

## **BAB 5**

### **KESIMPULAN DAN SARAN**

#### **5.1 Kesimpulan Penelitian**

Berdasarkan hasil penelitian ini dapat disimpulkan bahwa:

1. Simulasi dinamika molekul yang dilakukan selama 200 ns yang menghasilkan perhitungan rata-rata RMSD yang cukup stabil untuk semua atom protein 0,26 nm dan untuk atom penyusun tulang belakang 0,18 nm.
2. Hasil perhitungan RMSF menunjukkan bahwa pada bagian 7, 6, 8 dan 13 bersifat fleksibel dan pada masing-masing bagian terdapat residu asam amino yaitu F77, Q81, V82, Y109, P117 dan I118.
3. Hasil analisa dPCA dari 20000 konformasi menghasilkan enam struktur yang mengalami perubahan konformasi yang signifikan.
4. Interaksi yang dominan antara protein MIP dengan ligan adalah interaksi hidrofobik.
5. Interaksi antara protein MIP dengan ligan berubah selama simulasi dengan jumlah 4 struktur.

#### **5.2 Saran Penelitian**

Berdasarkan hasil yang diperoleh maka dapat disarankan:

1. Perhitungan energi bebas untuk mengetahui afinitas antara protein MIP dengan ligan (2-[2-(3,5-dimetil-2-oksoikloheksil)-2-hidroksietil-2,6-piperidindion-N-(3,5-dimetiladamantan-1-il)etanamida).

## DAFTAR PUSTAKA

- Aldeghi, M., Heifetz, A., Bodkin, M.J., Knapp, S. and Biggin, P.C. 2015, Accurate Calculation of The Absolute Free Energy of Binding for Drug Molecules, *Chemical Science*, **7(1)**: 207–218.
- Altis, A., Nguyen, P.H., Hegger, R. and Stock, G. 2007, Dihedral Angle Principal Component Analysis of Molecular Dynamics Simulations, *The Journal of Chemical Physics*, **126(24)**: 244111-1–244111-10.
- Arunan, E., Desiraju, G. R., Klein, R. A., Sadlej, J., Scheiner, S., Alkorta, I., Clary, D.C., Crabtree, R.H., Dannenberg, J.J., Hobza, P., Kjaergaard, H.G., Legon, A.C., Mennucci, B. and Nesbitt, D.J. 2011, Definition of The Hydrogen Bond (IUPAC Recommendations 2011), *Pure and Applied Chemistry*, **83(8)**: 1637–1641.
- Astuti, A.D. and Mutiara, A.B. 2009, Performance Analysis on Molecular Dynamics Simulation of Protein Using GROMACS, *Department of Informatics Engineering*, Jakarta.
- Ben-Shalom, I.Y., Case, D.A., Brozell, S.R., Cerutti, D.S., Cheatham, T.E., Cruzeiro, V.W.D., Darden, T.A., Duke, R.E., 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., Salomon-Ferrer, 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 Reference Manual (Covers Amber18 and AmberTools18)*, University of California, San Francisco.
- Beaute, J. 2019, ‘Epidemiology, Prevention and Control of Legionnaires’ Disease in Europe’, *Disertasi*, Doktor Epidemiologi Medis dan Biostatistik, Karolinska Institutet, Stockholm.
- Bussi, G., Donadio, D. and Parrinello, M. 2008, Canonical Sampling through Velocity-Rescaling, *The Journal of Chemical Physics*, **126(1)**: 014101-1–014101-7.

- Ceymann, A., Horstmann, M., Ehses, P., Schweimer, K., Paschke, A.K. and Fischer, G. 2008, Solution Structure of The *Legionella pneumophila* MIP-Rapamycin Complex, *BMC Strutral Biology*, **17(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.
- Cunha, B.A., Burillo, A. and Bouza, E. 2015, Legionnaires' Disease, *Lancet*, **387(10016)**: 376-385.
- 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.
- European Centre for Disease Prevention and Control, 2019, *Legionnaires' disease*, European Centre for Disease Prevention and Control, Stockholm.
- Ferreira, L.G., Santos, R.N.D., Olivia, G. and Andricopulo, A.D. 2015, Molecular Docking and Structure-Based Drug Design Strategies, *Molecule*, **20(7)**: 13384-13386.
- Frenkel, D. and Smit, B. 2002, *Understanding Molecular Simulation from Algorithms to Applications*, Academic Press, New York.
- Helbig, J.H., Konig, B., Knospe, H., Bubert, B., Yu, C., Luck, C.P., Riboldi-Tunnicliffe, A., Hilgenfeld, R., Jacobs, E., Hacker, J. and Fischer, G. 2003, The PPIase Active Site of *Legionella pneumophila* Mip Protein is Involved in the Infection of Eukaryotic Host Cells, *Biological Chemistry*, **384(1)**: 37-125.
- 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. and Dror, R.O. 2019, Molecular Dynamics Simulation for All, *Neuron*, **99(6)**: 1129-1143.
- Juli, C., Sippel, M., Jager, J., Thiele, A., Weiwig, M., Schweimer, K., Rosch, P., Steinert, M., Sottriffer, C.A. and Holzgrabe, U. 2011, Piceolic Acid Derivatives as Small-Molecule Inhibitors of The *Legionella* MIP Protein, *Journal of Medicinal Chemistry*, **54(1)**: 277–283.

