

BAB V

KESIMPULAN DAN SARAN

5.1 Kesimpulan Penelitian

Berdasarkan hasil penelitian ini dapat disimpulkan bahwa:

1. Simulasi dinamika molekul selama 40 ns memperlihatkan *domain motion* pada sisi aktif dan terjadinya *flipped state* dari ligan rapamycin.
2. Interaksi hidrofobik menstabilkan *flipped state* lebih dominan dari pada interaksi ikatan hidrogen.

5.2 Saran Penelitian

Berdasarkan hasil yang diperoleh maka dapat disarankan sebagai berikut:

1. Simulasi dinamika molekul untuk protein MIP pada struktur apo.
2. Simulasi dinamika molekul untuk protein yang mirip dengan protein MIP dan *family* FKBP dengan ligan rapamycin untuk mengetahui faktor yang berperan dalam selektivitas ligan.

DAFTAR PUSTAKA

- Abraham, M. J., van der Spoel, D., Lindahl, B., Hess, B. & the GROMACS development team. 2018, *GROMACS* User Manual version 2018. 2, The GROMACS Vol. 2, the Royal Institute of Technology and Uppsala University, Sweden.
- Altis, A., Nguyen, P. H., Hegger, R. & Stock, G. 2007. Dihedral angle principal component analysis of molecular dynamics simulations. *J. Chem. Phys.*, **126**, 244111.
- Altis, A., Otten, M., Nguyen, P. H., Hegger, R. & Stock, G. 2008. Construction of the free energy landscape of biomolecules via dihedral angle principal component analysis. *J. Chem. Phys.*, **128**, 245102.
- Bekker, H., Berendsen, H. J. C., Dijkstra, E. J., Achterop, S., van Drunen, R., van der Spoel, D., Sijbers, A., Keegstra, H., Reitsma, B. & Renardus, M. K. R., 1993, *GROMACS*: A parallel computer for molecular dynamics simulations, DeGroot, R. A. & Nadrchal, J, Singapore.
- Berendsen, H. J. C., van der Spoel, D. & Drunen, R. v. 1995. *GROMACS*: A message-passing parallel molecular dynamics implementation. *Computer Physics Communications*, **91**, 43-56.
- Bussi, G. & Parrinello, D. D. M. 2007. Canonical sampling through velocity rescaling. *The Journal of Chemical Physics*, **126**, 1-7.
- 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**.
- Cianciotto, N. P. 2001. Pathogenicity of *Legionella pneumophila*. *J. Med. Microbiol.*, **291**, 331-343.
- Departemen Kesehatan RI, 2003, Standar Pengolahan Spesimen *Legionella*, 1538, Jakarta: Departemen Kesehatan Republik Indonesia.
- Darden, T., York, D. & Pedersen, L. 1993. Particle mesh Ewald—an N.Log(N) method for Ewald sums in large systems. *J. Chem. Phys.*, **98**, 10089–10092.
- Da Silva, A. W. S. & Vranken, W. F. 2012. ACPYPE-AnterChamber

