

5. Publications

1. M. Yagi, J. Murray, K. Strand, S. Blystone, G. Interlandi, Y. Suda, M. Sobel; Heparin Modulates the Conformation and Signaling of Platelet Integrin $\alpha\text{IIb}\beta\text{3}$; *Thromb. Res.*, In press, 2011
2. J.E. Baio, T. Weidner, G. Interlandi, C. Mendoza-Barrera, H.E. Canavan, R. Michel, D.G. Castner; Probing albumin adsorption onto calcium phosphates by x-ray photoelectron spectroscopy and time-of-flight secondary ion mass spectrometry; *JVSTB*; 29(4), 2011
3. P. Aprikian*, G. Interlandi*, B. A. Kidd, I. Le Trong, V. Tchesnokova, O. Yakovenko, R. E. Stenkamp, W. E. Thomas, E. V. Sokurenko; Mechanically optimized structure of the adhesive fimbrial tip of *E. coli*; *PLoS Biology*; 9(5), 2011 (*Shared first authorship)
4. G. Interlandi and W. Thomas; The catch bond mechanism between von Willebrand Factor and platelet surface receptors investigated by molecular dynamics simulations; *Proteins: Structure, Function and Bioinformatics*; 78(11), 2506-2522, 2010
5. I. Le Trong, P. Aprikian, B. A. Kidd, M. Forero-Shelton, V. Tchesnokova, P. Rajagopal, V. Rodriguez, G. Interlandi, R. Klevit, V. Vogel, R. E. Stenkamp, E. V. Sokurenko, W. E. Thomas; Mechanical activation of the bacterial adhesive protein FimH involves allostery in a β -sandwich; *Cell*; 141(4), 645-655, 2010
6. G. Interlandi; Backbone conformations and side chain flexibility of two somatostatin mimics investigated by molecular dynamics simulations; *Proteins: Structure, Function and Bioinformatics*, 75, 659-670, 2009
7. G. Interlandi, S. K. Wetzel, G. Settanni, A. Plückthun, & A. Caffisch; Characterization and further stabilization of designed ankyrin repeat proteins by combining molecular dynamics simulations and experiments; *J. Mol. Biol.*, 375, 837-854, 2008
8. G. Interlandi, G. Settanni, & A. Caffisch; Unfolding transition state and intermediates of the tumor suppressor p16^{INK4a} investigated by molecular dynamics simulations; *Proteins: Structure, Function and Bioinformatics*, 64, 178-192, 2006
9. G. Interlandi, M. Ling, A.Y. Tu, D.W. Chung, W. E. Thomas; Type 2A von Willebrand disease mutations investigated by molecular dynamics simulations and proteolysis experiments; Under review