

## DAFTAR PUSTAKA

- Abdelmageed, M. I., Abdelmoneim, A. H., Mustafa, M. I., Elfadol, N. M., Murshed, N. S., Shantier, S. W., & Makhawi, A. M. (2020). Design of a Multiepitope-Based Peptide Vaccine against the e Protein of Human COVID-19: An Immunoinformatics Approach. *BioMed Research International*, 2020. <https://doi.org/10.1155/2020/2683286>
- Akondi, V. S., Menon, V., Baudry, J., & Whittle, J. (2022). Novel Big Data-Driven Machine Learning Models for Drug Discovery Application. *Molecules*, 27(3), 1–22. <https://doi.org/10.3390/molecules27030594>
- Astuti, A. D., & Mutiara, A. B. (2011). Simulasi dinamika molekuler protein dengan aplikasi gromacs. *Tehnik Informatika Dan Industri*, 1(2), 1–9.
- Chauhan, V., Rungta, T., Goyal, K., & Singh, M. P. (2019). Designing a multi-epitope based vaccine to combat Kaposi Sarcoma utilizing immunoinformatics approach. *Scientific Reports*, 9(1), 1–15. <https://doi.org/10.1038/s41598-019-39299-8>
- Chong, K. T., Thangavel, R. R., & Tang, X. (2008). Enhanced expression of murine  $\beta$ -defensins (MBD-1, -2, -3, and -4) in upper and lower airway mucosa of influenza virus infected mice. *Virology*, 380(1), 136–143. <https://doi.org/10.1016/j.virol.2008.07.024>
- Dar, H. A., Zaheer, T., Shehroz, M., Ullah, N., Naz, K., Muhammad, S. A., Zhang, T., & Ali, A. (2019). Immunoinformatics-aided design and evaluation of a potential multi-epitope vaccine against klebsiella pneumoniae. *Vaccines*, 7(3), 1–17. <https://doi.org/10.3390/vaccines7030088>
- Desai, R. R., Bhatt, D. H., Jasrai, Y. T., & Pandya, H. A. (2018). *Molecular Docking of Vascular Endothelial Growth Factor with Phytochemicals Molecular Docking of Vascular Endothelial Growth Factor with Phytochemicals for Anti-Angiogenesis*. May.
- Duits, L. A., Nibbering, P. H., Van Strijen, E., Vos, J. B., Mannesse-Lazeroms, S. P. G., Van Sterkenburg, M. A. J. A., & Hiemstra, P. S. (2003). Rhinovirus increases human  $\beta$ -defensin-2 and -3 mRNA expression in cultured bronchial epithelial cells. *FEMS Immunology and Medical Microbiology*, 38(1), 59–64. [https://doi.org/10.1016/S0928-8244\(03\)00106-8](https://doi.org/10.1016/S0928-8244(03)00106-8)
- Elengoe, A., Abu Naser, M., & Hamdan, S. (2014). Modeling and docking studies on novel mutants (K71L and T204V) of the ATPase domain of human heat shock 70 kDa protein 1. *International Journal of Molecular Sciences*, 15(4), 6797–6814. <https://doi.org/10.3390/ijms15046797>
- Firmansyah, M. A., Susilo, A., Haryanti, S. D., & Herowati, R. (2021a).