- Khan, S., Farooq, U. and Kurnikova, M. 2017, Protein Stability and Dynamics Influenced by Ligands in Extremophilic Complexes – a Molecular Dynamics Investigation, *Molecular BioSystem*, **13(9)**: 1874-1887.
- Leach, A.R. 2001, *Molecular modelling: principles and applications 2<sup>nd</sup> edition*, Pearson Education, England.
- Likhachev, I.V., Balabaev, N.K. and Galzitskaya, O.V. 2016, Available Instruments for Analyzing Molecular Dynamics Trajectories, *The Open Biochemistry Journal*, **10**: 1-11.
- Lins, L. and Brasseur, R. 1995, The Hydrophobic Effect in Protein Folding, *Faseb J*, **9(7)**: 535-540.
- Malau, N.D. and Sianturi, M. 2017, Molecular Dynamics Approach in Designing Thermostable Aspergillus niger Xylanase, *IOP Conference Series: Earth and Environmental Science*, **58**: 1-6.
- 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.
- Moehario, L.H., Robertus, T., Grace, Y. and Tjoa, E. 2019, Screening of Legionella pneumophila from Water Sources in The Hospitals in Jakarta, *Health Science Journal of Indonesia*, **10(1)**: 21-26.
- Norville, I.H., O'Shea, K., Sarkar-Tyson, M., Zheng, S., Titball, R.W., Varani, G. and Harmer, N.J. 2011, The Structure of a Burkholderia pseudomallei Immunophilin-Inhibitor Complex Reveals New Approaches to Antimicrobial Development, *Biochemical Journal Immediate Publication*, **437(3)**: 413–422.
- Phin, N., Parry-Ford, F., Harrison, T., Stagg, H.R., Zhang, N., Kumar, K., Lortholary, O., Zumla, A. and Abubakar, I. 2014, Epidemiology and Clinical Management of Legionnaires' Disease, *Lancet Infect Dis*, **14(10)**: 1011-1012.
- Rasch, J., Theuerkorn, M., Unal, C., Heinsohn, N., Tran, S., Fischer, G., Weiwad, M. and Steinert, M. 2015, Novel Cycloheximide Derivatives Targeting The Moonlighting Protein Mip Exhibit Specific Antimicrobial Activity Against *Legionella pneumophila*, *Bioengineering and Biotechnology*, **3**: 1-8.

- Reimer, A., Seufert, F., Weiwad, M., Ebert, J., Bzdyl, N.M., Kahler, C.M., Sarkar-Tyson, M., Holzgrabe, U., Rudel, T. and Kozjak-Pavlovic, V. 2016, Inhibitors of Macrophage Infectivity Potentiator-Like PPIases Affect Neisserial and Chlamydial Pathogenicity, *International Journal of Antimicrobial Agents*, **48(4)**: 8-401.
- Reva, B.A., Finkelstein, A.V. and Skolnick, J. 1998, What is The Probability of a Chance Prediction of a Protein Structure with a RMSD of 6 Å?, *Folding & Design*, **3(2)**: 141-147.
- Tinberg, C.E., Khare, S.D., Dou, J., Doyle, L., Nelson, J.W., Schena, A., Jankowski, W., Kalodimos, C.G., Johnsson, K., Stoddard, B.L. and Baker, D. 2013, Computational Design of Ligand-Binding Proteins with High Affinity and Selectivity, *Nature*, **501(7466)**: 212–216.
- Tong, M. and Jiang, Y. 2015, FK506-Binding Proteins and Their Diverse Functions, *Current Molecular Pharmacology*, **9(1)**: 48–65.
- Vogrin, A.J. and Hartland, E.L. 2016, *Human Emerging and Re-emerging Infections: Bacterial & Mycotic Infections*, JohnWiley & Sons Inc, Australia.
- Wang, J., Wolf, R.M., Caldwell, J.W., Kollman, P.A. and Case, D.A. 2004, Development and Testing of a General Amber Force Field, *Journal of Computational Chemistry*, **25(9)**: 1158-1171.
- World Health Organization, 2007, *Legionella and the prevention of legionellosis*, World Health Organization Press, Switzerland.
- Wu, W. and Owino, J. 2014, Applying Periodic Boundary Conditions in Finite Element Analysis, *Simulia Community Conference*, Amerika Serikat.