- Python Parser interface. *BMC Research Notes*, **5**, 367.
- Fields, B. S., Benson, R. F. & Besser, R. E. 2002. Legionella and Legionnaires' Disease: 25 Years of Investigation. *Clinical Microbiology Reviews*, **15**, 506–526.
- Granados, A., Podzamczer, D., Gudiol, F. & Manresa, F. 1989. Pneumonia due to *Legionella pneumophila* and pneumococcal pneumonia: similarities and differences on presentation. *Eur Respir J*, **2**, 130–134.
- Grzesiek, S. & Edwin, D. B. 2001. Hydrogen bonding. *Encyclopedia of Magnetic Resonance*, Switzerland.
- Gunsteren, W. F. V. & Mark, A. E. 1998. Validation of molecular dynamics simulation. *Journal Of Chemical Physics*, **108**, 6109-6116.
- Gupta, S. K., Imperiale, T. F. & Sarosi, G. A. 2001. Evaluation of the Winthrop-University Hospital Criteria to Identify *Legionella* Pneumonia. *Clinical Investigations*, **4**, 1064-1071.
- Hess, B., Bekker, H., Berendsen, H. J. C. & Lindahl, E. 2008. GROMACS 4: Algorithms for Highly Efficient, Load-Balanced, and Scalable Molecular Simulation. *J. Chem. Theory. Comput*, **4 (3)**, 435–447.
- Hess, B., Kutzner, C., van der Spoel, D. & Fraaije, J. 1997. LINCS: a linear constraint solver for molecular simulations. *J. Comput. Chem*, **18**, 1463–1472.
- Hornak, V., Abel, R., Ookur, A., Strockbine, B., Roitberg, A. & Simmerling, C. 2006. Comparison of multiple AMBER force fields and development of improved protein backbone parameters. *Proteins*, **65 (3)**, 712-725.
- Jeremy, M. B., John, L. T. & Lubert, S. 2002. *Biochemistry*, 5th Ed, W H Freeman, New York.
- Jorgensen, W. L., Chandrasekhar, J. & Madura, J. D. 1983. Comparison of simple potential functions for simulating liquid water. *J. Chem. Phys*, **79 (2)**, 926-935.
- Jorge Roig, M. D., Xavier Aguilar, M. D., Juan Ruiz, M. D., Christian Domingo, M. D., Eduardo Mesalles, M. D., Jose Manterola, M. D. & Jose Morera, M. D. 1991. Comparative Study of *Legionella pneumophila* and Other Nosocomial Acquired Pneumonias. *Chest*, **99**, 344-350.

- Li, J., Kim, S. G. & Blenis, J. 2014. Rapamycin: One Drug, Many Effects. *Cell Metabolism*, **19**, 373-379.
- Lindahl, E., Hess, B. & van der Spoel, D. 2001. C GROMACS 3.0: A Package for Molecular Simulation and Trajectory analysis. *J Mol Model*, **7**, 306-317.
- Ma'at, S. 2008. Menahan Atau Menekan Kekebalan (Imunosupresi) Untuk Pencangkokan Ginjal (Bagian II). *Indonesian Journal of Clinical Pathology and Medical Laborartory*, **14**, 110-122.
- Macfarlane, J., Miller, A., Smith, W. R., Morris, A. & Rose, D. 1984. Comparative radiographic features of community acquired legionnaires' disease, pneumococcal pneumonia, mycoplasma pneumonia, and psittacosis. *Thorax*, **39**, 28-33.
- Mcadam, P. R., Broek, C. W. V., Lindsay, D. S., Ward, M. J., Hanson, M. F., Gillies, M., Watson, M., Stevens, J. M., Edwards, G. F. & Fitzgerald, J. R. 2014. Gene flow in environmental Legionella pneumophila leads to genetic and pathogenic heterogeneity within a Legionnaires' disease outbreak. *Genome Biology*, **15**, 504-514.
- Miyamoto, S. & Kollman, P. A. 1992. Settle: An analytical version of the SHAKE and RATTLE algorithm for rigid water models. *J Comput. Chem*, **13 (8)**, 952-962.
- Moehario, L. H., Robertus, T., Grace, Y. & Tjoa, E. 2019. Screening of Legionella pneumophila from water sources in the hospitals in Jakarta. *Health Science Journal of Indonesia*, **10**, 21-26.
- Moffat, J. F. & Tompkins, L. S. 1992. A Quantitative Model of Intracellular Growth of Legionella pneumophila in Acanthamoeba castellanii. *Infection and Immunity*, **60**, 296-301.
- Molmeret, M. & Kwaik, Y. A. 2002. How does Legionella pneumophila exit the host cell? *Trends in Microbiology*, **6**, 258-260.
- Nilsson, V. P. a. L. 2008. Insights into structure, dynamics and hydration of locked nucleic acid (LNA) strand-based duplexes from molecular dynamics simulations. *Nucleic Acids Research*, **36**, 1508–1516.
- Páll, S., Abraham, M. J., Kutzner, C., Hess, B., Lindahl, E. 2015. Tackling Exascale Software Challenges in Molecular Dynamics simulations with GROMACS. In: Solving Software Challenges for Exascale. *Springer Internasional Publishing Switzerland*. **8759**. 3-27.
- Pronk, S., Páll, S., Schulz, R., Larsson, P., Bjelkmar, P., Apostolov, R.,