- Desain Vaksin Berbasis Epitop dengan Pendekatan Bioinformatika untuk Menekan Glikoprotein Spike SARS-CoV-2. *Jurnal Farmasi Indonesia*, 18(2), 82–96. <https://doi.org/10.31001/jfi.v18i2.1351>
- Firmansyah, M. A., Susilo, A., Haryanti, S. D., & Herowati, R. (2021b). *Desain Vaksin Berbasis Epitop dengan Pendekatan Bioinformatika untuk Menekan Glikoprotein Spike SARS-CoV-2 Epitope-Based Vaccine Design with Bioinformatics Approach to Suppress Spike Glycoprotein of SARS-CoV-2 1 . PENDAHULUAN Dunia saat ini memerangi pand. 18(2)*, 82–96.
- Gitman, M. R., Shaban, M. V., & Paniz-mondolfi, A. E. (2021). *Laboratory Diagnosis of SARS-CoV-2 Pneumonia*. 1–17.
- Joy, S., Vijayakumar, Y. M., & Sunhye, G. (2015). Role of computer-aided drug design in modern drug discovery. *Archives of Pharmacal Research*, 38(9), 1686–1701. <https://doi.org/10.1007/s12272-015-0640-5>
- Kandeel, M., Al-taher, A., Li, H., & Schwingenschlogl, U. (2020). *Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID- 19 . The COVID-19 resource centre is hosted on Elsevier Connect , the company ' s public news and information . January.*
- Kar, T., Narsaria, U., Basak, S., Deb, D., Castiglione, F., Mueller, D. M., & Srivastava, A. P. (2020). A candidate multi-epitope vaccine against SARS-CoV-2. *Scientific Reports*, 10(1), 1–24. <https://doi.org/10.1038/s41598-020-67749-1>
- Karplus, M., & McCammon, J. A. (2002). Molecular dynamics simulations of biomolecules. *Nature Structural Biology*, 9(9), 646–652. <https://doi.org/10.1038/nsb0902-646>
- Khan, M. T., Islam, M. J., Parihar, A., Islam, R., Jerin, T. J., Dhote, R., Ali, M. A., Laura, F. K., & Halim, M. A. (2021). Immunoinformatics and molecular modeling approach to design universal multi-epitope vaccine for SARS-CoV-2. *Informatics in Medicine Unlocked*, 24(December 2020), 100578. <https://doi.org/10.1016/j.imu.2021.100578>
- Klotman, M. E., & Chang, T. L. (2006). Defensins in innate antiviral immunity. *Nature Reviews Immunology*, 6(6), 447–456. <https://doi.org/10.1038/nri1860>
- Kuriata, A., Gierut, A. M., Oleniecki, T., Ciemny, M. P., Kolinski, A., Kurcinski, M., & Kmiecik, S. (2018). CABS-flex 2.0: A web server for fast simulations of flexibility of protein structures. *Nucleic Acids Research*, 46(W1), W338–W343. <https://doi.org/10.1093/nar/gky356>
- Liu, L., Wei, Q., Lin, Q., Fang, J., Wang, H., Kwok, H., Tang, H., Nishiura, K., Peng, J., Tan, Z., Wu, T., Cheung, K. W., Chan, K.

- H., Alvarez, X., Qin, C., Lackner, A., Perlman, S., Yuen, K. Y., & Chen, Z. (2019). Anti-spike IgG causes severe acute lung injury by skewing macrophage responses during acute SARS-CoV infection. *JCI Insight*, 4(4), 1–19. <https://doi.org/10.1172/jci.insight.123158>
- Naz, A., Shahid, F., Butt, T. T., Awan, F. M., Ali, A., & Malik, A. (2020). Designing Multi-Epitope Vaccines to Combat Emerging Coronavirus Disease 2019 (COVID-19) by Employing Immuno-Informatics Approach. *Frontiers in Immunology*, 11(July), 1–13. <https://doi.org/10.3389/fimmu.2020.01663>
- Nousias, S. (2011). *Diploma Thesis. 2019.*
- Puspaningtyas, A. R. (2013). DOCKING MOLEKUL DENGAN METODA MOLEGRO VIRTUAL DOCKER DARI EKSTRAK AIR Psidium guajava, Linn DAN Citrus sinensis, Peels SEBAGAI INHIBITOR PADA TIROSINASE UNTUK PEMUTIH KULIT. *Jurnal Kimia Terapan Indonesia*, 15(1), 31–39. <https://doi.org/10.14203/jkti.v15i1.102>
- Qin, S., & Zhou, H. (2007). *Structural bioinformatics meta-PPISP : a meta web server for protein-protein interaction site prediction.* 23(24), 3386–3387. <https://doi.org/10.1093/bioinformatics/btm434>
- Rahman, N., Ali, F., Basharat, Z., Shehroz, M., Khan, M. K., Jeandet, P., Nepovimova, E., Kuca, K., & Khan, H. (2020). Vaccine design from the ensemble of surface glycoprotein epitopes of SARS-CoV-2: An immunoinformatics approach. *Vaccines*, 8(3), 1–17. <https://doi.org/10.3390/vaccines8030423>
- Rakib, A., Ahmed, S., Jahan, N., Chowdhury, M., Akter, T., Nainu, F., Paul, A., Shahriar, A., & Montakim, A. (2020). *Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19 . The COVID-19 resource centre is hosted on Elsevier Connect , the company ' s public news and information . January.*
- Shey, R. A., Ghogomu, S. M., Esoh, K. K., Nebangwa, N. D., Shintouo, C. M., Nongley, N. F., Asa, B. F., Ngale, F. N., Vanhamme, L., & Souopgui, J. (2019). In-silico design of a multi-epitope vaccine candidate against onchocerciasis and related filarial diseases. *Scientific Reports*, 9(1), 1–18. <https://doi.org/10.1038/s41598-019-40833-x>
- Tahir Ul Qamar, M., Saleem, S., Ashfaq, U. A., Bari, A., Anwar, F., & Alqahtani, S. (2019). Epitope-based peptide vaccine design and target site depiction against Middle East Respiratory Syndrome Coronavirus: An immune-informatics study. *Journal of Translational Medicine*, 17(1), 1–14. <https://doi.org/10.1186/s12967-019-2116-8>
- Tartof, S. Y., Slezak, J. M., Fischer, H., Hong, V., Ackerson, B. K., Ranasinghe, O. N., Frankland, T. B., Ogun, O. A., Zamparo, J. M.,

