

DAFTAR PUSTAKA

- Abir, M. H., Rahman, T., Das, A., Etu, S. N., Nafiz, I. H., Rakib, A., Mitra, S., Emran, T. Bin, Dhama, K., Islam, A., Siyadatpanah, A., Mahmud, S., Kim, B., & Hassan, M. M. (2022). Pathogenicity and virulence of Marburg virus. *Virulence*, 13(1), 609–633. <https://doi.org/10.1080/21505594.2022.2054760>
- Banerjee, A., & Mitra, P. (2020). Ebola Virus VP35 Protein: Modeling of the Tetrameric Structure and an Analysis of Its Interaction with Human PKR. In *Journal of Proteome Research* (Vol. 19, Issue 11). <https://doi.org/10.1021/acs.jproteome.0c00473>
- Bateman, A., Martin, M. J., Orchard, S., Magrane, M., Agivetova, R., Ahmad, S., Alpi, E., Bowler-Barnett, E. H., Britto, R., Bursteinas, B., Bye-A-Jee, H., Coetzee, R., Cukura, A., da Silva, A., Denny, P., Dogan, T., Ebenezer, T. G., Fan, J., Castro, L. G., ... Teodoro, D. (2021). UniProt: the universal protein knowledgebase in 2021. *Nucleic Acids Research*, 49(D1), D480–D489. <https://doi.org/10.1093/nar/gkaa1100>
- Bibi, S., Ullah, I., Zhu, B., Adnan, M., Liaqat, R., Kong, W. B., & Niu, S. (2021). In silico analysis of epitope-based vaccine candidate against tuberculosis using reverse vaccinology. *Scientific Reports*, 11(1), 1–16. <https://doi.org/10.1038/s41598-020-80899-6>
- Bourne, P. E. E., & Weissig, H. (2003). *Structural Bioinformatics*. WILEY-LISS. <https://www.pdfdrive.com/structural-bioinformatics-d191453837.html/>
- Burley, S. K., Berman, H. M., Bhikadiya, C., Bi, C., Chen, L., Di Costanzo, L., Christie, C., Dalenberg, K., Duarte, J. M., Dutta, S., Feng, Z., Ghosh, S., Goodsell, D. S., Green, R. K., Guranović, V., Guzenko, D., Hudson, B. P., Kalro, T., Liang, Y., ... Zardecki, C. (2019). RCSB Protein Data Bank: Biological macromolecular structures enabling research and education in fundamental biology, biomedicine, biotechnology and energy. *Nucleic Acids Research*, 47(D1), D464–D474. <https://doi.org/10.1093/nar/gky1004>
- Chatanaka, M. K., Ulndreaj, A., Sohæi, D., & Prassas, I. (2022). Immunoinformatics: Pushing the boundaries of immunology research and

- medicine. *ImmunoInformatics*, 5(August 2021), 100007. <https://doi.org/10.1016/j.immuno.2021.100007>
- Chen, 2021. (2021). *Chen, 2021.pdf*. 22(8), 609–632.
- Corporation, M. (2021). *Windows Notepad*. Microsoft Store. <https://apps.microsoft.com/store/detail/windows-notepad/9MSMLRH6LZF3?hl=enus&gl=us>
- Cross, R. W., Bornholdt, Z. A., Prasad, A. N., Borisevich, V., Agans, K. N., Deer, D. J., Abelson, D. M., Kim, D. H., Shestowsky, W. S., Campbell, L. A., Bunyan, E., Geisbert, J. B., Fenton, K. A., Zeitlin, L., Porter, D. P., & Geisbert, T. W. (2021). Combination therapy protects macaques against advanced Marburg virus disease. *Nature Communications*, 12(1), 1–10. <https://doi.org/10.1038/s41467-021-22132-0>
- Dimitrov, I., Bangov, I., Flower, D. R., & Doytchinova, I. (2014). AllerTOP v.2 - A server for in silico prediction of allergens. *Journal of Molecular Modeling*, 20(6). <https://doi.org/10.1007/s00894-014-2278-5>
- 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). <https://doi.org/10.1038/s41392-020-00352-y>
- Du, Z., Su, H., Wang, W., Ye, L., Wei, H., Peng, Z., Anishchenko, I., Baker, D., & Yang, J. (2021). The trRosetta server for fast and accurate protein structure prediction. *Nature Protocols*, 16(12), 5634–5651. <https://doi.org/10.1038/s41596-021-00628-9>
- Firmansyah, M. A., Susilo, A., Haryanti, S., & Herowati, R. (2021). Desain Vaksin Berbasis Epitop dengan Pendekatan Bioinformatika untuk Menekan Glikoprotein Spike SARS-CoV-2. *Jurnal Farmasi Indonesia*, 18, 82–96. <https://doi.org/10.31001/jfi.v18i2.1351>
- Heo, L., Park, H., & Seok, C. (2013). GalaxyRefine: Protein structure refinement driven by side-chain repacking. *Nucleic Acids Research*, 41(Web Server issue), 384–388. <https://doi.org/10.1093/nar/gkt458>

