Atomistic insights into the binding process in the column chromatography

S.Yasami Khiabani[a], H.Rahimi[b]*
[a] Department of Biomedical Engineering, AmirKabir University of Technology, Tehran, Iran
[b] Molecular Medicine Department, Biotechnology Research Center, Pasteur Institute of Iran, Tehran, Iran
* rahimi.h1981@gmail.com

Abstract: Protein purification is a critical and cost consuming step in the production of therapeutic protein. column chromatography is the most use it method for protein purification which composed of the bead, spacer arm adopted to connect ligand and the support, the mobile phase. Although there are many studies on the chromatography design until now the principle of selecting the suitable beads are unknown. In this project molecular dynamics simulation used to provide atomistic insights into the structural parameters of beads. Results showed that the volume, surface, and the charge of the beads play roles as critical parameters in the design of column chromatography.

Keywords: Molecular Dynamics, Chromatography, Protein Purification

References

[1] S. J. Marrink, H. J. Risselada, S. Yefimov, D. P. Tieleman, and A. H. De Vries, "The MARTINI Force Field : Coarse Grained Model for Biomolecular Simulations The MARTINI Force Field : Coarse Grained Model for Biomolecular Simulations," *J. Phys. Chem. B*, vol. 111, no. June, pp. 7812–7824, 2007.

[2] D. H. De Jong, G. Singh, W. F. D. Bennett, T. a Wassenaar, L. V Sch, X. Periole, P. Tieleman, and S. J. Marrink, "Improved Parameters For F or The Martini Coarse- Coarse - Grained Protein Force Field," *J. Chem. Theory Comput.*, vol. 9, no. 1, pp. 687–697, 2012.

[3] L. Monticelli, S. K. Kandasamy, X. Periole, R. G. Larson, D. P. Tieleman, and S. J. Marrink, "The MARTINI coarse grained force field: extension to proteins," *J. Chem. Theory Comput.*, vol. 4, no. 5, pp. 819–834, 2008.

[4] M. Salvalaglio, M. Paloni, B. Guelat, M. Morbidelli, and C. Cavallotti, "A two level hierarchical model of protein retention in ion exchange chromatography," *J. Chromatogr. A*, vol. 1411, pp. 50–62, 2015.

[5] L. Zamolo, V. Busini, D. Moiani, D. Moscatelli, and C. Cavallotti, "Molecular dynamic investigation of the interaction of supported affinity ligands with monoclonal antibodies," *Biotechnol. Prog.*, vol. 24, no. 3, pp. 527–539, 2008.

[6] M. Salvalaglio, L. Zamolo, V. Busini, D. Moscatelli, and C. Cavallotti, "Molecular modeling of Protein A affinity chromatography," *J. Chromatogr. A*, vol. 1216, no. 50, pp. 8678–8686, 2009.

[7] C. Boi, V. Busini, M. Salvalaglio, C. Cavallotti, and G. C. Sarti, "Understanding ligand-protein interactions in affinity membrane chromatography for antibody purification," *J. Chromatogr. A*, vol. 1216, no. 50, pp. 8687–8696, 2009.

[8] J. Liang, G. Fieg, and S. Jakobtorweihen, "Molecular Dynamics Simulations of a Binary Protein Mixture Adsorption onto Ion-Exchange Adsorbent," *Ind. Eng. Chem. Res.*, vol. 54, no. 10, pp. 2794–2802, 2015.

[9] W. Beckner, Y. He, and J. Pfaendtner, "Chain Flexibility in Self-Assembled Monolayers Affects Protein Adsorption and Surface Hydration: A Molecular Dynamics Study," *J. Phys. Chem. B*, p. acs.jpcb.6b05882, 2016.