

# VLADIMIR VACIC

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## EDUCATION AND TRAINING

- **Postdoctoral Research Scientist, Columbia University**, New York, NY 2010 - present  
Specializing in genetics of neurological diseases and functional genomics.
- **Postdoctoral Fellow, Cold Spring Harbor Laboratory**, Cold Spring Harbor, NY 2008-2010  
Specialized in genetics and systems biology of psychiatric diseases.
- **Ph.D. Computer Science, University of California, Riverside**, Riverside, CA 2004-2008  
Specialized in computational biology. Dean's Graduate Fellowship.
- **M.S. Computer and Information Sciences, Temple University**, Philadelphia, PA 2003-2004  
Specialized in machine learning and data mining.
- **B.S. Computer Science and Mathematics, University of Bridgeport**, Bridgeport, CT 1998-2002  
Academic Excellence Scholarship. President's List. Graduated *Summa Cum Laude*.

## RESEARCH

- **Intern, Siemens Corporate Research**, Princeton, NJ 2007  
Developed data analysis tools as part of the Personalized Healthcare group.
- **Research Assistant, Indiana University School of Medicine**, Indianapolis, IN 2004, 2005  
Interned at the Center for Computational Biology and Bioinformatics.

## TEACHING

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

## SERVICE

- Program committee member for the International Workshop on Data Mining in Bioinformatics - BIODDD (2011), IEEE International Conference on Application-specific Systems, Architectures and Processors (ASAP) - Bioinformatics Track (2009, 2010, 2012).
- Reviewer for (*journals*) Nucleic Acids Research, Genome Biology, Bioinformatics, PLoS Computational Biology, Molecular Biology and Evolution, BMC Structural Biology, Pattern Recognition, PLoS One, Algorithms for Molecular Biology; (*conferences*) Intelligent Systems for Molecular Biology (ISMB), Pacific Symposium on Biocomputing (PSB), Computational Systems Bioinformatics (CSB), Workshop on Algorithms in Bioinformatics (WABI), ACM SIGKDD Conference on Knowledge Discovery and Data Mining (KDD), IEEE International Conference on Data Mining (ICDM), SIAM Data Mining (SDM), Combinatorial Pattern Matching (CPM).
- President of the Upsilon Pi Epsilon (Honor Society for the Computing Sciences) Bridgeport Delta Chapter at the University of Bridgeport (2001-2002).

## AWARDS AND DISTINCTIONS

PSB 2008 travel award sponsored by the National Institutes of Health.

Member of the Phi Kappa Phi and Upsilon Pi Epsilon Honor Societies at University of Bridgeport.

## PUBLICATIONS

1. **Vacic V**, Iakoucheva LM. **Disease mutations in disordered regions - exception to the rule?** *Mol Biosyst.* 8(1):27-32. (2012)
2. Malhotra D, McCarthy S, Michaelson JJ, **Vacic V**, Burdick KE, Yoon S, Cichon S, Corvin A, Gary S, Gershon ES, Gill M, Karayiorgou M, Kelsoe JR, Krastoshevsky O, Krause V, Leibenluft E, Levy DL, Makarov V, Bhandari A, Malhotra AK, McMahon FJ, Nöthen MM, Potash JB, Rietschel M, Schulze TG, Sebat J. **High frequencies of *de novo* CNVs in bipolar disorder and schizophrenia.** *Neuron.* 72(6):951-63. (2011)
3. **Vacic V**, McCarthy SE, Malhotra D, Murray F, Cho HH, Peoples A, Makarov V, Yoon S, Bhandari A, Corominas R, Iakoucheva LM, Krastoshevsky O, Krause V, Larach Walters V, Welsh DK, Craig D, Kelsoe JR, Gershon ES, Leal SM, Dell Aquila M, Morris DW, Gill M, Corvin A, Insel PA, McClellan J, King MC, Karayiorgou M, Levy DL, DeLisi LE, Sebat J. **Duplications of the neuropeptide receptor VIPR2 confer significant risk for schizophrenia.** *Nature*, 471(7339):499-503. (2011)
4. Radivojac P, **Vacic V**, Haynes C, Cocklin RR, Mohan A, Heyen JW, Goebel MG, Iakoucheva LM. **Identification, analysis and prediction of protein ubiquitination sites.** *Proteins*, 78(2):365-380. (2010)
5. **Vacic V**, Iakoucheva LM, Lonardi S, Radivojac P. **Graphlet kernels for prediction of functional residues in protein structures.** *J Comput Biol*, 17(1):55-72. (2010)
6. 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, Bhardwaj N. **Immune profile and mitotic index of metastatic melanoma lesions enhance clinical staging in predicting patient survival.** *Proc Natl Acad Sci USA*, 106(48):20429-34. (2009)
7. 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 LM, Crow TJ, Christian SL, Lieberman J, Stroup S, Lehtimäki 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, Nöthen 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, Sebat J. **Microduplications of 16p11.2 are associated with schizophrenia.** *Nat Genet*, 41:1223-7. (2009)
8. Dunker AK, Oldfield CJ, Meng J, Romero P, Yang JY, Chen JW, **Vacic V**, Obradovic Z, Uversky VN. **The unfoldomics decade: an update on intrinsically disordered proteins.** *BMC Genomics*, 9(S2):S1. (2008)
9. Jin H, **Vacic V**, Girke T, Lonardi S, Zhu J-K. **Small RNAs and the regulation of cis-natural antisense transcripts in Arabidopsis.** *BMC Mol Biol*, 9:6. (2008)
10. **Vacic V**, Jin H, Zhu J-K, Lonardi S. **A probabilistic method for small RNA flowgram matching.** *Pac Symp Biocomput*, 13:75-86. (2008)
11. Fu Z, Chen X, **Vacic V**, Nan P, Zhong Y, Jiang T. **MSOAR: A high-throughput ortholog assignment system based on genome rearrangement.** *J Comput Biol*, 14(9):1160-75. (2007)
12. **Vacic V**, Uversky VN, Dunker AK, Lonardi S. **Composition Profiler: a tool for discovery and visualization of amino acid composition differences.** *BMC Bioinformatics*, 8:211. (2007)