- Huang Lab. (2021). *HDOCK SERVER*. Lab of Biophysics and Molecular Modeling. <http://hdock.phys.hust.edu.cn/>
- Huy, T. X. N., Nguyen, T. T., Reyes, A. W. B., Vu, S. H., Min, W. G., Lee, H. J., Lee, J. H., & Kim, S. (2021). Immunization With a Combination of Four Recombinant Brucella abortus Proteins Omp16, Omp19, Omp28, and L7/L12 Induces T Helper 1 Immune Response Against Virulent *B. abortus* 544 Infection in BALB/c Mice. *Frontiers in Veterinary Science*, 7(January), 1–10. <https://doi.org/10.3389/fvets.2020.577026>
- IEDBAR. (2023). *IEDB Analysis Resource*. IEDBAR. <http://tools.iedb.org/main/>
- Janeway CA Jr, Travers P, Walport M, et al. (2001). *Immunobiology: The Immune System in Health and Disease*. 5th edition. Garland Science. <https://www.ncbi.nlm.nih.gov/books/NBK27156/>
- Jayashree R, K. M. (2020). Immunoinformatics and Epitope Prediction. *Methods in Molecular Biology*, 155–172.
- 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>
- Khairkhah, N., Aghasadeghi, M. R., Namvar, A., & Bolhassani, A. (2020). Design of novel multiepitope constructs-based peptide vaccine against the structural S, N and M proteins of human COVID-19 using immunoinformatics analysis. *PLoS ONE*, 15(10 October), 1–28. <https://doi.org/10.1371/journal.pone.0240577>
- Khasana, A. S. N., Hartono, N. L. S., Permatasari, V. O., Ramadhan, D. L., & Sumadi, F. A. N. (2023). in Silico Design of B-Cell Epitope Based Peptide Vaccine for Varicella Zoster Virus. *Indonesian Journal of Biotechnology and Biodiversity*, 7(1), 1–11. <https://doi.org/10.47007/ijobb.v7i1.157>
- Lamiable, A., Thevenet, P., Rey, J., Vavrusa, M., Derreumaux, P., & Tuffery, P. (2016). PEP-FOLD3: faster denovo structure prediction for linear peptides in

- solution and in complex. *Nucleic Acids Research*, 44(1), W449–W454. <https://doi.org/10.1093/nar/gkw329>
- Mahmud, S. M. N., Rahman, M., Kar, A., Jahan, N., & Khan, A. (2019). Designing of an Epitope- Based Universal Peptide Vaccine against Highly Conserved Regions in RNA Dependent RNA Polymerase Protein of Human Marburg Virus: A Computational Assay. *Anti-Infective Agents*, 18(3), 294–305. <https://doi.org/10.2174/2211352517666190717143949>
- Naveed, M., Tehreem, S., Arshad, S., Bukhari, S. A., Shabbir, M. A., Essa, R., Ali, N., Zaib, S., Khan, A., Al-Harrasi, A., & Khan, I. (2021). Design of a novel multiple epitope-based vaccine: An immunoinformatics approach to combat SARS-CoV-2 strains. *Journal of Infection and Public Health*, 14(7), 938–946. <https://doi.org/10.1016/j.jiph.2021.04.010>
- NetCTL. (2023). *NetCTL-1.2 Predection of CTL epitopes in protein sequences*. DTU Health Tech. <https://services.healthtech.dtu.dk/services/NetCTL-1.2/>
- Nyakarahuka, L., Ojwang, J., Tumusiime, A., Balinandi, S., Whitmer, S., Kyazze, S., Kasozi, S., Wetaka, M., Makumbi, I., Dahlke, M., Borchert, J., Lutwama, J., Ströher, U., Rollin, P. E., Nichol, S. T., & Shoemaker, T. R. (2017). Isolated case of marburg virus disease, Kampala, Uganda, 2014. *Emerging Infectious Diseases*, 23(6), 1001–1004. <https://doi.org/10.3201/eid2306.170047>
- Oluwagbemi, O. O., Oladipo, E. K., Kolawole, O. M., Oloke, J. K., Adelusi, T. I., Irewolede, B. A., Dairo, E. O., Ayeni, A. E., Kolapo, K. T., Akindiya, O. E., Oluwasegun, J. A., Oluwadara, B. F., & Fatumo, S. (2022). Bioinformatics, Computational Informatics, and Modeling Approaches to the Design of mRNA COVID-19 Vaccine Candidates. *Computation*, 10(7). <https://doi.org/10.3390/computation10070117>
- Ong, E., He, Y., & Yang, Z. (2020). Epitope promiscuity and population coverage of Mycobacterium tuberculosis protein antigens in current subunit vaccines under development. *Infection, Genetics and Evolution*, 80(January), 104186. <https://doi.org/10.1016/j.meegid.2020.104186>
- Paul, S., Sidney, J., Sette, A., & Peters, B. (2016). TepiTool: A pipeline for

