# Vladimir Vacic

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## WORK EXPERIENCE

**Senior Scientist, Computational Biology**, **23andMe, Inc.**, South San Francisco, CA 2018 - present
**Senior Scientist, Computational Biology**, Mountain View, CA 2015 - 2018

**Manager, Computational Biology, New York Genome Center**, New York, NY 2013 - 2015
**Bioinformatics Scientist** 2012 - 2013

**Intern, Computational Biology, New York Genome Center**, New York, NY 2007
With Daniel Fasulo. Developed data analysis tools as part of the Personalized Healthcare group.

**Research Assistant, Indiana University School of Medicine**, Indianapolis, IN 2004, 2005
Interened in Keith Dunker's group at the Center for Computational Biology and Bioinformatics.

**Java Developer, Divine Inc., Enterprise Portal Division,** Fairfield, CT 2001 - 2002
Contributed to development of the financial portal product.

**Director of Technology, ArtXone Inc.**, Westport, CT 1999 - 2000
Managed all aspects of technology for an Internet start-up.

## EDUCATION AND TRAINING

**Postdoctoral Research Scientist, Columbia University**, New York, NY 2010 - 2012
With Itsik Pe'er. Specialized in genetics of neurological disease and functional genomics.

**Postdoctoral Fellow, Cold Spring Harbor Laboratory**, Cold Spring Harbor, NY 2008 - 2010
With Jonathan Sebat. Specialized in genetics and systems biology of psychiatric diseases.

**Ph.D. Computer Science, University of California, Riverside**, Riverside, CA 2004 - 2008
With Stefano Lonardi. Specialized in computational biology, with a focus on protein bioinformatics.

**M.S. Computer and Information Sciences, Temple University**, Philadelphia, PA 2003 - 2004
Specialized in machine learning and data mining, with a focus on bioinformatics.

**B.S. Computer Science** and **Mathematics, University of Bridgeport,** Bridgeport, CT 1998 - 2002
Double major, graduated *Summa Cum Laude*.

## CERTIFICATIONS

**New York Academy of Sciences**, New York, NY 2012, 2013

- From Scientist to CSO: A leadership course for scientists in business, academia, government and research institutes.
- From Idea to IPO: The technology venture course.

## SERVICE

- Program committee member for the ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (2015), IEEE International Conference on Application-specific Systems, Architectures and Processors (ASAP) - Bioinformatics Track (2009, 2010, 2012), International Workshop on Data Mining in Bioinformatics - BIOKDD (2011).
- Reviewer for (journals) Algorithms for Molecular Biology, American Journal of Psychiatry, Bioinformatics, BMC Structural Biology, Genome Biology, Journal of Theoretical Biology, Molecular Biology and Evolution, Nucleic Acids Research, Pattern Recognition, PeerJ, PLoS Computational Biology, PLoS One; (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).

