DAFTAR PUSTAKA

Ahmadi, A., Zorofchian Moghadamtousi, S., Abubakar, S., & Zandi, K. (2015). Antiviral potential of algae polysaccharides isolated from marine sources: A review. *BioMed Research International*, *2015*. https://doi.org/10.1155/2015/825203

Boopathi, S., Poma, A. B., & Kolandaivel, P. (2020). Novel 2019 coronavirus structure, mechanism of action, antiviral drug promises and rule out against its treatment. *Journal of Biomolecular Structure and Dynamics*, *39*(9), 1–10. https://doi.org/10.1080/07391102.2020.1758788

Carossino, M., Thiry, E., de la Grandière, A., & Barrandeguy, M. E. (2014). Novel vaccination approaches against equine alphavirus encephalitides. *Vaccine*, *32*(3), 311–319. https://doi.org/10.1016/j.vaccine.2013.11.071

Case, D. A., Walker, R. C., Cheatham, T. E., Simmerling, C., Roitberg, A., Merz, K. M., … Darden, T. (2018). Amber 2018. *University of California, San Francisco. 2018*, 1–923. Diambil dari http://ambermd.org/contributors.html%0Ahttp://ambermd.org/doc12/Amber18.pdf

CenterDC. (2021). SARS-CoV-2 Variant Classifications and Definitions. *Cdc*, 1–10. Diambil dari https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-info.html

Cosconati, S., Forli, S., Perryman, A. L., Harris, R., Goodsell, D. S., & Olson, A. J. (2010). *Cosconati2010.Pdf*. 597–607.

Dea, F., Putri, C., & Sukohar, A. (2021). the Developments on Therapeutic Approaches for COVID-19. *Medical Profession Journal of Lampung*, *11*(2), 200–204. https://doi.org/10.53089/MEDULA.V11I2.312

Desheng, L., Jian, G., Yuanhua, C., Wei, C., Huai, Z., & Mingjuan, J. (2011). Molecular dynamics simulations and MM/GBSA methods to investigate binding mechanisms of aminomethylpyrimidine inhibitors with DPP-IV. *Bioorganic and Medicinal Chemistry Letters*, *21*(22), 6630–6635. https://doi.org/10.1016/j.bmcl.2011.09.093

Dolecek, T. A., & Granditis, G. (1991). Dietary polyunsaturated fatty acids and mortality in the Multiple Risk Factor Intervention Trial (MRFIT). *World review of nutrition and dietetics*, *66*, 205–216. https://doi.org/10.1159/000419291

Etesami, E., Saba, F., Noroozi, M., Amoozegar, M. A., Khaniki, G. B., & Fazeli, A. S. (2017). Caspian Sea's Navicula salinicola Hustedt 1939 and effect of the prolonged culture on its fatty acid profile. *Int. J. Aquat. Biol.*, *5*(4), 268–274. Diambil dari https://ij-aquaticbiology.com/index.php/ijab/article/view/271

Gupta, S., & Varadwaj, P. K. (2018). A Brief Overview on Molecular Dynamics Simulation of Biomolecular. *International journal of pharmaceutical sciences and research*, *9*(4), 1333–1350. https://doi.org/10.13040/IJPSR.0975-8232.9(4).1333-50

Hartenian, E., Nandakumar, D., Lari, A., Ly, M., Tucker, J. M., & Glaunsinger, B. A. (2020). The molecular virology of coronaviruses. *The Journal of Biological Chemistry*, *295*(37), 12910. https://doi.org/10.1074/JBC.REV120.013930

Henderson, R., Edwards, R. J., Mansouri, K., Janowska, K., Stalls, V., Gobeil, S. M. C., … Acharya, P. (2020). Controlling the SARS-CoV-2 spike glycoprotein conformation. *Nature Structural and Molecular Biology*, *27*(10), 925–933. https://doi.org/10.1038/s41594-020-0479-4

Hoffmann, M., Kleine-Weber, H., Schroeder, S., Krüger, N., Herrler, T., Erichsen, S., … 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

Janowski, P., Liu, C., Deckman, J., & Case, D. (2015). Molecular dynamics simulation of triclinic lysozyme in a crystal lattice. *Protein Science*, *25*. https://doi.org/10.1002/pro.2713

Kurnia, D. (2020). KANDUNGAN KIMIA DARI Navicula sp dan BIOAKTIVITASNYA. *Indonesia Natural Research Pharmaceutical Journal*, *5*(1), 65–69. https://doi.org/10.52447/inspj.v5i1.4049

López-Camacho, E., García-Godoy, M. J., García-Nieto, J., Nebro, A. J., & Aldana-Montes, J. F. (2016). A new multi-objective approach for molecular docking based on rmsd and binding energy. *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, *9702*, 65–77. https://doi.org/10.1007/978-3-319-38827-4_6

Lu, R., Zhao, X., Li, J., Niu, P., Yang, B., Wu, H., … 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

Markou, G., Chatzipavlidis, I., & Georgakakis, D. (2012). Effects of phosphorus concentration and light intensity on the biomass composition of Arthrospira (Spirulina) platensis. *World Journal of Microbiology and Biotechnology*, *28*(8), 2661–2670. https://doi.org/10.1007/s11274-012-1076-4

Merz, C. R., & Main, K. L. (2015). Microalgae (diatom) production - The aquaculture and biofuel nexus. *2014 Oceans - St. John's, OCEANS 2014*. https://doi.org/10.1109/OCEANS.2014.7003242

