of the ARTIC version 3 and version 4 SARS-CoV-2 primers and their impact on the detection of the G142D amino acid substitution in the spike protein. *Microbiology spectrum*, 9(3), e01803-21.
- Dearlove, B., Lewitus, E., Bai, H., Li, Y., Reeves, D. B., Joyce, M. G., ... & Rolland, M. (2020). A SARS-CoV-2 vaccine candidate would likely match all currently circulating variants. *Proceedings of the National Academy of Sciences*, 117(38), 23652-23662.
- Dhanda, S. K., Vir, P., & Raghava, G. P. (2013). Designing of interferon-gamma inducing MHC class-II binders. *Biology direct*, 8(1), 1-15.
- Dhawan, D. (2017). Clinical Next-Generation Sequencing: Enabling Precision Medicine. *Progress and Challenges in Precision Medicine*, 35–54. <https://doi.org/10.1016/B978-0-12-809411-2.00002-7>

- Dong, Y., Dai, T., Wei, Y., Zhang, L., Zheng, M., & Zhou, F. (2020). A systematic review of SARS-CoV-2 vaccine candidates. *Signal transduction and targeted therapy*, 5(1), 1-14.
- Esakandari, H., Nabi-Afjadi, M., Fakkari-Afjadi, J., Farahmandian, N., Miresmaeili, S. M., & Bahreini, E. (2020). A comprehensive review of COVID-19 characteristics. *Biological procedures online*, 22, 1-10.
- European Centre for Disease Prevention and Control. (2021). Sequencing of SARS-CoV-2: first update. Stockholm. Retrieved from <https://www.ecdc.europa.eu/sites/default/files/documents/Sequencing-of-SARS-CoV-2-first-update.pdf>.
- Firmansyah, M. J. (2022). 90% of covid cases in Indonesia omicron: Health ministry. Tempo. Retrieved May 20, 2022, from <https://en.tempo.co/read/1561610/90-of-covid-cases-in-indonesia-omicron-health-ministry>
- Garstka, M. A., Fish, A., Celie, P. H., Joosten, R. P., Janssen, G. M., Berlin, I., ... & Neefjes, J. (2015). The first step of peptide selection in antigen presentation by MHC class I molecules. *Proceedings of the National Academy of Sciences*, 112(5), 1505-1510.
- Goodwin, S., McPherson, J. D., & McCombie, W. R. (2016). Coming of age: ten years of next-generation sequencing technologies. *Nature Reviews Genetics* 2016 17:6, 17(6), 333–351. <https://doi.org/10.1038/nrg.2016.49>
- Grudlewska-Buda, K., Wiktorczyk-Kapischke, N., Wałecka-Zacharska, E., Kwiecińska-Piróg, J., Buszko, K., Leis, K., Juszczuk, K., Gospodarek-Komkowska, E., & Skowron, K. (2021). Sars-cov-2—morphology, transmission and diagnosis during pandemic, review with element of meta-analysis. *Journal of Clinical Medicine*, 10(9). <https://doi.org/10.3390/JCM10091962/S1>
- Gunadi, M. S. H., Wibawa, H., Marcellus, V. S., Slamet, I. T., Supriyati, E., El Khair, R., ... & Wibawa, T. (2021). Is the infection of the SARS-CoV-2 Delta variant associated with the outcomes of COVID-19 patients?. *Frontiers in medicine*, 8.
- Gupta, A. K., & Gupta, U. D. (2014). Next Generation Sequencing and Its Applications. *Animal Biotechnology: Models in Discovery and Translation*, 345–367. <https://doi.org/10.1016/B978-0-12-416002-6.00019-5>
- Gustiananda, M., Sulistyo, B. P., Agustriawan, D., & Andarini, S. (2021). Immunoinformatics Analysis of SARS-CoV-2 ORF1ab Polyproteins to Identify Promiscuous and Highly Conserved T-Cell Epitopes to Formulate Vaccine for Indonesia and the World Population. *Vaccines*, 9(12), 1459.

