

# 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

1. Vacic V, Iakoucheva LM, Lonardi S, and Radivojac P. "Graphlet kernels for prediction of functional residues in protein structures." *J Comput Biol*. In press.
2. Bogunovic D, O'Neill DW, Belitskaya-Levy I, Vacic V, Yu Y-L, Adams S, Darvishian F, Berman R, Shapiro R, Pavlick AC, Lonardi S, Zavadil J, Osman I, and Bhardwaj N. "Immune profile and mitotic index of metastatic melanoma lesions enhance clinical staging in predicting patient survival." *Proc Natl Acad Sci USA*. In press.
3. McCarthy S, Makarov V, Kirov G, Addington A, McClellan J, Yoon S, Perkins D, Dickel DE, Kusenda M, Krastoshevsky O, Krause V, Kumar RA, Grozeva D, Malhotra D, Walsh T, Zackai EH, Kaplan P, Ganesh J, Krantz ID, Spinner NB, Roccanova P, Bhandari A, Pavon K, Lakshmi B, Leotta A, Kendall J, Lee Y, Vacic V, Gary S, Iakoucheva L, Crow TJ, Christian SL, Lieberman J, Stroup S, Lehtimki T, Puura K, Haldeman-Englert C, Pearl J, Goodell M, Willour VL, DeRosse P, Steele J, Kassem L, Wolff J, Chitkara N, McMahon F, Malhotra AK, Potash JB, Schulze T, Nthen MM, Cichon S, Rietschel M, Leibenluft E, Kustanovich V, Lajonchere CM, Sutcliffe JS, Skuse D, Gill M, Gallagher L, Mendell NR, Wellcome Trust Case Control Consortium, Craddock N, Owen MJ, O'Donovan MC, Shaikh TH, Susser E, DeLisi LE, Sullivan PF, Deutsch CK, Rapoport J, Levy DL, King MC, and Sebat J. "Microduplications of 16p11.2 are associated with schizophrenia." *Nat Genet*. 41:1223-7. (2009)
4. Radivojac P, Vacic V, Haynes C, Cocklin RR, Mohan A, Heyen JW, Goebel MG, and Iakoucheva LM. "Identification, analysis and prediction of protein ubiquitination sites." *Proteins*. In press.
5. 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)
6. Vacic V, Jin H, Zhu J-K, and Lonardi S. "A probabilistic method for small RNA flowgram matching." *Pac Symp Biocomput*, 13:75-86. (2008)
7. 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 Mol Biol*, 9:6. (2008)
8. Fu Z, Chen X, Vacic V, Nan P, Zhong Y, and Jiang T. "MSOAR: A high-throughput ortholog assignment system based on genome rearrangement." *J Comput Biol*, 14(9):1160-75. (2007)
9. 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." *J Proteome Res*, 6(6):2351-66. (2007)
10. 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)
11. 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 Res*, 35:D786-93. (2007)
12. Mohan A, Oldfield CJ, Radivojac P, Vacic V, Cortese MS, Dunker AK, and Uversky VN. "Analysis of Molecular Recognition Features (MoRFs)." *J Mol Biol*, 362(5):1043-59. (2006)
13. 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)
14. Fu Z, Chen X, Vacic V, Nan P, Zhong Y, and Jiang T. "A parsimony approach to genome-wide ortholog assignment." *RECOMB'06*, Venice, Italy. (2006)
15. 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): 137-40. (2005)

## POSTERS

Vacic V, McCarthy SE, Yoon S, Malhotra D, Makarov V, Iakoucheva L, and Sebat J. “Estimating significance of CNV-pathway associations in schizophrenia.” Poster presented at the *RECOMB Systems Biology Satellite Meeting*, Cambridge, Massachusetts. (2009)

Kusenda M, Vacic V, Yoon S, Wigler M, and Sebat J. “The effect of chr16p11.2 microdeletions and microduplications on gene expression in Autism Spectrum Disorders and Schizophrenia.” Poster presented at the *American Society for Human Genetics Meeting*, Honolulu, Hawaii. (2009)

Bogunovic D, O’Neill D, Belitskaya-Levy I, Vacic V, Adams S, Darvishian F, Pavlick A, Zavadil J, Osman I, and Bhardwaj N. “Use of gene expression profile and mitotic index of metastatic melanoma lesions as an adjunct to TNM staging in predicting patient survival.” Poster presented at the *American Society for Clinical Oncology Meeting*, Orlando, Florida. (2009)

Kusenda M, Yoon S, 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, 2010).

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.