

## **BAB 5**

### **KESIMPULAN DAN SARAN**

#### **5.1. Kesimpulan**

Berdasarkan hasil penelitian yang telah dilakukan maka dapat disimpulkan hasil dari Simulasi dinamika kompleks MIP-*rapamycin* pada konsentrasi garam fisiologis yang dilakukan selama 400 ns, dapat dipaparkan sebagai berikut :

1. Simulasi dinamika kompleks yang dilakukan selama waktu 400 ns menghasilkan nilai rata-rata dari perhitungan RMSD untuk semua atom protein 0,2745 nm dan nilai rata-rata untuk atom tulang belakang 0,1983 nm.
2. Hasil nilai rata-rata dari perhitungan RMSF untuk semua atom protein 0,1444 nm dan nilai rata-rata untuk atom tulang belakang 0,0964 nm. Pada RMSF sub bagian 6 dan 13 berfluktuasi lebih rendah.
3. Interaksi ikatan hidrogen yang terbentuk selama waktu 400 ns, yaitu pada residu Q78, I83, Y109, dan D66.
4. Interaksi ikatan hidrofobik antara residu W86 dengan gugus pipekolil dari ligan *rapamycin* stabil dengan jarak rata-rata 0,4661 nm.

#### **5.2. Saran**

Pada penelitian simulasi dinamika kompleks MIP-*rapamycin* pada konsentrasi garam fisiologis dapat dilanjutkan dengan perhitungan energi bebas.

## DAFTAR PUSTAKA

- Abraham, M.J., van der Spoel, D., Lindahl, E, dan Hess, B. 2018, GROMACS User Manual version 2018, *Royal Institute of Technology and Uppsala University*, **2**, <https://www.gromacs.org/>.
- Aldeghi, M., Heifetz, A., Bodkin, M.J., Knapp, S. and Biggin, P.C. 2015, Accurate Calculationof The Absolute Free Energy of Binding for Drug Molecules, *Chemical Science*, **7(1)**: 207–218.
- Bussi, G., Donadio, D. and Parrinello, M. 2008, Canonical Sampling through Velocity-Rescaling, *The Journal of Chemical Physics*, **126(1)**: 014101-1– 014101-7.
- Bogunia, M., & Makowski, M. 2020, Influence of ionic strength on hydrophobic interactions in water: dependence on solute size and shape. *The Journal of Physical Chemistry B*, **124(46)**: 10326-10336.
- Case, D., Ben-Shalom, I., Brozell, S., Cerutti, D., Cheatham, T. I., Cruzeiro, V., Darden, T., Duke, R., Ghoreishi, D., Gilson, M. K., Gohlke, H., Goetz, A. W., Greene, D., Harris, R., Homeyer, N., Huang, Y., Izadi, S., Kovalenko, A., Kurtzman, T., Lee, T. S., LeGrand, S., Li, P., Lin, C., Liu, J., Luchko, T., Luo, R., Mermelstein, D. J., Merz, K. M., Miao, Y., Monard, G., Nguyen, C., Nguyen, H., Omelyan, I., Onufriev, A., Pan, F., Qi, R., Roe, D. R., Roitberg, A., Sagui, C., Schott-Verdugo, S., Shen, J., Simmerling, C. L., Smith, J., SalomonFerrer, R., Swails, J., Walker, R.C., Wang, J., Wei, H., Wolf, R. M., Wu, X., Xiao, L., York, D.M., and Kollman, P.A. 2018, Amber 2018 References Manual (Covers Amber18 and AmberTools18), University of California, San Francisco.
- Ceymann, A., Horstmann, M., Ehses, P., Schweimer, K., Paschke, A. K., Steinert, M., & Faber, C. 2008, Solution structure of the Legionella pneumophila Mip-rapamycin complex. *BMC Structural Biology*, **8**: 1-12.
- Childers, M. and Daggett, V. 2018, Validating Molecular Dynamics Simulations Against Experimental Observables in Light of Underlying Conformational Ensembles, *The Journal of Physical Chemistry B*, **122(26)**: 6673-6689.