- Harvey, W. T., Carabelli, A. M., Jackson, B., Gupta, R. K., Thomson, E. C., Harrison, E. M., Ludden, C., Reeve, R., Rambaut, A., Peacock, S. J., & Robertson, D. L. (2021). SARS-CoV-2 variants, spike mutations and immune escape. *Nature Reviews Microbiology* 2021 19:7, 19(7), 409–424. <https://doi.org/10.1038/s41579-021-00573-0>
- Heather, J. M., & Chain, B. (2016). The sequence of sequencers: The history of sequencing DNA. *Genomics*, 107(1), 1. <https://doi.org/10.1016/J.YGENO.2015.11.003>
- Hoffmann, M., Kleine-Weber, H., Schroeder, S., Krüger, N., Herrler, T., Erichsen, S., Schiergens, T. S., Herrler, G., Wu, N. H., Nitsche, A., Müller, M. A., Drosten, C., & Pöhlmann, S. (2020). SARS-CoV-2 Cell Entry Depends on ACE2 and TMPRSS2 and Is Blocked by a Clinically Proven Protease Inhibitor. *Cell*, 181(2), 271-280.e8. <https://doi.org/10.1016/J.CELL.2020.02.052>
- Hu, B., Guo, H., Zhou, P., & Shi, Z. L. (2020). Characteristics of SARS-CoV-2 and COVID-19. *Nature Reviews Microbiology* 2020 19:3, 19(3), 141–154. <https://doi.org/10.1038/s41579-020-00459-7>
- Huang, Y., Yang, C., Xu, X. F., Xu, W., & Liu, S. W. (2020). Structural and functional properties of SARS-CoV-2 spike protein: potential antiviral drug development for COVID-19. *Acta Pharmacologica Sinica*, 41(9), 1141-1149.
- Jakhar, R., & Gakhar, S. K. (2020). An immunoinformatics study to predict epitopes in the envelope protein of SARS-CoV-2. *Canadian Journal of Infectious Diseases and Medical Microbiology*, 2020.
- James, P. (2020). *Nanopore sequencing the SARS-CoV-2 genome: Introduction to Protocol*. Oxford Nanopore Technologies. Retrieved July 18, 2022, from <https://nanoporetech.com/resource-centre/nanopore-sequencing-sars-cov-2-genome-introduction-protocol>
- Jayaweera, M., Perera, H., Gunawardana, B., & Manatunge, J. (2020). Transmission of COVID-19 virus by droplets and aerosols: A critical review on the unresolved dichotomy. *Environmental Research*, 188, 109819. <https://doi.org/10.1016/J.ENVRES.2020.109819>
- Kadam, S. B., Sukhramani, G. S., Bishnoi, P., Pable, A. A., & Barvkar, V. T. (2021). SARS-CoV-2, the pandemic coronavirus: Molecular and structural insights. *Journal of Basic Microbiology*, 61(3), 180–202. <https://doi.org/10.1002/JOBM.202000537>
- Kim, D., Lee, J. Y., Yang, J. S., Kim, J. W., Kim, V. N., & Chang, H. (2020). The architecture of SARS-CoV-2 transcriptome. *Cell*, 181(4), 914-921.
- Konings, F., Perkins, M. D., Kuhn, J. H., Pallen, M. J., Alm, E. J., Archer, B. N., ... & Van Kerkhove, M. D. (2021). SARS-CoV-2 Variants of Interest and Concern naming scheme conducive for global discourse. *Nature Microbiology*, 1-3.