- computational prediction of T cell epitope candidates. In *Current Protocols in Immunology* (Vol. 2016). <https://doi.org/10.1002/cpim.12>
- Porter, D. P., Weidner, J. M., Gomba, L., Bannister, R., Blair, C., Jordan, R., Wells, J., Wetzel, K., Garza, N., Tongeren, S. Van, Donnelly, G., Steffens, J., Moreau, A., Bearss, J., Lee, E., Bavari, S., Cihlar, T., & Warren, T. K. (2020). *Remdesivir (GS-5734) Is Efficacious in Cynomolgus Macaques Infected With Marburg Virus.* 222, 1894–1901. <https://doi.org/10.1093/infdis/jiaa290>
- Prasasty, V. D., & Istyastono, E. P. (2019). Data of small peptides in SMILES and three-dimensional formats for virtual screening campaigns. *Data in Brief*, 27, 104607. <https://doi.org/10.1016/j.dib.2019.104607>
- Rawal, K., Sinha, R., Abbasi, B. A., Chaudhary, A., Nath, S. K., Kumari, P., Preeti, P., Saraf, D., Singh, S., Mishra, K., Gupta, P., Mishra, A., Sharma, T., Gupta, S., Singh, P., Sood, S., Subramani, P., Dubey, A. K., Strych, U., ... Bottazzi, M. E. (2021). Identification of vaccine targets in pathogens and design of a vaccine using computational approaches. *Scientific Reports*, 11(1), 1–25. <https://doi.org/10.1038/s41598-021-96863-x>
- Renadi, S., Pratita, A. T. K., Mardianingrum, R., & Ruswanto, dan R. (2023). The Potency of Alkaloid Derivates as Anti-Breast Cancer Candidates: In Silico Study. *Jurnal Kimia Valensi*, 9(1), 89–108. <https://doi.org/10.15408/jkv.v9i1.31481>
- Reynolds, P., & Marzi, A. (2019). Ebola and Marburg virus diseases AER 2019. *Virus Genes*, 53(4), 501–515.
- Rezaldi, F., Taupiqurohman, O., Fadillah, M. F., Rochmat, A., Humaedi, A., & Fadhilah, F. (2021). Identifikasi Kandidat Vaksin COVID-19 Berbasis Peptida dari Glikoprotein Spike SARS CoV-2 untuk Ras Asia secara In Silico. *Jurnal Biotek Medisiana Indonesia*, 10(1), 77–85. <https://ejournal2.litbang.kemkes.go.id/index.php/jbmi/article/view/5031/2299>
- Ruswanto, R., Mardianingrum, R., Nofianti, T., Fizriani, R., & Siswandono, S. (2023). Computational Study of Bis-(1-(Benzoyl)-3-Methyl Thiourea)