- Darden, T., York, D. and Pedersen, L. 1993, Particle mesh Ewald: An N - log(N) method for Ewald sums in large systems, *The Journal of Chemical Physics*, **98**(12): 10089-10092.
- Gattuso, G., Rizzo, R., Lavoro, A., Spoto, V., Porciello, G., Montagnese, C., ... & Salmeri, M. 2022, Overview of the clinical and molecular features of *Legionella pneumophila*: Focus on novel surveillance and diagnostic strategies. *Antibiotics*, **11**(3): 370.
- Hess, B., Bekker, H., Berendsen, H.J.C. and Fraaije, J.G.E.M. 1997, LINCS: A Linear Constraint Solver for Molecular Simulations, *Journal of Computational Chemistry*, **18**: 1463–1472.
- Hollingsworth, S. A., & Dror, R. O. 2018, Molecular dynamics simulation for all. *Neuron*, **99**(6): 1129-1143.
- Humphrey W. 1996, VMD-visual molecular dynamics. *Journal of molecular graphics*, **14**: 33-38.
- Iliadi, V., Staykova, J., Iliadis, S., Konstantinidou, I., Sivikh, P., Romanidou, G., ... & Konstantinidis, T. G. 2022, *Legionella pneumophila*: The Journey from the Environment to the Blood. *Journal of Clinical Medicine*, **11**(20): 6126.
- Juli, C., Sippel, M., Jäger, J., Thiele, A., Weiwig, M., Schweimer, K., ... & Holzgrabe, U. 2011, Pipecolic acid derivatives as small-molecule inhibitors of the *Legionella* MIP protein. *Journal of medicinal chemistry*, **54**(1): 277-283.
- Jomehzadeh, N., Moosavian, M., Saki, M., & Rashno, M. 2019, Legionella and legionnaires' disease: An overview. *Journal of Acute Disease*, **8**(6): 221-232.
- Jorgensen W.L., Chandrasekhar J., Madura J.D., Impey R.W., Klein, M.L. 1983, Comparison of simple potential functions for simulating liquid water, *Journal of Chemical Physics*, **79**: 926-935.
- Likhachev, I. V., Balabaev, N. K., & Galzitskaya, O. V. 2016, Available instruments for analyzing molecular dynamics trajectories. *The open biochemistry journal*, **10**: 1.
- Lindorff-Larsen, K., Piana, S., Palmo, K., Maragakis, P., Klepeis, J. L., Dror, R. O., & Shaw, D. E. 2010, Improved side-chain torsion potentials for the Amber ff99SB protein force field. *Proteins: Structure, Function, and Bioinformatics*, **78**(8): 1950-1958.

- Liu, Y., Yang, F., Zou, S., & Qu, L. 2019, Rapamycin: a bacteria-derived immunosuppressant that has anti-atherosclerotic effects and its clinical application. *Frontiers in Pharmacology*, **9**: 1520.
- Mobley, D.L., Bayly, C.I., Cooper, M.D. and Dill, K.A. 2009, Predictions of Hydration Free Energies from All-Atom Molecular Dynamics Simulations, *The Journal of Physical Chemistry B*, **113(14)**: 4533–4537.
- Patodia, S., Bagaria, A., & Chopra, D. 2014, Molecular dynamics simulation of proteins: a brief overview. *Journal of Physical Chemistry & Biophysics*, **4(6)**: 1.
- Reimer, A., Seufert, F., Weiwad, M., Ebert, J., Bzdy, N. M., Kahler, C. M., Kozjak-Pavlovic, V. 2016, Inhibitors of macrophage inf ectivity potentiator-like PPIases affect neisserial and chlamydial pathogenicity, *International Journal of Antimicrobial Agents*, **48(4)**: 401–408.
- Terry, C. A., Fernández, M. J., Gude, L., Lorente, A., & Grant, K. B. 2011, Physiologically relevant concentrations of NaCl and KCl increase DNA photocleavage by an N-substituted 9-aminomethylanthracene DYE. *Biochemistry*, **50(47)**: 10375-10389.
- Tong, M., & Jiang, Y. 2016, FK506-binding proteins and their diverse functions. *Current molecular pharmacology*, **9(1)**, 48-65.
- Ünal, C. M., & Steinert, M. 2014, Microbial peptidyl-prolyl cis/trans isomerases (PPIases): virulence factors and potential alternative drug targets. *Microbiology and molecular biology reviews*, **78(3)**: 544-571.