- Krishnan, A., Hamilton, J. P., Alqahtani, S. A., & Woreta, T. A. (2021). COVID-19: An overview and a clinical update. *World Journal of Clinical Cases*, 9(1), 8. <https://doi.org/10.12998/WJCC.V9.I1.8>
- Kumar, S., Nyodu, R., Maurya, V. K., & Saxena, S. K. (2020). Morphology, Genome Organization, Replication, and Pathogenesis of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). *Coronavirus Disease 2019 (COVID-19)*, 23. https://doi.org/10.1007/978-981-15-4814-7_3
- Lam, T. T. Y., Jia, N., Zhang, Y. W., Shum, M. H. H., Jiang, J. F., Zhu, H. C., Tong, Y. G., Shi, Y. X., Ni, X. B., Liao, Y. S., Li, W. J., Jiang, B. G., Wei, W., Yuan, T. T., Zheng, K., Cui, X. M., Li, J., Pei, G. Q., Qiang, X., ... Cao, W. C. (2020). Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins. *Nature* 2020 583:7815, 583(7815), 282–285. <https://doi.org/10.1038/s41586-020-2169-0>
- Lambisia, A. W., Mohammed, K. S., Makori, T. O., Ndwiga, L., Mburu, M. W., Morobe, J. M., Mora, E. O., Musyoki, J., Murunga, N., Mwangi, J. N., Nokes, D. J., Agoti, C. N., Ochola-Oyier, L. I., & Githinji, G. (2022). Optimization of the SARS-CoV-2 ARTIC Network V4 Primers and Whole Genome Sequencing Protocol. *Frontiers in medicine*, 9, 836728. <https://doi.org/10.3389/fmed.2022.836728>
- Lauring, A. S., & Malani, P. N. (2021). Variants of SARS-CoV-2. *JAMA*, 326(9), 880–880. <https://doi.org/10.1001/JAMA.2021.14181>
- Lebeau, G., Vagner, D., Frumence, É., Ah-Pine, F., Guillot, X., Nobécourt, E., Raffray, L., & Gasque, P. (2020). Deciphering SARS-CoV-2 Virologic and Immunologic Features. *International Journal of Molecular Sciences* 2020, Vol. 21, Page 5932, 21(16), 5932. <https://doi.org/10.3390/IJMS21165932>
- Li, H., Wang, Y., Ji, M., Pei, F., Zhao, Q., Zhou, Y., Hong, Y., Han, S., Wang, J., Wang, Q., Li, Q., & Wang, Y. (2020). Transmission Routes Analysis of SARS-CoV-2: A Systematic Review and Case Report. *Frontiers in Cell and Developmental Biology*, 8. <https://doi.org/10.3389/FCELL.2020.00618>
- Lotfi, M., Hamblin, M. R., & Rezaei, N. (2020). COVID-19: Transmission, prevention, and potential therapeutic opportunities. *Clinica Chimica Acta; International Journal of Clinical Chemistry*, 508, 254. <https://doi.org/10.1016/J.CCA.2020.05.044>
- Lu, H., Giordano, F., & Ning, Z. (2016). Oxford Nanopore MinION Sequencing and Genome Assembly. *Genomics, Proteomics & Bioinformatics*, 14(5), 265–279. <https://doi.org/10.1016/J.GPB.2016.05.004>
- Lu, R., Zhao, X., Li, J., Niu, P., Yang, B., Wu, H., Wang, W., Song, H., Huang, B., Zhu, N., Bi, Y., Ma, X., Zhan, F., Wang, L., Hu, T., Zhou, H., Hu, Z., Zhou, W., Zhao, L., ... Tan, W. (2020). Genomic

- characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. *The Lancet*, 395(10224), 565–574.
[https://doi.org/10.1016/S0140-6736\(20\)30251-8](https://doi.org/10.1016/S0140-6736(20)30251-8)
- Ma, E. (2018). *Correcting Ambiguous Base Labels in DNA Sequencing using Neural Networks and its Impact on DNA Barcoding Applications* (Doctoral dissertation, University of Guelph).
- Majumdar, P., & Niyogi, S. (2021). SARS-CoV-2 mutations: The biological trackway towards viral fitness. *Epidemiology & Infection*, 149.
- Malik, Y. A. (n.d.). *Properties of Coronavirus and SARS-CoV-2*.
- Marques-Pereira, C., Pires, M. N., Gouveia, R. P., Pereira, N. N., Caniceiro, A. B., Rosário-Ferreira, N., & Moreira, I. S. (2022). SARS-CoV-2 membrane protein: from genomic data to structural new insights. *International journal of molecular sciences*, 23(6), 2986.
- Marshall, J. S., Warrington, R., Watson, W., & Kim, H. L. (2018). An introduction to immunology and immunopathology. *Allergy, Asthma and Clinical Immunology*, 14(2), 1–10.
<https://doi.org/10.1186/S13223-018-0278-1/TABLES/4>
- Mishra, S. (2020). Designing of cytotoxic and helper T cell epitope map provides insights into the highly contagious nature of the pandemic novel coronavirus SARS-CoV-2. *Royal Society open science*, 7(9), 201141.
- Naqvi, A. A. T., Fatima, K., Mohammad, T., Fatima, U., Singh, I. K., Singh, A., Atif, S. M., Hariprasad, G., Hasan, G. M., & Hassan, M. I. (2020). Insights into SARS-CoV-2 genome, structure, evolution, pathogenesis and therapies: Structural genomics approach. *Biochimica et Biophysica Acta. Molecular Basis of Disease*, 1866(10), 165878.