Morris, G. M., Huey, R., & Olson, A. J. (2008). UNIT using AutoDock for ligand-receptor docking. In *Current Protocols in Bioinformatics*. https://doi.org/10.1002/0471250953.bi0814s24

Muttaqin, F. Z. (2019). Molecular Docking and Molecular Dynamic Studies of Stilbene Derivative Compounds As Sirtuin-3 (Sirt3) Histone Deacetylase Inhibitor on Melanoma Skin Cancer and Their Toxicities Prediction. *Journal of Pharmacopolium*, *2*(2), 112–121. https://doi.org/10.36465/jop.v2i2.489

Prieto-Martínez, F. D., Arciniega, M., & Medina-Franco, J. L. (2018). Acoplamiento Molecular: Avances Recientes y Retos. *TIP Revista Especializada en Ciencias Químico-Biológicas, 21*, 65–87. https://doi.org/10.22201/fesz.23958723e.2018.0.143

Romano T. Kroemer. (2007). Structure-Based Drug Design: Docking and Scoring. *Current Protein & Peptide Science*, *8*(4), 312–328. https://doi.org/10.2174/138920307781369382

Salmaso, V., & Moro, S. (2018). Bridging molecular docking to molecular dynamics in exploring ligand-protein recognition process: An overview. *Frontiers in Pharmacology*, *9*(AUG), 1–16. https://doi.org/10.3389/fphar.2018.00923

Sanders, J. M., Monogue, M. L., Jodlowski, T. Z., & Cutrell, J. B. (2020). Pharmacologic Treatments for Coronavirus Disease 2019 (COVID-19): A Review. *JAMA*, *323*(18), 1824–1836. https://doi.org/10.1001/JAMA.2020.6019

Sargsyan, K., Grauffel, C., & Lim, C. (2017). How Molecular Size Impacts RMSD Applications in Molecular Dynamics Simulations. *Journal of Chemical Theory and Computation*, *13*(4), 1518–1524. https://doi.org/10.1021/acs.jctc.7b00028

Singh, E., Khan, R. J., Jha, R. K., Amera, G. M., Jain, M., Singh, R. P., … Singh, A. K. (2020).

A comprehensive review on promising anti-viral therapeutic candidates identified against main protease from SARS-CoV-2 through various computational methods. *Journal of Genetic Engineering and Biotechnology*, *18*(1). https://doi.org/10.1186/s43141-020-00085-z

Sliwoski, G., Kothiwale, S., Meiler, J., & Lowe, E. W. (2014). Computational methods in drug discovery. *Pharmacological Reviews*, *66*(1), 334–395. https://doi.org/10.1124/pr.112.007336

Sterling, T., & Irwin, J. J. (2015). ZINC 15 - Ligand Discovery for Everyone. *Journal of Chemical Information and Modeling*, *55*(11), 2324–2337. https://doi.org/10.1021/ACS.JCIM.5B00559

Tay, M. Z., Poh, C. M., Rénia, L., MacAry, P. A., & Ng, L. F. P. (2020). The trinity of COVID-19: immunity, inflammation and intervention. *Nature Reviews Immunology*, *20*(6), 363–374. https://doi.org/10.1038/s41577-020-0311-8

Udugama, B., Kadhiresan, P., Kozlowski, H. N., Malekjahani, A., Osborne, M., Li, V. Y. C., … Chan, W. C. W. (2020). Diagnosing COVID-19: The Disease and Tools for Detection. *ACS nano*, *14*(4), 3822–3835. https://doi.org/10.1021/acsnano.0c02624

Vivar-sierra, A., Hern, P., Vergara-castañeda, A., Ram, G., Pinto-almaz, R., Salazar, J. R., & Loza-mej, M. A. (2021). *In Silico Study of Polyunsaturated Fatty Acids as Potential SARS-CoV-2 Spike Protein Closed Conformation Stabilizers :*

Wardani, F. (2012). Studi Derivat Ribavirin dan GTP Sebagai Inhibitor Untuk NS5 Metiltransferase Virus Dengue. *Fakultas MIPA, Universitas Indonesia*.

World Health Organization. (2021). WHO Coronavirus (COVID-19) Dashboard. WHO Coronavirus (COVID-19) Dashboard With Vaccination Data. *WHO*, hal. 1–5. Diambil dari https://covid19.who.int/

Xie, H., Li, Y., Yu, F., Xie, X., Qiu, K., & Fu, J. (2015). An Investigation of Molecular Docking and Molecular Dynamic Simulation on Imidazopyridines as B-Raf Kinase Inhibitors. *International Journal of Molecular Sciences*, *16*(11), 27350–27361. https://doi.org/10.3390/ijms161126026

Ylilauri, M., & Pentikäinen, O. T. (2013). MM/GBSA as a tool to understand the binding affinities of filamin-peptide interactions. *Journal of Chemical Information and Modeling*,

53(10), 2626–2633. https://doi.org/10.1021/ci4002475

Zhang, D., Lin, Y., Chen, X., Zhao, W., Chen, D., Gao, M., … Lu, Y. (2019). Docking- and pharmacophore-based virtual screening for the identification of novel Mycobacterium tuberculosis protein tyrosine phosphatase B (MptpB) inhibitor with a thiobarbiturate scaffold. *Bioorganic Chemistry*, *85*(September 2018), 229–239. https://doi.org/10.1016/j.bioorg.2018.12.038

Zhang, S., Qiao, S., Yu, J., Lan, J., Zhang, L., & Wang, X. (2021). *evolution*. 1–12.

Zhou, P., Yang, X. Lou, 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*, *579*(7798), 270–273. https://doi.org/10.1038/s41586-020-2012-7