- Gray, S., Valluri, S. R., Pan, K., Angulo, F. J., Jodar, L., & McLaughlin, J. M. (2021). Effectiveness of mRNA BNT162b2 COVID-19 vaccine up to 6 months in a large integrated health system in the USA: a retrospective cohort study. *The Lancet*, 398(10309), 1407–1416. [https://doi.org/10.1016/S0140-6736\(21\)02183-8](https://doi.org/10.1016/S0140-6736(21)02183-8)
- Van Zundert, G. C. P., Rodrigues, J. P. G. L. M., Trellet, M., Schmitz, C., Kastritis, P. L., Karaca, E., Melquiond, A. S. J., Van Dijk, M., De Vries, S. J., & Bonvin, A. M. J. J. (2016a). The HADDOCK2.2 Web Server: User-Friendly Integrative Modeling of Biomolecular Complexes. *Journal of Molecular Biology*, 428(4), 720–725. <https://doi.org/10.1016/j.jmb.2015.09.014>
- Van Zundert, G. C. P., Rodrigues, J. P. G. L. M., Trellet, M., Schmitz, C., Kastritis, P. L., Karaca, E., Melquiond, A. S. J., Van Dijk, M., De Vries, S. J., & Bonvin, A. M. J. J. (2016b). The HADDOCK2.2 Web Server: User-Friendly Integrative Modeling of Biomolecular Complexes. *Journal of Molecular Biology*, 428(4), 720–725. <https://doi.org/10.1016/j.jmb.2015.09.014>
- Walls, A. C., Park, Y. J., Tortorici, M. A., Wall, A., McGuire, A. T., & Velesler, D. (2020). Structure, Function, and Antigenicity of the SARS-CoV-2 Spike Glycoprotein. *Cell*, 181(2), 281-292.e6. <https://doi.org/10.1016/j.cell.2020.02.058>
- Yu, Z., Kan, R., Ji, H., Wu, S., Zhao, W., Shuian, D., & Liu, J. (2020). *Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID- 19 . The COVID-19 resource centre is hosted on Elsevier Connect , the company ' s public news and information . January.*
- Zhang, H., Penninger, J. M., Li, Y., Zhong, N., & Slutsky, A. S. (2020). Angiotensin-converting enzyme 2 (ACE2) as a SARS-CoV-2 receptor: molecular mechanisms and potential therapeutic target. *Intensive Care Medicine*, 46(4), 586–590. <https://doi.org/10.1007/s00134-020-05985-9>