<https://doi.org/10.1016/J.BBADIS.2020.165878>
- Niesen, M., Anand, P., Silvert, E., Suratekar, R., Pawlowski, C., Ghosh, P., ... & Soundararajan, V. (2021). COVID-19 vaccines dampen genomic diversity of SARS-CoV-2: Unvaccinated patients exhibit more antigenic mutational variance. *medRxiv*.
- Noh, J. Y., Jeong, H. W., & Shin, E. C. (2021). SARS-CoV-2 mutations, vaccines, and immunity: implication of variants of concern. *Signal Transduction and Targeted Therapy*, 6(1), 1-2.
- Ogishi, M., & Yotsuyanagi, H. (2019). Quantitative prediction of the landscape of T cell epitope immunogenicity in sequence space. *Frontiers in immunology*, 10, 827.
- Ophinni, Y., Hasibuan, A. S., Widhani, A., Maria, S., Koesnoe, S., Yunihastuti, E., Karjadi, T. H., Rengganis, I., & Djauzi, S. (2020). COVID-19 Vaccines: Current Status and Implication for Use in Indonesia. *Acta medica Indonesiana*, 52(4), 388–412.
- Oude Munnink, B. B., Worp, N., Nieuwenhuijse, D. F., Sikkema, R. S., Haagmans, B., Fouchier, R. A. M., & Koopmans, M. (2021). The next phase of SARS-CoV-2 surveillance: real-time molecular

- epidemiology. *Nature Medicine* 2021; 27(9), 1518–1524.
<https://doi.org/10.1038/s41591-021-01472-w>
- Pal, M., Berhanu, G., Desalegn, C., & Kandi, V. (2020). Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2): An Update. *Cureus*, 12(3).
<https://doi.org/10.7759/CUREUS.7423>
- Pascual-Iglesias, A., Canton, J., Ortega-Prieto, A. M., Jimenez-Guardeño, J. M., & Regla-Nava, J. A. (2021). An Overview of Vaccines against SARS-CoV-2 in the COVID-19 Pandemic Era. *Pathogens* 2021, Vol. 10, Page 1030, 10(8), 1030.
<https://doi.org/10.3390/PATHOGENS10081030>
- Peck, K. M., & Lauring, A. S. (2018). Complexities of Viral Mutation Rates. *Journal of Virology*, 92(14).
<https://doi.org/10.1128/JVI.01031-17/ASSET/24D089E9-DAC2-41E5-847F-8AA925BCF80D/ASSETS/GRAPHIC/ZJV0141836750002.JPG>
- Ricci, D., Etna, M. P., Rizzo, F., Sandini, S., Severa, M., & Coccia, E. M. (2021). Innate Immune Response to SARS-CoV-2 Infection: From Cells to Soluble Mediators. *International Journal of Molecular Sciences*, 22(13). <https://doi.org/10.3390/IJMS22137017>
- Robishaw, J. D., Alter, S. M., Solano, J. J., Shih, R. D., DeMets, D. L., Maki, D. G., & Hennekens, C. H. (2021). Genomic surveillance to combat COVID-19: challenges and opportunities. *The Lancet Microbe*, 2(9), e481–e484. [https://doi.org/10.1016/S2666-5247\(21\)00121-X](https://doi.org/10.1016/S2666-5247(21)00121-X)
- Satarker, S., & Nampoothiri, M. (2020). Structural Proteins in Severe Acute Respiratory Syndrome Coronavirus-2. *Archives of Medical Research*, 51(6), 482.
<https://doi.org/10.1016/J.ARCMED.2020.05.012>
- Schoeman, D., & Fielding, B. C. (2019). Coronavirus envelope protein: current knowledge. *Virology journal*, 16(1), 1-22.
- Sharun, K., Dhama, K., Pawde, A. M., Gortázar, C., Tiwari, R., Katherine Bonilla-Aldana, D., Rodriguez-Morales, A. J., de La Fuente, J., Michalak, I., Attia, Y. A., Gort Azar C, C., de La Fuente, J. E., Pandit, P., Dayal, D., Chikitsa, U. P., Vishwavidyalaya, V., Go, E., & Sansthan, A. (2021). SARS-CoV-2 in animals: potential for unknown reservoir hosts and public health implications. <Https://Doi.Org/10.1080/01652176.2021.1921311>, 41(1), 181–201.