**PUBLICATIONS**

38. Frank MO, Koyama T, Rhrissorrakrai K, Robine N, Utro F, Emde AK, Chen BJ, Arora K, Shah M, Geiger H, Felice V, Dikoglu E, Rahman S, Fang A, **Vacic V**, Bergmann EA, Moore Vogel JL, Reeves C, Khaira D, Calabro A, Kim D, Lamendola-Essel MF, Esteves C, Agius P, Stolte C, Boockvar J, Demopoulos A, Placantonakis DG, Golfinos JG, Brennan C, Bruce J, Lassman AB, Canoll P, Grommes C, Daras M, Diamond E, Omuro A, Pentsova E, Orange DE, Harvey SJ, Posner JB, Michelini VV, Jobanputra V, Zody MC, Kelly J, Parida L, Wrzeszczynski KO, Royyuru AK, Darnell RB. (2019) Sequencing and curation strategies for identifying candidate glioblastoma treatments. *BMC Medical Genomics.* Accepted.
37. Jansen PR, Watanabe K, Stringer S, Skene N, Bryois J, Hammerschlag AR, de Leeuw CA, Benjamins J, Muñoz-Manchado AB, Nagel M, Savage JE, Tiemeier H, White T, The 23andMe Research Team, Tung JY, Hinds DA, **Vacic V**, Sullivan PF, van der Sluis S, Polderman TJC, Smit AB, Hjerling-Leffler J, Van Someren EJW, Posthuma D. (2019) Genome-wide analysis of insomnia (N=1,331,010) identifies novel loci and functional pathways. *Nature Genetics*. Accepted.
36. Narzisi G, Corvelo A, Arora K, Bergmann E, Shah M, Musunuri R, Emde AK, Robine N, **Vacic V**, Zody MC. (2018) Genome-wide somatic variant calling using localized colored de Bruijn graphs. *Communications Biology*. 1:20.
35. Fejzo MS, Sazonova OV, Sathirapongsasuti JF, Hallgrímsdóttir IB, 23andMe Research Team, **Vacic V**, MacGibbon KW, Schoenberg FP, Mancuso N, Slamon DJ, Mullin PM. (2018) Placenta and appetite genes GDF15 and IGFBP7 are associated with hyperemesis gravidarum. *Nature Communications.* 9(1):1178.
34. Wrzeszczynski KO, Frank MO, Koyama T, Rhrissorrakrai K, Robine N, Utro F, Emde AK, Chen BJ, Arora K, Shah M, **Vacic V**, Norel R, Bilal E, Bergmann EA, Moore Vogel JL, Bruce J, Lassman A, Canoll P, Grommes C, Harvey S, Parida L, Michelini VV, Zody MC, Jobanputra V, Royyuru AK, Darnell RB. (2017) Comparing sequencing assays and human-machine analyses in actionable genomics for glioblastoma. *Neurology: Genetics*. 3(4):e164.
33. Fang H, Bergmann EA, Arora K, **Vacic V**, Zody MC, Iossifov I, O'Rawe JA, Wu Y, Jimenez Barron LT, Rosenbaum J, Ronemus M, Lee Y, Wang Z, Dikoglu E, Jobanputra V, Lyon GJ, Wigler M, Schatz MC, Narzisi G. (2016) Indel variant analysis of short-read sequencing data with Scalpel. *Nature Protocols*. 11(12):2529-2548.
32. Bagrodia A, Lee BH, Lee W, Cha EK, Sfakianos JP, Iyer G, Pietzak EJ, Gao SP, Zabor EC, Ostrovnaya I, Kaffenberger SD, Syed A, Arcila ME, Chaganti RS, Kundra R, Eng J, Hreiki J, **Vacic V**, Arora K, Oschwald DM, Berger MF, Bajorin DF, Bains MS, Schultz N, Reuter VE, Sheinfeld J, Bosl GJ, Al-Ahmadie AH, Solit DB, Feldman DR. Genetic determinants of cisplatin-resistance in patients with advanced germ cell tumors. *Journal of Clinical Oncology*. 34(33):4000-4007.
31. Bergmann EA, Chen BJ, Arora K, **Vacic V**, Zody MC. (2016) Conpair: concordance and contamination estimator for matched tumor – normal pairs. *Bioinformatics*. 32(20):3196-3198.
30. Freudenberg-Hua Y, Li W, Abhyankar AV, **Vacic V**, Cortes V, Ben-Avraham D, Koppel J, Greenwald B, Germer S, T2D-GENES Consortium, Darnell RB, Barzilai N, Freudenberg J, Atzmon G, Davies P. (2016) Differential burden of rare protein truncating variants in Alzheimer's disease patients compared to centenarians. *Human Molecular Genetics*. 25(14):3096-3105.
29. Hatlen MA, Arora K, **Vacic V**, Grabowska EA, Liao W, Riley-Gillis B, Oschwald DM, Wang L, Joergens JE, Shih AH, Rapaport F, Gu S, Voza F, Asai T, Neel BG, Kharas MG, Gonen M, Levine RL, Nimer SD. (2016) Integrative genetic analysis of mouse and human AML identifies cooperating disease alleles. *The Journal of Experimental Medicine*. 213(1):25-34.