- Platinum (II) Complex Derivatives as Anticancer Candidates. *Advances and Applications in Bioinformatics and Chemistry*, 16(January), 15–36. <https://doi.org/10.2147/AABC.S392068>
- Sami, S. A., Marma, K. K. S., Mahmud, S., Khan, M. A. N., Albogami, S., El-Shehawi, A. M., Rakib, A., Chakraborty, A., Mohiuddin, M., Dhama, K., Uddin, M. M. N., Hossain, M. K., Tallei, T. E., & Emran, T. Bin. (2021). Designing of a Multi-epitope Vaccine against the Structural Proteins of Marburg Virus Exploiting the Immunoinformatics Approach. *ACS Omega*, 6(47), 32043–32071. <https://doi.org/10.1021/acsomega.1c04817>
- Sanami, S., Alizadeh, M., Nosrati, M., Dehkordi, K. A., Azadegan-Dehkordi, F., Tahmasebian, S., Nosrati, H., Arjmand, M. H., Ghasemi-Dehnoo, M., Rafiei, A., & Bagheri, N. (2021). Exploring SARS-COV-2 structural proteins to design a multi-epitope vaccine using immunoinformatics approach: An in silico study. *Computers in Biology and Medicine*, 133(January), 104390. <https://doi.org/10.1016/j.combiomed.2021.104390>
- Santoso, A. R., & Sidarta, E. (2021). Pengaruh evolusi virus H3N2 pada perubahan hemaglutinin, neuraminidase dan efeknya terhadap Major Histocompatibility Complex (MHC) kelas II di Indonesia pada tahun 2005-2019. In *Tarumanagara Medical Journal* (Vol. 3, Issue 2, pp. 220–229). <https://doi.org/10.24912/tmj.v4i1.13712>
- Schulze, M. S. E. D., Anders, A. K., Sethi, D. K., & Call, M. J. (2013). Disruption of Hydrogen Bonds between Major Histocompatibility Complex Class II and the Peptide N-Terminus Is Not Sufficient to Form a Human Leukocyte Antigen-DM Receptive State of Major Histocompatibility Complex Class II. *PLoS ONE*, 8(7), 1–15. <https://doi.org/10.1371/journal.pone.0069228>
- Shu, T., Gan, T., Bai, P., Wang, X., Qian, Q., Zhou, H., Cheng, Q., Qiu, Y., Yin, L., Zhong, J., & Zhou, X. (2019). Ebola virus VP35 has novel NTPase and helicase-like activities. *Nucleic Acids Research*, 47(11), 5837–5851. <https://doi.org/10.1093/nar/gkz340>
- Smiline Girija, A. S. (2020). Delineating the Immuno-Dominant Antigenic Vaccine

- Peptides Against gacS-Sensor Kinase in *Acinetobacter baumannii*: An in silico Investigational Approach. *Frontiers in Microbiology*, 11(September), 1–10. <https://doi.org/10.3389/fmicb.2020.02078>
- Syakuran, L. "Abdan. (2020). Desain Kandidat Vaksin SARS-CoV-2 Menggunakan Pendekatan Imunoinformatica. *ResearchGate*, 1–11. <https://doi.org/10.13140/802.2.33453.31202>.
- Tahir ul Qamar, M., Rehman, A., Tusleem, K., Ashfaq, U. A., Qasim, M., Zhu, X., Fatima, I., Shahid, F., & Chen, L. L. (2020). Designing of a next generation multiepitope based vaccine (MEV) against SARS-CoV-2: Immunoinformatics and in silico approaches. *PLoS ONE*, 15(12 December 2020), 1–25. <https://doi.org/10.1371/journal.pone.0244176>
- Tamam, B., Syah, D., N. Lioe, H., T. Suhartono, M., & Ananta Kusuma, W. (2018). Beberapa Penciri Berbasis Sekuens Untuk Mengenali Sifat Fungsional Peptida Bioaktif: Studi Eksplorasi. *Jurnal Teknologi Dan Industri Pangan*, 29(1), 1–9. <https://doi.org/10.6066/jtip.2018.29.1.1>
- Walker, J. M., Gasteiger, E., Hoogland, C., Gattiker, A., Duvaud, S., Wilkins, M. R.. Appel, R. D., & Bairoch, A. (2005). *The Proteomics Protocols Handbook Edited Protein Identification and Analysis Tools on the ExPASy Server (J. Walker, Ed.)*. Springer Science & Business Media. <http://www.expasy.org/tools/>
- 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(MAR), 1–16. <https://doi.org/10.3389/fimmu.2017.00292>
- Yan, Y., Zhang, D., Zhou, P., Li, B., & Huang, S. Y. (2017). HDOCK: A web server for protein-protein and protein-DNA/RNA docking based on a hybrid strategy. *Nucleic Acids Research*, 45(W1), W365–W373. <https://doi.org/10.1093/nar/gkx407>