

## DAFTAR PUSTAKA

- Alberts, B., Johnson, A., Lewis, J., Raff, M., Roberts, K., & Walter, P. (2002). *Molecular biology of the cell* (4th ed.). Garland Science.
- Anfinsen, C. B. (1973). Principles that govern the folding of protein chains. *Science*, 181(4096), 223–230. <https://doi.org/10.1126/science.181.4096.223>
- Atisattapong, W., & Marupanthorn, P. (2021). Wang–Landau sampling for estimation of the reliability of physical networks. *Computer Physics Communications*, 262, 107831. <https://doi.org/10.1016/j.cpc.2021.107831>
- Böckenhauer, H. J., & Bongartz, D. (2007). Protein folding in the HP model on grid lattices with diagonals. *Discrete Applied Mathematics*, 155(2), 230–256. <https://doi.org/10.1016/j.dam.2006.04.031>
- Bozkurt, A., & Sengul, A. (2021). Monte Carlo approach for calculation of mass energy absorption coefficients of some amino acids. *Nuclear Engineering and Technology*, 53(9), 3044–3050. <https://doi.org/10.1016/j.net.2021.04.004>
- Cimorelli, L., Covelli, C., De Vincenzo, A., Pianese, D., & Molino, B. (2021). Sedimentation in Reservoirs: Evaluation of Return Periods Related to Operational Failures of Water Supply Reservoirs with Monte Carlo Simulation. *Journal of Water Resources Planning and Management*, 147(1), 1–12. [https://doi.org/10.1061/\(asce\)wr.1943-5452.0001307](https://doi.org/10.1061/(asce)wr.1943-5452.0001307)
- Dill, K. A., & MacCallum, J. L. (2012). The protein-folding problem, 50 years on. *Science*, 338(6110), 1042–1046. <https://doi.org/10.1126/science.1219021>
- Dobson, C. M. (2003). Protein folding and misfolding. *Nature*, 426(6968), 884–890. <https://doi.org/10.1038/nature02261>
- Farris, A. C. K., Seaton, D. T., & Landau, D. P. (2021). Effects of lattice constraints in coarse-grained protein models. *Journal of Chemical Physics*, 154(8). <https://doi.org/10.1063/5.0038184>
- Farris, A. C. K., Wüst, T., & Landau, D. P. (2019). Statistical physics meets biochemistry: Wang-Landau sampling of the HP model of protein folding. *American Journal of Physics*, 87(4), 310–316. <https://doi.org/10.1119/1.5093292>
- Gershenson, A., Gosavi, S., Faccioli, P., & Wintrode, P. L. (2020). Successes and challenges in simulating the folding of large proteins. *Journal of Biological Chemistry*, 295(1), 15–33. <https://doi.org/10.1074/jbc.REV119.006794>
- Gracia, B., Montes, P., Gutierrez, A. M., Arun, B., & Karras, G. I. (2024). Protein-folding chaperones predict structure-function relationships and cancer risk in BRCA1 mutation carriers. *Cell Reports*, 43(2), 113803. <https://doi.org/10.1016/j.celrep.2024.113803>
- Katili, A. S. (2009). Struktur Dan Fungsi Protein Kolagen. *Jurnal Pelangi Ilmu*, 2(5), 19–29.