28. Kusenda M, **Vacic V**, Malhotra D, Rodgers L, Pavon K, Meth J, Kumar RA, Christian SL, Peeters H, Cho SS, Addington A, Rapoport JL, Sebat J. (2015) The influence of microdeletions and microduplications of 16p11.2 on global transcription profiles. *Journal of Child Neurology*. 30(14):1947-53.
27. Goes FS, McGrath J, Avramopolous D, Woylec P, Pirooznia M, Ruczinski I, Nestadt G, Kenny EE, **Vacic V**, Peters I, Lencz T, Darvasi A, Mulle JG, Warren ST, Pulver AE. (2015) Genome-wide association of schizophrenia in the Ashkenazi Jews. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*. 168(8):649-59.
26. Beltran H, Eng K, Mosquera JM, Sigaras A, Romanel A, Rennert H, Kossai M, Paul C, Faltas B, Fontugne J, Park K, Banfelder J, Prandi D, Madhukar N, Zhang T, Padilla J, Greco N, McNary TJ, Herrscher E, Wilkes D, MacDonald TY, Xue H, **Vacic V**, Emde AK, Oschwald D, Tan AY, Collins C, Gleave ME, Wang Y, Chakravarty D, Schiffman M, Kim R, Robinson BD, Nanus DM, Tagawa ST, Campagne F, Xiang JZ, Smogorzewska A, Demichelis F, Rickman D, Sboner A, Elemento O, Rubin MA. (2015) Whole-exome sequencing of metastatic cancer and biomarkers of treatment response. *JAMA Oncology*. 1(4):466-474.
25. Freudenberg-Hua Y, Freudenberg J, **Vacic V**, Abhyankar A, Emde AK, Ben-Avraham D, Barzilai N, Oschwald DM, Christen E, Koppel J, Greenwald B, Darnell RB, Germer S, Atzmon G, Davies P. (2014) Disease variants in genomes of 44 centenarians. *Molecular Genetics and Genomic Medicine*. 2(5):438-50.
24. Brannon AR, Vakiani E, Sylvester BE, Scott SN, McDermott G, Shah RN, Kania K, Viale A, Oschwald DM, **Vacic V**, Emde AK, Cercek A, Yaeger R, Kemeny NE, Saltz LB, Shia J, D'Angelica MI, Weiser MR, Solit DB, Berger MF. (2014) Comparative sequencing analysis reveals high genomic concordance between matched primary and metastatic colorectal cancer lesions. *Genome Biology*. 5(8):454.
23. **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, Atzmon G, Burns ER, Ostrer H, Hakonarson H, Bergman A, Barzilai N, Darvasi A, Peter I, Guha S, Lencz T, Giladi N, Marder K, Pe'er I, Bressman SB, Orr-Urtreger A. (2014) Genome-wide mapping of IBD segments in an Ashkenazi PD cohort identifies associated haplotypes. *Human Molecular Genetics*. 3(17):4693-702.
22. Corominas R, Yang X, Lin GN, Kang S, Shen Y, Ghamsari L, Broly M, Rodriguez M, Tam S, Trigg SA, Fan C, Yi S, Tasan M, Lemmens I, Kuang X, Zhao N, Malhotra D, Michaelson JJ, **Vacic V**, Calderwood MA, Roth FP, Tavernier J, Horvath S, Salehi-Ashtiani K, Korkin D, Sebat J, Hill DE, Hao T, Vidal M, Iakoucheva LM. (2014) Protein interaction network of alternatively-spliced isoforms from brain links genetic risk factors for autism. *Nature Communications*. 5:3650.
21. Honeyman JN, Simon EP, Robine N, Chiaroni-Clarke R, Darcy DG, Lim IIP, Gleason CE, Murphy JM, Rosenberg BR, Teegan L, Takacs CN, Botero S, Belote R, Germer S, Emde AK, **Vacic V**, Bhanot U, LaQuaglia MP, Simon SM. (2014) Detection of a recurrent DNAJB1-PRKACA chimeric transcript in fibrolamellar hepatocellular carcinoma. *Science*. 343(6174):1010-4.
20. Carmi S, Palamara PF, **Vacic V**, Lencz T, Darvasi A, Pe'er I. (2013) The variance of identity-by-descent sharing in the Wright-Fisher model. *Genetics*. 193(3):911-28.
19. **Vacic V**, Markwick PRL, Oldfield CJ, Zhao X, Haynes C, Uversky VN, Iakoucheva LM. (2012) Disease-associated mutations disrupt functionally important regions of intrinsic protein disorder. *PLoS Computational Biology*. 8(10):e1002709.
18. **Vacic V**, Iakoucheva LM. (2012) Disease mutations in disordered regions - exception to the rule? *Molecular BioSystems* (themed issue on intrinsically disordered proteins). 8(1):27-32.
17. 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, Nothen MM, Potash JB, Rietschel M, Schulze TG, Sebat J. (2011) High frequencies of de novo CNVs in bipolar disorder and schizophrenia. *Neuron*. 72(6):951-63.
16. **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, and Sebat J. (2011) Duplications of the neuropeptide receptor VIPR2 confer significant risk for schizophrenia. *Nature*. 471(7339):499-503.

