

VLADIMIR VACIC

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Postdoctoral Fellow current
Cold Spring Harbor Laboratory Cold Spring Harbor, NY

EDUCATION

Ph.D. Computer Science (Bioinformatics)	2008
University of California, Riverside	Riverside, CA
M.S. Computer and Information Sciences (Machine Learning and Data Mining)	2004
Temple University	Philadelphia, PA
B.S. Computer Science and Mathematics (double major), <i>Summa Cum Laude</i>	2002
University of Bridgeport	Bridgeport, CT

RESEARCH

Graduate Student Researcher	2006-2008
Algorithms and Computational Biology Lab, UC Riverside	Riverside, CA
Intern	Summer, Fall 2007
Personalized Healthcare Group, Siemens Corporate Research	Princeton, NJ
Research Assistant	Summers 2004, 2005
Center for Comp. Biology and Bioinformatics, Indiana University School of Medicine	Indianapolis, IN
Research Assistant	2003-2004
Center for Information Science and Technology, Temple University	Philadelphia, PA

TEACHING

Teaching Assistant	2004-2006
Computer Science and Engineering Department, UC Riverside	Riverside, CA
Teaching Assistant	2003-2004
Computer and Information Sciences Department, Temple University	Philadelphia, PA

AWARDS AND DISTINCTIONS

PSB 2008 travel award sponsored by the National Institutes of Health.
Dean's Graduate Fellowship award at the University of California, Riverside (2004-2006).
Academic Excellence Scholarship at the University of Bridgeport (1998-2002).
President's List at the University of Bridgeport for all semesters (1998-2002).
Member of the Phi Kappa Phi and Upsilon Pi Epsilon Honor Societies at University of Bridgeport.

PUBLICATIONS

Protein Function and Structure

Vacic V, Iakoucheva LM, Lonardi S, and Radivojac P. "Graphlet kernels for prediction of functional residues in protein structures." *Journal of Computational Biology*. To appear.

Dunker AK, Oldfield CJ, Meng J, Romero P, Yang JY, Chen JW, Vacic V, Obradovic Z, and Uversky VN. "The unfoldomics decade: an update on intrinsically disordered proteins." *BMC Genomics*, 9(S2):S1. (2008)

Vacic V, Oldfield CJ, Mohan A, Radivojac P, Cortese MS, Uversky VN, and Dunker AK. "Characterization of molecular recognition features, MoRFs, and their binding partners." *Journal of Proteome Research*, 6(6):2351-66. (2007)

Sickmeier M, Hamilton J, LeGall T, Vacic V, Uversky VN, Cortese MS, Tompa P, Obradovic Z, and Dunker AK. "DisProt: the database of disordered proteins." *Nucleic Acids Research*, 35(Database issue):D786-93. (2007)

Mohan A, Oldfield CJ, Radivojac P, Vacic V, Cortese MS, Dunker AK, and Uversky VN. "Analysis of Molecular Recognition Features (MoRFs)." *Journal of Molecular Biology*, 362(5):1043-59. (2006)

Vucetic S, Obradovic Z, Vacic V, Radivojac P, Peng K, Iakoucheva LM, Cortese MS, Lawson JD, Brown CJ, Sikes JG, Newton CD, and Dunker AK. "DisProt: a database of protein disorder." *Bioinformatics*, 21(1): 137-140. (2005)

Sequence Analysis

Vacic V, Uversky VN, Dunker AK, and Lonardi S. "Composition Profiler: a tool for discovery and visualization of amino acid composition differences." *BMC Bioinformatics*. 8:211. (2007)

Vacic V, Iakoucheva LM, and Radivojac P. "Two Sample Logo: a graphical representation of the differences between two sets of sequence alignments." *Bioinformatics*, 22(12):1536-7. (2006)

Small RNAs

Vacic V, Jin H, Zhu J-K, and Lonardi S. "A probabilistic method for small RNA flowgram matching." *Pacific Symposium on Biocomputing, PSB'08*. 13:75-86. (2008)

Jin H, Vacic V, Girke T, Lonardi S, and Zhu J-K. "Small RNAs and the regulation of cis-natural antisense transcripts in Arabidopsis." *BMC Molecular Biology*. 9:6. (2008)

Genomics

Fu Z, Chen X, Vacic V, Nan P, Zhong Y, and Jiang T. "MSOAR: A high-throughput ortholog assignment system based on genome rearrangement." *Journal of Computational Biology*. 14(9):1160-75. (2007)

Fu Z, Chen X, Vacic V, Nan P, Zhong Y, and Jiang T. "A parsimony approach to genome-wide ortholog assignment." *ACM Annual Conference on Research in Computational Molecular Biology, RECOMB'06*, Venice, Italy. (2006)

POSTERS

Kusenda M, Seungtai Y, Vacic V, Wigler M, and Sebat J. "The effect of chr16p11.2 microdeletions and microduplications on gene expression in Autism Spectrum Disorders." Poster presented at the *American Society of Human Genetics Meeting*, Philadelphia, Pennsylvania. (2008)

Vacic V, Oldfield CJ, Mohan A, Radivojac P, Cortese MS, Uversky VN, and Dunker AK. "Analysis

of molecular recognition feature complexes.” Poster presented at the *51st Biophysical Society Annual Meeting*, Baltimore, Maryland. (2007)

Dunker AK, Mohan A, Vacic V, Radivojac P, Oldfield CJ, Cortese MS, and Uversky VN. “Molecular Recognition Features, MoRFs.” Poster presented at the *50th Biophysical Society Annual Meeting*, Salt Lake City, Utah. (2006)

Vacic V, Riggen S, Lewis A, Patterson E, Sickmeier M, Baird J, Hamilton J, Kim D, Cortese MS, Chen J, Radivojac P, Uversky VN, Vucetic S, Obradovic Z, and Dunker AK. “DisProt: a database of protein disorder.” Poster presented at the *Indiana Proteomics Symposium*, Bloomington, Indiana. (2004)

SERVICES

President of the Upsilon Pi Epsilon (Honor Society for the Computing Sciences) Bridgeport Delta Chapter at the University of Bridgeport (2001-2002).

Program committee member for the IEEE International Conference on Application-specific Systems, Architectures and Processors (ASAP) - Bioinformatics Track (2009).

Reviewer for (*journals*) Nucleic Acids Research, Bioinformatics, BMC Structural Biology, Pattern Recognition, Algorithms for Molecular Biology, IEEE Communications Letters; (*conferences*) Pacific Symposium on Biocomputing (PSB), Computational Systems Bioinformatics (CSB), Workshop on Algorithms in Bioinformatics (WABI), IEEE International Conference on Data Mining (ICDM), SIAM Data Mining (SDM), Combinatorial Pattern Matching (CPM), IEEE International Conference on Tools with Artificial Intelligence.