Gianluca Interlandi Curriculum Vitae

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1. Education/training

Institution and location	Dates attended	Degree	Conferred	Field of study
ETH, Zürich, Switzerland	1995-2000	BA, MS	11/2000	Physics
University of Zürich, Switzerland	2001-2005	PhD	02/2006	Biochemistry
Univeristy of Washington, Seattle WA	2006-2012	Postdoc		Bioengineering

2. Positions

2001-2005	Graduate fellow, University of Zürich, Zürich, Switzerland
2006-2012	Postdoctoral fellow, University of Washington, Seattle, WA
2012-present	Research Scientist, University of Washington, Seattle, WA

3. Qualifications

Academic scientific skills. Expertise with various molecular simulation packages, e.g., NAMD, CHARMM, GROMACS, VMD. Knowledge of RosettaDock. Good understanding of various experimental techniques in the area of biology, e.g., circular dichroism, stopped flow, flow chamber, single molecule force spectroscopy. Scientific publication and grant writing skills. Peer review of manuscripts.

Information technology skills. Programming in C++, java, HTML. Scripting in TCL, Unix shell. Administration of Linux servers, Linux beowulf clusters, data storage servers.

Language skills (oral and written). Italian, German, English, French, Spanish.

4. Experience

Postdoctoral fellow in the group of prof. W. Thomas at the Department of Bioengineering, University of Washington. Molecular dynamics simulations of the regulation of von Willebrand Factor A domains. Molecular dynamics simulations of fimbrial tip proteins.

Graduate fellow in the department of biochemistry at the University of Zürich, Switzerland. Molecular dynamics simulations of structured peptides and ankyrin repeat proteins. Combine computational results with experimental data to engineer more stable proteins.

Internship in the computing and controls group of the Swiss Synchrotron Light Source, Villigen, Switzerland (summer 1998, three months). Construction of an online visualization tool of a technical database.

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 αIIbβ3; *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. Caflisch; 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. Caflisch; 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