DAFTAR PUSTAKA

Alexander, J. A. N., Radaeva, M., King, D. T., Chambers, H. F., Cherkasov, A., Chatterjee, S. S., & Strynadka, N. C. J. (2020). Structural analysis of avibactam-mediated activation of the bla and mec divergons in methicillin-resistant Staphylococcus aureus. *Journal of Biological Chemistry*, *295*(32), 10870–10884. https://doi.org/10.1074/jbc.RA120.013029

Alexander, J. A. N., Worrall, L. J., Hu, J., Vuckovic, M., Satishkumar, N., Poon, R., Sobhanifar, S., Rosell, F. I., Jenkins, J., Chiang, D., Mosimann, W. A., Chambers, H. F., Paetzel, M., Chatterjee, S. S., & Strynadka, N. C. J. (2023). Structural basis of broad-spectrum β-lactam resistance in Staphylococcus aureus. *Nature*, *613*(7943), 375–382. https://doi.org/10.1038/s41586-022-05583-3

Asri, R. C., & Rasyid, R. (2017). *Artikel Penelitian Identifikasi MRSA pada Diafragma Stetoskop di Ruang Rawat Inap dan HCU Bagian Penyakit Dalam*. *6*(2), 239–244.

Boundy, S., Safo, M. K., Wang, L., Musayev, F. N., O'Farrell, H. C., Rife, J. P., & Archer, G. L. (2013). Characterization of the Staphylococcus aureus rRNA methyltransferase encoded by orfx, the gene containing the staphylococcal chromosome cassette mec (SCCmec) insertion site. *Journal of Biological Chemistry*, *288*(1), 132–140. https://doi.org/10.1074/jbc.M112.385138

Burley, S. K., Berman, H. M., Kleywegt, G. J., & Markley, J. L. (2018). *HHS Public Access*. 627–641. https://doi.org/10.1007/978-1-4939-7000-1

Calon, N. S., & Antikanker, O. (2018). *Uji in silico Aktivitas Sitotoksik dan Toksisitas Senyawa Turunan N - (Benzoil) - N ' - feniltiourea Sebagai Calon Obat Antikanker*. *March*. https://doi.org/10.20961/jpscr.v3i1.16266

Daina, A., Michielin, O., & Zoete, V. (2017). SwissADME : a free web tool to evaluate pharmacokinetics , drug- likeness and medicinal chemistry friendliness of small molecules. *Nature Publishing Group*, *October 2016*, 1–13. https://doi.org/10.1038/srep42717

Der, D. M. F., Karls, E., & Tübingen, U. (2018). *Nanoparticle-based*

delivery of nucleic acids for targeting multidrug-resistant bacteria. April.

Design, L. (n.d.). *PHARMACOPHORE AND LIGAND-BASED DESIGN WITH BIOVIA DISCOVERY STUDIO*.

Dewi, R. S., Anggraeni, A., Bahti, H. H., & Yusuf, M. (2022). Simulasi Dinamika Molekuler Ligan Disekunderbutil ditiofosfat (DSBDTP) Untuk Ekstraksi Logam Tanah Jarang. *SainsMath: Jurnal MIPA Sains Terapan*, *20*(3), 1–9.

Gondokesumo, M. E., & Kurniawan, I. M. (2019). Molecular docking study of sappan wood extract to inhibit PBP2A enzyme on methicillin-resistant Staphylococcus aureus (MRSA). *Journal of Basic and Clinical Physiology and Pharmacology*, *30*(6), 1–9. https://doi.org/10.1515/jbcpp-2019-0282

Guan, S., Zhong, L., Yu, H., Wang, L., Jin, Y., Liu, J., Xiang, H., Yu, H., Wang, L., & Wang, D. (2022). Molecular docking and proteomics reveals the synergistic antibacterial mechanism of theaflavin with β-lactam antibiotics against MRSA. *Frontiers in Microbiology*, *13*(November), 1–13. https://doi.org/10.3389/fmicb.2022.993430

Kamarudin, A. A., Sayuti, N. H., Saad, N., Razak, N. A. A., & Esa, N. M. (2021). Eleutherine bulbosa (Mill.) urb. bulb: Review of the pharmacological activities and its prospects for application. *International Journal of Molecular Sciences*, *22*(13). https://doi.org/10.3390/ijms22136747

Kim, S., Thiessen, P. A., Bolton, E. E., Chen, J., Fu, G., Gindulyte, A., Han, L., He, J., He, S., Shoemaker, B. A., Wang, J., Yu, B., Zhang, J., & Bryant, S. H. (2016). *PubChem Substance and Compound databases*. *44*(September 2015), 1202–1213. https://doi.org/10.1093/nar/gkv951

Lade, H., & Kim, J. S. (2021). Bacterial targets of antibiotics in methicillin-resistant staphylococcus aureus. *Antibiotics*, *10*(4). https://doi.org/10.3390/antibiotics10040398

Lakhundi, S., & Zhang, K. (2018). *crossm*. *31*(4), 1–103.