- Shirts, M. R., Smith, J. C., Kasson, P. M., van der Spoel, D., Hess, B., Lindahl, E. 2013. GROMACS 4.5: a high-throughput and highly parallel open source molecular simulation toolkit. *Bioinformatics*, 1–10.
- Ruiz, M., Ewig, S., Marcos, M. A., Martinez, J. A., Arancibia, F., Mensa, J. & Torres, A. 1999. Etiology of Community-Acquired Pneumonia: Impact of Age, Comorbidity, and Severity. *Am J Respir Crit Care Med*, **160**, 397–405.
- Ryckaert , J. P. & Ciccotti, G. Berendsen, H. J. 1977. Numerical Integration of the Cartesian Equations of Motion of a System with Constraints: Molecular Dynamics of N-Alkanes. *J Comput Phys.*, **23** (3), 327–341.
- Shalom, B., D, C., S, B., D, C., T, C., V, C., T, D., R, D., D, G. & M, G. 2018. *Amber 2018 Reference Manual (Covers Amber18 and AmberTools18)*, University of California, San Francisco.
- Sippel, M. 2010. Computational Structure-based Design Approaches: Targeting HIV-1 Integrase and the *Macrophage Infectivity Potentiator* of *Legionella pneumophila*. Dissertation, Universität Würzburg.
- Smith, L. I. 2002. *A tutorial on Principal Components Analysis*, **85**, 1-26.
- Sopena, N., Sabria-Leal, M., Pedro-Botet, M. L., Padilla, E., Dominguez, J., Morera, J. & Tudela, P. 1998. Comparative Study of the Clinical Presentation of Legionella Pneumonia and Other Community-Acquired Pneumonias. *CHEST*, **113**, 1195-1200.
- Stout, J. E. & U, V. L. Y. 1997. Legionellosis. *The New England Journal of Medicine*, **337**, 682-687.
- Sturgill-Koszycki, S. & Swanson, M. S. 2000. Legionella pneumophila Replication Vacuoles Mature into Acidic, Endocytic Organelles. *J. Exp. Med.*, **192**, 1261-1272.
- Tully, M., Williams, A. & Fitzgeorge, R. B. 1992. Transposon mutagenesis in *Legionella pneumophila* If. -- Mutants exhibiting impaired intracellular growth within cultured macrophages and reduced virulence in vivo. *Res. Microbiol*, **143**, 481-488.
- Van der Spoel, D., Lindahl, E., Hess, B., Groenhof, G., Mark, A. E. & Berendsen, H. J. C. 2005. *GROMACS*: Fast, Flexible, and Free. *Journal of Computational Chemistry*, **26** (16), 1702-1718.

- Wang, J., Wolf, R. M., Caldwell, J. W., Kollman, P. A. & Case, D. A. 2004. Development and Testing of a General Amber Force Field. *J Chem Theory Comput*, **25**, 1157–1174.
- Weiner, P. K. & Kollman, P. A. 1981. AMBER: Assisted Model Building with Energy Refinement. A General Program for Modeling Molecules and Their Interactions. *Journal of Computational Chemistry*, **2**, 287-303.
- Yu, V. L., Kroboth, F. J., Shonnard, J., Brown, A., Mcdearman, S. & Magnusson, M. 1982. Legionnaires' Disease: New Clinical Perspective from a Prospective Pneumonia Study. *The American Journal of Medicine*, **73**, 357-361.