

## **BAB 5**

### **SIMPULAN**

#### **5.1 Simpulan**

Simulasi selama 20 ns menghasilkan dua klaster Ago yang berada dalam kesetimbangan. Interaksi Ago-siRNA bersifat dinamis dan didominasi oleh interaksi elektrostatik dari ikatan hidrogen. Hanya dua dari sembilan ikatan hidrogen yang dipertahankan. Tiga ikatan hidrogen tidak tampak sama sekali, dua ikatan hidrogen berada dalam kesetimbangan, sedangkan dua lainnya bertahan kira-kira selama 10 ns. Fleksibilitas sisi aktif terutama disebabkan oleh residu 128GLN tetapi tidak terjadi penyimpangan pada rotasi sudut dihedral rantai utama residu tersebut.

#### **5.2 Alur Penelitian Selanjutnya**

Perlu adanya analisa sampling konformasi lebih lanjut untuk struktur siRNA selama simulasi.

## DAFTAR PUSTAKA

Adams, A., 2005, RNA Therapeutic Enter Clinical Trials, **The Scientist**, 19(1), pp.28.

Agrawal, N., P.V.N. Dasaradhi, A. Mohmmmed, P. Malhotra, R. Bhatnagar, S. Mukherjee, 2003, RNA Interference: Biology, Mechanism and Applications, **Microbiology and Molecular Biology Reviews**, 67(4), pp.657-685.

Berendsen, H.J.C., 1995, **A Molecular Dinamycs Simulations: The Limits and Beyond**, Delivered in: Proceeding of The 2<sup>nd</sup> International Symposium on Algorithms for Macromolecular Modelling, Berlin, May 21-24, pp.1997.

Brooks, B.R., R.E. Bruccoleri, B.D. Olafson, D.J. States, S. Swaminathan, M. Karplus, 1983, CHARMM: A Program for Macromolecular Energy, Minimization, and Dynamics Calculations, **Journal of Computer Chemical**, 4, pp.187-217.

Chaudhury S., M.A. Olson, G. Tawa, A. Wallqvist, and M.S. Lee, 2011, Efficient conformational sampling in explicit solvent using a hybrid replica exchange molecular dynamics method, **Journal of Chemical Teory and Computation**, pp.1-4.

Couzin, J., 2002, Small RNAs Make Big Splash, **Science**, pp.2296-2297.

Dorsett and Tuschi, 2004, Applications in Functional Genomics and Potential as Therapeutics, **Nature**, 2, pp.318-329.

Estrada, T., R. Armen, and M. Taufer, 2010, **Automatic Selection of Near-Native Protein-Ligand Conformations using A Hierarchical Clustering and Volunteer Computing**, Delivered in: Proceedings of the First ACM International Conference on Bioinformatics and Computational Biology, New York, pp.204-213.

Feig, M., J. Karanicolas, and C.L. Brooks, 2004, MMTSB Tool Set: Enhanced Sampling and Multiscale Modelling Methods for Applications in Structural Biology, **Journal of Molecular Graphics and Modelling**, 22, pp.377–395.

Fire, A., SiQun Xu, M.K. Montgomery, S.A. Kostas, S.E. Driver, and C.C. Mello, 1998, Potent and Specific Genetic Interference by Double-Stranded RNA in *Caenorhabditis elegans*, **Nature**, 391, pp.806-811.

Margaretha, F., 2010, Uji Stabilitas Kompleks siRNA-Protein Argonaute dengan Simulasi Dinamika Molekul, **Skripsi Sarjana**, Universitas Katolik Widya Mandala, Surabaya.

Hess, B., H. Bekker, H.J. Berendsen, J.G.E.M. Fraaije, 1997, LINCS: A Linear Constraint Solver for Molecular Simulations, **Journal of Computer Chemical**, 18, pp.1463-1472.

Humphrey, W., A. Dalke, K. Schulten, 1996, VMD : Visual Molecular Dynamics, **J Mol Graph**, 14, pp.33-38.

Ikeda, K., M. Satoh, K.M. Pauley, M.J. Fritzler, W.H. Reeves, and E.K.L. Chan, 2006, Detection of the Argonaute Protein Ago2 and microRNAs in the RNA Induced Silencing Complex (RISC) Using Monoclonal Antibody, **Journal of Immunol Methods**, 317(1-2), pp.38-44.

