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**Network Analysis Reveals the Recognition Mechanism for Mannose-binding Lectins** YUNJIE ZHAO, YIREN JIAN, CHEN ZENG, Department of Physics, The George Washington University, COMPUTATIONAL BIOPHYSICS LAB TEAM — The specific carbohydrate binding of mannose-binding lectin (MBL) protein in plants makes it a very useful molecular tool for cancer cell detection and other applications. The biological states of most MBL proteins are dimeric. Using dynamics network analysis on molecular dynamics (MD) simulations on the model protein of MBL, we elucidate the short- and long-range driving forces behind the dimer formation. The results are further supported by sequence coevolution analysis. We propose a general framework for deciphering the recognition mechanism underlying protein-protein interactions that may have potential applications in signaling pathways.

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