Dario Ghersi

Postdoctoral Fellow
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Education

Ph.D. Computational Biology, Mount Sinai/New York University, 2010

M.D. University of Genoa, Italy, 2004, 110/110 *Summa Cum Laude*

Awards

American-Italian Cancer Foundation Postdoctoral Fellowship, 2011-2013

NBCR Scholarship, 2007, University of California, San Diego

Medal for academic achievements, 2004, University of Genoa

Research Experience

Postdoctoral Fellow   2010-present
Mona Singh   Princeton University
Development of computational methods for the analysis of protein interactions and their alterations
in pathology

PhD Student   2006-2010
Roberto Sanchez   Mount Sinai School of Medicine
Development of computational methods to detect and characterize protein binding sites

Research Assistant   2004-2005
Franco Celada   NYU Medical Center
Mathematical modeling of the immune system with a multiagent-based simulator. Development of
routines to model crossreactivity in T cell-mediated immune response to viral infections.

Teaching Experience

Mentoring of over ten undergraduate students (summer internships and senior independent research),
Princeton University, 2010-2013

Teaching Assistant, Computational Immunology, University of Genoa, Fall 2001

First-author publications

Ghersi D, Singh M, "molBLOCKS: a suite to break down small molecules into fragments and analyze their distribution", *Bioinformatics* 2014, 10.1093/bioinformatics/btu173

Ghersi D, Singh M, "Interaction-based discovery of functionally important genes in cancers", *Nucleic Acids Research* 2013, 10.1093/nar/gkt1305

Ghersi D, Singh M, "Disentangling the complex relationship between function, network features and disease: an application to cancer and Mendelian disorders", *BMC Systems Biology* 2013, 7:5

Ghersi D, Sanchez R, "Automated Identification of Binding Sites for Phosphorylated Ligands in Protein Structures", *Proteins* 2012, 80:2347-58

Ghersi D, Sanchez R, "Beyond structural genomics: computational approaches for the identification of ligand binding sites in protein structures", *Journal of Structural and Functional Genomics* 2011, 12(2):109

Ghersi D, Sanchez R, "EasyMIFs and SiteHound: tools for the identification of ligand-binding sites in protein structures", *Bioinformatics* 2009, 25(23):3185-6

Ghersi D, Sanchez R, "Improving accuracy and efficiency of blind protein-ligand docking by focusing on predicted binding sites", *Proteins* 2009, 4(2):417-24

Other publications

Chakravarty S, Ghersi D, Sanchez R, "Systematic Assessment of Accuracy of Comparative Model of Proteins Belonging to Different Structural Fold Classes", *J Mol Mod* 2011, 17(11):2831

Calcagno C, Puzone R, Pearson YE, Cheng Y, Ghersi D, Selin LK, Welsh RM, Celada F "Computer simulations of heterologous immunity: highlights of an interdisciplinary cooperation", *Autoimmunity* 2011, 44(4):304

Zhang Q, Chakravarty S, Ghersi D, Plotnikov AN, Sanchez R, Zhou MM, "Biochemical Profiling of Histone Binding Selectivity of the Yeast Bromodomain Family", *PLoS One* 2010, 5(1):e8903

Hernandez M, Ghersi D, Sanchez R, "SITEHOUND-web: a server for ligand binding site identification in protein structures", *Nucleic Acids Research* 2009, 37(Web Server issue): W413-W416

Cheng Y, Ghersi D, Calcagno C, Selin LK, Puzone R, Celada F, "A discrete computer model of the immune system reveals competitive interactions between the humoral and cellular branch and between cross-reacting memory and naive responses", *Vaccine* 2009, 27(6):833-45

Bahl K, Kim SK, Calcagno C, Ghersi D, Puzone R, Celada F, Selin LK, Welsh RM "IFN-induced attrition of CD8 T cells in the presence or absence of cognate antigen during the early stages of viral infections", *J Immunol* 2006, 176(7):4284-95

Cornberg M, Chen AT, Wilkinson LA, Brehm MA, Kim SK, Calcagno C, Ghersi D, Puzone R, Celada F, Welsh RM, Selin LK "Narrowed TCR repertoire and viral escape as a consequence of heterologous immunity", *J Clin Invest* 2006, 116(5):1443-56

Selin LK, Cornberg M, Brehm MA, Kim SK, Calcagno C, Ghersi D, Puzone R, Celada F, Welsh RM "CD8 memory T cells: cross-reactivity and heterologous immunity", *Semin Immunol* 2004 16(5):335-47

Invited Talks

"Making life computable: the challenges of data-driven biology", ETS, Princeton, NJ, 2013.

"Protein interactions: from molecules to networks", Nanyang Technological University, Singapore, 2012.

"Increasing accuracy and speed of protein-ligand docking approaches", University of Sheffield, U.K., 2009.

"Computational approaches to detect and exploit protein binding sites", Cold Spring Harbor, NY, 2008.

Service

Referee for *PLoS Computational Biology, Nucleic Acids Research, Bioinformatics, IEEE Transactions on Computational Biology and Bioinformatics*

Software Development

molBLOCKS – for breaking down small molecules into fragments and analyzing their composition (`http://compbio.cs.princeton.edu/molblocks`)

CanBind – for exploring protein binding sites mutated in human cancers (`http://canbind.princeton.edu`)

fcsampling – for carrying out functionally-constrained sampling (`http://compbio.cs.princeton.edu/fcsampling`)

EasyMIFs and **SiteHound** – for computing Interaction Energy Maps and performing binding site identification in protein structures (`http://sitehound.sanchezlab.org`)

Skills

Programming languages: C/C++, Python, R, Lisp, Octave/Matlab, Mathematica

Operating systems: Linux, Mac OS X, Windows

Database design and implementation (MySQL)

Software: MODELLER (comparative modeling), AutoDock (molecular docking)

References

Prof. Mona Singh, (`mona@cs.princeton.edu`), Dept. of Computer Science and Lewis-Sigler Institute for Comparative Genomics, Princeton University, Princeton, NJ, Tel. +1 609-258-7059

Prof. Roberto Sanchez (`roberto.sanchez@mssm.edu`), Dept. of Structural and Chemical Biology, Mount Sinai School of Medicine, New York, NY, Tel. +1 212-659-8648

Prof. Ming-Ming Zhou (`ming-ming.zhou@mssm.edu`), Dept. of Structural and Chemical Biology, Mount Sinai School of Medicine, Tel. +1 212-659-8652

Prof. Franco Celada (`franco.celada@nyumc.org`), Dept. of Pathology, Hospital for Joint Diseases, NYU, New York, NY, Tel. +1 212-598-6507