<https://doi.org/10.1080/01652176.2021.1921311>
- Surjit, M., & Lal, S. K. (2009). The Nucleocapsid Protein of the SARS Coronavirus: Structure, Function and Therapeutic Potential. *Molecular Biology of the SARS-CoVavirus*, 129–151.
https://doi.org/10.1007/978-3-642-03683-5_9
- Tarke, A., Sidney, J., Methot, N., Yu, E. D., Zhang, Y., Dan, J. M., Goodwin, B., Rubiro, P., Sutherland, A., Wang, E., Frazier, A., Ramirez, S. I., Rawlings, S. A., Smith, D. M., da Silva Antunes, R., Peters,

- B., Scheuermann, R. H., Weiskopf, D., Crotty, S., Grifoni, A., ... Sette, A. (2021). Impact of SARS-CoV-2 variants on the total CD4+ and CD8+ T cell reactivity in infected or vaccinated individuals. *Cell reports Medicine*, 2(7), 100355. <https://doi.org/10.1016/j.xcrm.2021.100355>
- Tarke, A., Sidney, J., Methot, N., Yu, E. D., Zhang, Y., Dan, J. M., Goodwin, B., Rubiro, P., Sutherland, A., Wang, E., Frazier, A., Ramirez, S. I., Rawlings, S. A., Smith, D. M., da Silva Antunes, R., Peters, B., Scheuermann, R. H., Weiskopf, D., Crotty, S., ... Sette, A. (2021). Impact of SARS-CoV-2 variants on the total CD4+ and CD8+ T cell reactivity in infected or vaccinated individuals. *Cell Reports Medicine*, 2(7). <https://doi.org/10.1016/j.xcrm.2021.100355>
- Tarke, A., Sidney, J., Methot, N., Zhang, Y., Dan, J. M., Goodwin, B., ... & Sette, A. (2021). Negligible impact of SARS-CoV-2 variants on CD4+ and CD8+ T cell reactivity in COVID-19 exposed donors and vaccinees. *Biorxiv*.
- Tenda, E. D., Asaf, M. M., Pradipta, A., Kumaheri, M. A., & Susanto, A. P. (2021). The COVID-19 surge in Indonesia: what we learned and what to expect. *Breathe*, 17(4).
- Thomas, S. (2020). The Structure of the Membrane Protein of SARS-CoV-2 Resembles the Sugar Transporter SemiSWEET. *Pathogens and Immunity*, 5(1), 342.
- Troyano-Hernández, P., Reinosa, R., & Holguín, Á. (2021). Evolution of SARS-CoV-2 Envelope, Membrane, Nucleocapsid, and Spike Structural Proteins from the Beginning of the Pandemic to September 2020: A Global and Regional Approach by Epidemiological Week. *Viruses 2021*, Vol. 13, Page 243, 13(2), 243. <https://doi.org/10.3390/V13020243>
- Ullah, H., Ullah, A., Gul, A., Mousavi, T., & Khan, M. W. (2021). Novel coronavirus 2019 (COVID-19) pandemic outbreak: A comprehensive review of the current literature. *Vacunas (English Edition)*, 22(2), 106–113. <https://doi.org/10.1016/J.VACUNE.2020.09.005>
- Vita, R., Mahajan, S., Overton, J. A., Dhanda, S. K., Martini, S., Cantrell, J. R., ... & Peters, B. (2019). The immune epitope database (IEDB): 2018 update. *Nucleic acids research*, 47(D1), D339-D343.
- V'kovski, P., Kratzel, A., Steiner, S., Stalder, H., & Thiel, V. (2020). Coronavirus biology and replication: implications for SARS-CoV-2. *Nature Reviews Microbiology* 2020 19:3, 19(3), 155–170. <https://doi.org/10.1038/s41579-020-00468-6>
- Wang, C. C., Prather, K. A., Sznitman, J., Jimenez, J. L., Lakdawala, S. S., Tufekci, Z., & Marr, L. C. (2021). Airborne transmission of respiratory viruses. *Science*, 373(6558).
- Wang, P., Sidney, J., Dow, C., Mothé, B., Sette, A., & Peters, B. (2008). A systematic assessment of MHC class II peptide binding predictions and evaluation of a consensus approach. *PLoS computational biology*, 4(4), e1000048.