13. **Vacic V**, Oldfield CJ, Mohan A, Radivojac P, Cortese MS, Uversky VN, Dunker AK. **Characterization of molecular recognition features, MoRFs, and their binding partners.** *J Proteome Res*, 6(6):2351-66. (2007)
14. Sickmeier M, Hamilton J, LeGall T, **Vacic V**, Uversky VN, Cortese MS, Tompa P, Obradovic Z, Dunker AK. **DisProt: the database of disordered proteins.** *Nucleic Acids Res*, 35:D786-93. (2007)
15. Mohan A, Oldfield CJ, Radivojac P, **Vacic V**, Cortese MS, Dunker AK, Uversky VN. **Analysis of Molecular Recognition Features (MoRFs).** *J Mol Biol*, 362(5):1043-59. (2006)
16. **Vacic V**, Iakoucheva LM, Radivojac P. **Two Sample Logo: a graphical representation of the differences between two sets of sequence alignments.** *Bioinformatics*, 22(12):1536-7. (2006)
17. Fu Z, Chen X, **Vacic V**, Nan P, Zhong Y, Jiang T. **A parsimony approach to genome-wide ortholog assignment.** *RECOMB'06*, Venice, Italy. (2006)
18. Vucetic S, Obradovic Z, **Vacic V**, Radivojac P, Peng K, Iakoucheva LM, Cortese MS, Lawson JD, Brown CJ, Sikes JG, Newton CD, Dunker AK. **DisProt: a database of protein disorder.** *Bioinformatics*, 21(1): 137-40. (2005)

## MANUSCRIPTS IN REVIEW

1. **Vacic V**, Zhao X, Oldfield CJ, Haynes C, Friedman AJ, Markwick PRL, Uversky VN, Iakoucheva LM. **Disease-associated mutations disrupt functionally important regions of intrinsic protein disorder.**
2. **Vacic V**, Ozelius LJ, Clark LN, Bar-Shira A, Gana-Weisz M, Gurevich T, Gusev A, Kedmi M, Kenny EE, Liu X, Mejia-Santana H, Mirelman A, Raymond D, Saunders-Pullman R, Desnick RJ, Burns ER, Ostrer H, Hakonarson H, Bergman A, Atzmon G, Barzilai N, Darvasi A, Peter I, Guha S, Lencz T, Giladi N, Marder K, Pe'er I, Bressman SB, Orr-Urtreger A. **Genome-wide mapping of identical-by-descent segments in an Ashkenazi Parkinson disease cohort identifies associated haplotypes.**

## POSTERS

- **Vacic V**, Dewal N, LaFramboise T, Freedman ML, Pe'er I. Strategies for analyzing allele specificity in ChIP-seq data. *ICHG/ASHG*, Montreal, Canada. (2011)
- Sebat J, McCarthy S, **Vacic V**, Burdick KE, Cichon S, Corvin A, Gary S, Gershon ES, Karayiorgou M, Kelsoe JR, Krastoshevsky O, Krause V, Leibenluft E, Levy DL, Malhotra A, McMahon F, Michaelson J, Potash J, Reitschel J, Schulz T, Malhotra D. De novo copy number variants confer risk for early onset bipolar disorder and schizophrenia. *ICHG/ASHG*, Montreal, Canada. (2011)
- **Vacic V**, Kenny EE, Gusev A, Peter I, Cho G, Atzmon G, Ostrer H, Bressman SB, Ozelius L, Pe'er I. Admixture in Ashkenazi Jewish cohorts and implications for association studies. *ASHG*, Washington, DC. (2010)
- **Vacic V**, McCarthy SE, Yoon S, Malhotra D, Makarov V, Iossifov I, Iakoucheva L, Sebat J. Estimating significance of CNV-pathway associations in schizophrenia. *RECOMB Systems Biology*, Cambridge, MA. (2009)
- Kusenda M, **Vacic V**, Yoon S, Wigler M, Sebat J. The effect of chr16p11.2 microdeletions and microduplications on gene expression in Autism Spectrum Disorders and Schizophrenia. *ASHG*, Honolulu, HI. (2009)
- Bogunovic D, O'Neill D, Belitskaya-Levy I, **Vacic V**, Adams S, Darvishian F, Pavlick A, Zavadil J, Osman I, Bhardwaj N. Use of gene expression profile and mitotic index of metastatic melanoma lesions as an adjunct to TNM staging in predicting patient survival. *ASCO*, Orlando, FL. (2009)
- **Vacic V**, Oldfield CJ, Mohan A, Radivojac P, Cortese MS, Uversky VN, Dunker AK. Analysis of molecular recognition feature complexes. *Biophysical Society Annual Meeting*, Baltimore, MD. (2007)