Mahasenan, K. V., Molina, R., Bouley, R., Batuecas, M. T., Fisher, J. F., Hermoso, J. A., Chang, M., & Mobashery, S. (2017). Conformational dynamics in penicillin-binding protein 2a of

methicillin-resistant staphylococcus aureus, allosteric communication network and enablement of catalysis. *Journal of the American Chemical Society*, *139*(5), 2102–2110. https://doi.org/10.1021/jacs.6b12565

Marrero, A., Mallorquí-Fernández, G., Guevara, T., García-Castellanos, R., & Gomis-Rüth, F. X. (2006). Unbound and Acylated Structures of the MecR1 Extracellular Antibiotic-sensor Domain Provide Insights into the Signal-transduction System that Triggers Methicillin Resistance. *Journal of Molecular Biology*, *361*(3), 506–521. https://doi.org/10.1016/j.jmb.2006.06.046

Masumi, M., Noormohammadi, F., Kianisaba, F., Nouri, F., Taheri, M., & Taherkhani, A. (2022). Methicillin-Resistant Staphylococcus aureus: Docking-Based Virtual Screening and Molecular Dynamics Simulations to Identify Potential Penicillin-Binding Protein 2a Inhibitors from Natural Flavonoids. *International Journal of Microbiology*, *2022*. https://doi.org/10.1155/2022/9130700

Mlynarczyk-bonikowska, B., Kowalewski, C., Krolak-ulinska, A., & Marusza, W. (2022). *Molecular Mechanisms of Drug Resistance in Staphylococcus aureus*.

Morris, G. M., Huey, R., Lindstrom, W., Sanner, M. F., Belew, R. K., Goodsell, D. S., & Olson, A. J. (2010). *NIH Public Access*. *30*(16), 2785–2791. https://doi.org/10.1002/jcc.21256.AutoDock4

Nandhini, P., Kumar, P., Mickymaray, S., Alothaim, A. S., Somasundaram, J., & Rajan, M. (2022). Recent Developments in Methicillin-Resistant Staphylococcus aureus (MRSA) Treatment: A Review. *Antibiotics*, *11*(5), 1–21. https://doi.org/10.3390/antibiotics11050606

Pagadala, N. S., Syed, K., & Tuszynski, J. (2017). Software for molecular docking : a review. *Biophysical Reviews*, 91–102. https://doi.org/10.1007/s12551-016-0247-1

Pedretti, A., Mazzolari, A., Vistoli, G., Farmaceutica, C., Pratesi, P., & Farmacia, F. (2004). *VEGA ZZ : a versatile toolkit for drug design and protein modelling*. *21*(2002), 20133.

Pisano, M. B., Kumar, A., Medda, R., Gatto, G., Pal, R., Fais, A., Era,

B., Cosentino, S., Uriarte, E., Santana, L., Pintus, F., & Matos, M. J. (2019). Antibacterial Activity and Molecular Docking Studies of a Selected Series of Hydroxy-3-arylcoumarins. *Molecules*, *24*(15), 1–12. https://doi.org/10.3390/molecules24152815

Ri, K. K. (n.d.). *No Title*.

Sabe, V. T., Ntombela, T., Jhamba, L. A., Maguire, G. E. M., Govender, T., Naicker, T., & Kruger, H. G. (2021). European Journal of Medicinal Chemistry Current trends in computer aided drug design and a highlight of drugs discovered via computational techniques : A review. *European Journal of Medicinal Chemistry*, *224*, 113705. https://doi.org/10.1016/j.ejmech.2021.113705

Shore, A. C., & Coleman, D. C. (2013). Staphylococcal cassette chromosome mec: Recent advances and new insights. *International Journal of Medical Microbiology*, *303*(6–7), 350–359. https://doi.org/10.1016/j.ijmm.2013.02.002

Singh, B. K. (2018). *COMPUTER AIDED DRUG DESIGN : AN OVERVIEW*. *8*(5), 504–509.