- Wang, Y., Yang, Q., & Wang, Z. (2014). The evolution of nanopore sequencing. *Frontiers in Genetics*, 5(DEC), 449. [https://doi.org/10.3389/FGENE.2014.00449/BIBTEX](https://doi.org/10.3389/FGENE.2014.00449)
- Wieczorek, M., Abualrous, E. T., Sticht, J., Álvaro-Benito, M., Stolzenberg, S., Noé, F., & Freund, C. (2017). Major histocompatibility complex (MHC) class I and MHC class II proteins: conformational plasticity in antigen presentation. *Frontiers in immunology*, 8, 292.
- Williams, T. C., & Burgers, W. A. (2021). SARS-CoV-2 evolution and vaccines: cause for concern?. *The Lancet Respiratory Medicine*, 9(4), 333-335.
- Wong, N. A., & Saier, M. H. (2021). The SARS-CoV-2 Infection Cycle: A Survey of Viral Membrane Proteins, Their Functional Interactions and Pathogenesis. *International Journal of Molecular Sciences*, 22(3), 1–63. <https://doi.org/10.3390/IJMS22031308>
- Woo, H. G., & Shah, M. (2021). Omicron: A heavily mutated SARS-CoV-2 variant exhibits stronger binding to ACE2 and potently escape approved COVID-19 therapeutic antibodies. *bioRxiv*.
- World Health Organization. (n.d.). *Tracking Sars-Cov-2 Variants*. World Health Organization. Retrieved November 30, 2021, from <https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/>.
- World Health Organization. (n.d.). *WHO coronavirus (COVID-19) Dashboard*. World Health Organization. Retrieved September 17, 2021, from <https://covid19.who.int/>.
- Wu, Y. C., Chen, C. S., & Chan, Y. J. (2020). The outbreak of COVID-19: An overview. *Journal of the Chinese Medical Association*, 83(3), 217–220.
- Yadav, R., Chaudhary, J. K., Jain, N., Chaudhary, P. K., Khanra, S., Dhamija, P., Sharma, A., Kumar, A., & Handu, S. (2021). Role of Structural and Non-Structural Proteins and Therapeutic Targets of SARS-CoV-2 for COVID-19. *Cells*, 10(4). <https://doi.org/10.3390/CELLS10040821>
- Yang, H., & Rao, Z. (2021). Structural biology of SARS-CoV-2 and implications for therapeutic development. *Nature Reviews Microbiology* 2021 19:11, 19(11), 685–700. <https://doi.org/10.1038/s41579-021-00630-8>
- Yuan, M., Wu, N. C., Zhu, X., Lee, C. C. D., So, R. T. Y., Lv, H., Mok, C. K. P., & Wilson, I. A. (2020). A highly conserved cryptic epitope in the receptor binding domains of SARS-CoV-2 and SARS-CoV. *Science*, 368(6491), 630–633.
- Zhao, J., Cui, W., & Tian, B. P. (2020). The Potential Intermediate Hosts for SARS-CoV-2. *Frontiers in Microbiology*, 11, 2400. <https://doi.org/10.3389/FMICB.2020.580137/BIBTEX>
- Zheng, J. (2020). SARS-CoV-2: an Emerging Coronavirus that Causes a Global Threat. *International Journal of Biological Sciences*, 16(10), 1678. <https://doi.org/10.7150/IJBS.45053>
- Zhou, P., Yang, X. lou, Wang, X. G., Hu, B., Zhang, L., Zhang, W., Si, H. R., Zhu, Y., Li, B., Huang, C. L., Chen, H. D., Chen, J., Luo, Y., Guo, H., Jiang, R. di, Liu, M. Q., Chen, Y., Shen, X. R., Wang, X., ...

Shi, Z. L. (2020). A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature*, 579(7798), 270. <https://doi.org/10.1038/S41586-020-2012-7>

Zhu, N., Zhang, D., Wang, W., Li, X., Yang, B., Song, J., Zhao, X., Huang, B., Shi, W., Lu, R., Niu, P., Zhan, F., Ma, X., Wang, D., Xu, W., Wu, G., Gao, G. F., & Tan, W. (2020). A Novel Coronavirus from Patients with Pneumonia in China, 2019. *New England Journal of Medicine*, 382(8), 727–733