Kelley, L.A., S.P. Gardner, and M.J. Sutcliffe, 1996, An Automated Approach for Clustering an Ensemble of NMR-Derived Protein Structures into Conformationally Related Subfamilies, **Protein Eng**, Vol. 9, pp.1063-1065.

Laakso, R., 2005, **Protein Structure Analysis**., pp.3.

Lindahl, E., B. Hess, D. Van der Spoel, 2001, GROMACS 3.0: A Package for Molecular Simulation and Trajectory Analysis, **Journal of Molecular Model.**, 7, pp.306-317.

Lucentini, J., 2004, Silencing Cancer, **The Scientist**, 18(17), pp.14-15.

Ma, Jin-Bao, K. Ye, and D.J. Patel, 2004, Structural Basis for Overhang-Specific Small Interfering RNA Recognition by the PAZ Domain, **Letters to Nature**, Vol. 429, Nature Publishing Group, USA.

Malik, A., 2005, RNA Therapeutic, Pendekatan Baru dalam Terapi Gen, **Majalah Ilmu Kefarmasian**, Vol. II, No.2, Departemen Farmasi FMIPA-UI, Depok, pp.51-61.

Melnikova I., 2007, RNA-based therapies, **Nature Publishing Group(6)**, pp.863-864.

- Napoli, C., C. Lemieux, and R. Jorgensen, 1990, **Plant Cell**, 2, pp.279-289.
- Novalia, M., 2011, Perhitungan Energi Bebas Kompleks Protein Argonaute-siRNA dan Kompleks Protein Argonaute-siLNA, **Skripsi Sarjana**, Universitas Katolik Widya Mandala, Surabaya.
- Novina , C.D. and P.A. Sharp, 2004, The RNAi Revolution, **Nature**, 430, pp.161-164.
- Pande, V. and Nilsson L., 2007, **Insight Into Structure, Dynamics and Hydration of Locked Nucleic Acid (LNA) Strand-Based Duplexes from Molecular Dynamics Simulations**, Department of Biosciences and Nutrition, Karolinska Institute, Sweden, pp.1508-1509.
- Pande, V., L. Nilsson, 2008, Insights into Structure, Dynamics and Hydration of Locked Nucleic Acid (LNA) Strand-Based Duplexes from Molecular Dynamics Simulations, **Nucleic Acids Research**, Vol. 36, No. 5, Oxford University Press, Sweden, pp.1508-1516.
- Pray, L.A., 2004, Viroids, Viruses, and RNA Silencing, **The Scientist**, 18(16), pp.23.
- Provost, P., D. Dishart., J. Doucet, D. Frendewey, B. Samulessong, and O. Rådmark, 2002, Ribonuclease Activity and RNA Binding of Recombinant Human Dicer, **The EMBO Jurnal**, 21(21), pp.5864-5874.
- Saenger, W., 1984, **Principles of Nucleic Acid Structure**, Springer-verlag, New York.
- Song J.J., Liu J., Tolia N., Schneiderman J., Smith S., Martienssen R., Hannon G., and Tor L.J., 2003, The Crystal Structure of The Argonaute 2 PAZ Domain Reveals an RNA-binding Motif in RNAi Effector Complexes, **Natural Structure Biology**, 10, pp.1026-1032.
- Tang, G., 2005, siRNA and miRNA : An Insight into RISCs, **TRENDS in Molecular Medicine**, 30(2).
- Van der Krol, A.R., L.A. Mur, M. Beld, J.N.M. MOI, and A.R. Stuitje, 1990, Flavonoid Genes in Petunia: Addition of a Limited Number of Gene Copies May Lead to a Suppression of Gene Expression, **Plant Cell**, 2, pp.291-299.

Van der Spoel, D., E. Lindahl, B. Hess, G. Groenhof, A. Mark and H.J.C. Berendsen, 2005, GROMACS: Fast, Flexible and Free, **Journal of Computer Chemical**, 26, pp.1701-1718.

Van Gunsteren, W.F. and A.E. Mark, 1998, Validation of Molecular Dynamics Simulation, **Journal of Chemical Physics**, 108(15), pp.6109-6116.

Weiner, P.K., P.A. Kollman, 1981, AMBER: Assisted Model Building with Energy Refinement. A General Program for Modelling Molecules and Their Interactions, **Journal of Computer Chemical**, 2, pp.287-303.