- Khoury, G. A., Smadbeck, J., Kieslich, C. A., & Floudas, C. A. (2014). Protein folding and de novo protein design for biotechnological applications. *Trends in Biotechnology*, 32(2), 99–109. <https://doi.org/10.1016/j.tibtech.2013.10.008>
- Kurbanova, D. R., Murtazaev, A. K., Ramazanov, M. K., & Magomedov, M. A. (2023). Phase transitions in the four-state Potts model with competing exchange interactions: Application of the Wang-Landau algorithm. *Physica E: Low-Dimensional Systems and Nanostructures*, 148(May 2022), 115626. <https://doi.org/10.1016/j.physe.2022.115626>
- Kwak, W. (2012). Wang-Landau Algorithm in a Two-Dimensional Spin-1 Blume-Capel Model. *Physics Procedia*, 34, 80–83. <https://doi.org/10.1016/j.phpro.2012.05.013>
- Lee, J. H., Kim, S. Y., & Lee, J. (2015). Study on collapse and folding transitions of a lattice protein using exact enumeration. *AIP Advances*, 5(12). <https://doi.org/10.1063/1.4938021>
- Li, Y., Kang, H., Ye, K., Yin, S., & Li, X. (2018). *FoldingZero: Protein Folding from Scratch in Hydrophobic-Polar Model*. Nips, 1–10. <http://arxiv.org/abs/1812.00967>
- Li, Y. W., Wüst, T., & Landau, D. P. (2011). Monte Carlo simulations of the HP model (the “ising model” of protein folding). *Computer Physics Communications*, 182(9), 1896–1899. <https://doi.org/10.1016/j.cpc.2010.12.049>
- Musdalifah, Safrullah, & Surungan, T. (2023). Studi Perubahan Sifat Struktur dan Termodinamik Pelipatan Protein Model HOP Menggunakan Simulasi Monte Carlo dengan Algoritma Wang-Landau. In *Prosiding Seminar Nasional Fisika*, 2(1), 568-576.
- Pabisi, E. H. (2024). *Numerasi Eksak pada Pelipatan Protein Model Protein Kisi*. Universitas Hasanuddin. Makassar.
- Pattanasiri, B., Li, Y. W., Landau, D. P., Wüst, T., & Triampo, W. (2013). Thermodynamics and structural properties of a confined HP protein determined by Wang-Landau simulation. *Journal of Physics: Conference Series*, 454(1). <https://doi.org/10.1088/1742-6596/454/1/012071>
- Shi, G., Farris, A. C. K., Wüst, T., & Landau, D. P. (2016). Folding in a semi-flexible lattice model for Crambin. *Journal of Physics: Conference Series*, 686(1), 0–7. <https://doi.org/10.1088/1742-6596/686/1/012001>
- Shi, G., Wüst, T., & David, P. L. (2017). Replica Exchange Wang - Landau Simulation of Lattice Protein Folding Funnels. *Journal of Physics: Conference Series*, 905(1). <https://doi.org/10.1088/1742-6596/905/1/012016>
- Shi, G., Wüst, T., & Landau, D. P. (2016). Characterizing folding funnels with replica exchange Wang-Landau simulation of lattice proteins. *Physical Review E*, 94(5), 1–5. <https://doi.org/10.1103/PhysRevE.94.050402>
- Shi, G., Wüst, T., & Landau, D. P. (2018). Elucidating thermal behavior, native

- contacts, and folding funnels of simple lattice proteins using replica exchange Wang-Landau sampling. *Journal of Chemical Physics*, 149(16). <https://doi.org/10.1063/1.5026256>
- Silantyeva, I. A., & Vorontsov-Velyaminov, P. N. (2012). Thermodynamic properties of star shaped polymers investigated with Wang-Landau Monte Carlo simulations. *Macromolecular Symposia*, 317–318(1), 267–275. <https://doi.org/10.1002/masy.201200015>
- Taylor, M. P., Paul, W., & Binder, K. (2016). On the polymer physics origins of protein folding thermodynamics. *Journal of Chemical Physics*, 145(17). <https://doi.org/10.1063/1.4966645>
- Wüst, T., & Landau, D. P. (2012). Optimized Wang-Landau sampling of lattice polymers: Ground state search and folding thermodynamics of HP model proteins. *Journal of Chemical Physics*, 137(6). <https://doi.org/10.1063/1.4742969>
- Yang, X., & Chen, Z. (2023). A hybrid approach based on Monte Carlo simulation-VIKOR method for water quality assessment. *Ecological Indicators*, 150(April), 110202. <https://doi.org/10.1016/j.ecolind.2023.110202>
- Zhang, Z., Farris, A. C. K., Shi, G., Wüst, T., & Landau, D. P. (2019). Crambin Homologues in the H0P Lattice Model. *Journal of Physics: Conference Series*, 1290(1), 0–6. <https://doi.org/10.1088/1742-6596/1290/1/012018>