

Combining Brownian and Molecular Dynamics to simulate protein-protein docking subject to biochemical constraints

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I will describe the use of Brownian dynamics simulations to simulate the diffusional association of proteins to compute association rates, characterize diffusional encounter complexes and investigate the factors influencing the protein-protein binding process [1, 2]. I will then present a computational procedure to predict the structures of protein-protein complexes by a combination of Brownian dynamics and molecular dynamics simulations constrained by biochemical data [3]. Applications to structurally and functionally diverse protein complexes with different determinants of protein-protein binding, including enzyme-inhibitor, signal transduction and electron transfer complexes, will be presented [3, 4].

[1] Gabdoulline, R.R., Wade, R.C. Biomolecular Diffusional Association *Curr. Opin. Struct. Biol.* (2002) 12, 204-213.

[2] Spaar, A., Dammer, C., Gabdoulline, R.R., Wade, R.C., Helms, V. Diffusional encounter of barnase and barstar. *Biophys. J.* (2006) 90, 1913-1924.

[3] Motiejunas, D., Gabdoulline, R.R., Wang, T., Feldman-Salit, A., Johann, T., Winn, P.J. and Wade, R.C. Protein-protein docking by simulating the process of association subject to biochemical constraints, *Proteins*, in press.

[4] Karyakin, A., Motiejunas, D., Wade, R.C., Jung, C. FTIR studies of the redox partner interaction in cytochrome P450. The Pdx-P450cam couple. *BBA General Subjects* (2007) 3, 420-431.