15. Radivojac P, **Vacic V**, Haynes C, Cocklin RR, Mohan A, Heyen JW, Goebl MG, and Iakoucheva LM. (2010) Identification, analysis and prediction of protein ubiquitination sites. *Proteins: Structure, Function, and Bioinformatics*. 78(2):365-380.
14. **Vacic V**, Iakoucheva LM, Lonardi S, and Radivojac P. (2010) Graphlet kernels for prediction of functional residues in protein structures. *Journal of Computational Biology.* 17(1):55-72. web site
13. 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. (2009) Immune profile and mitotic index of metastatic melanoma lesions enhance clinical staging in predicting patient survival. *Proceedings of the National Academy of Sciences.* 106(48):20429-34.
12. McCarthy SE, 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, 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, and Sebat J. (2009) Microduplications of 16p11.2 are associated with schizophrenia. *Nature Genetics.* 41:1223-7.
11. Dunker AK, Oldfield CJ, Meng J, Romero P, Yang JY, Chen JW, **Vacic V**, Obradovic Z, and Uversky VN. (2008) The unfoldomics decade: an update on intrinsically disordered proteins. *BMC Genomics*. 9(S2):S1.
10. Jin H, **Vacic V**, Girke T, Lonardi S, and Zhu J-K. (2008) Small RNAs and the regulation of cis-natural antisense transcripts in Arabidopsis. *BMC Molecular Biology*. 9:6.
9. **Vacic V**, Jin H, Zhu J-K, and Lonardi S. (2008) A probabilistic method for small RNA flowgram matching. *Pacific Symposium on Biocomputing, PSB'08*, 13:75-86.
8. Fu Z, Chen X, **Vacic V**, Nan P, Zhong Y, and Jiang T. (2007) MSOAR: a high-throughput ortholog assignment system based on genome rearrangement. *Journal of Computational Biology.* 14(9):1160-75.
7. **Vacic V**, Uversky VN, Dunker AK, and Lonardi S. (2007) Composition Profiler: a tool for discovery and visualization of amino acid composition differences. *BMC Bioinformatics*. 8:211.
6. **Vacic V**, Oldfield CJ, Mohan A, Radivojac P, Cortese MS, Uversky VN, and Dunker AK. (2007) Characterization of molecular recognition features, MoRFs, and their binding partners. *Journal of Proteome Research*. 6(6):2351-66.
5. Sickmeier M, Hamilton JA, LeGall T, **Vacic V**, Cortese MS, Tantos A, Szabo B, Tompa P, Chen J, Uversky VN, Obradovic Z, and Dunker AK. (2007) DisProt: the database of disordered proteins. *Nucleic Acids Research*. 35:D786-93.
4. Mohan A, Oldfield CJ, Radivojac P, **Vacic V**, Cortese MS, Dunker AK, and Uversky VN. (2006) Analysis of molecular recognition features (MoRFs). *Journal of Molecular Biology*, 362(5):1043-59.
3. **Vacic V**, Iakoucheva LM, and Radivojac P. (2006) Two Sample Logo: a graphical representation of the differences between two sets of sequence alignments. *Bioinformatics*, 22(12):1536-7.
2. Fu Z, Chen X, **Vacic V**, Nan P, Zhong Y, and Jiang T. (2006) A parsimony approach to genome-wide ortholog assignment. *ACM Annual Conference on Research in Computational Molecular Biology, RECOMB'06*, Venice, Italy. 2005
1. 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. (2005) Disprot: a database of protein disorder. *Bioinformatics*, 21(1): 137-140. (2005)

**PATENT APPLICATIONS**

- WO 2015048367. Fusion proteins and methods of use thereof. Robine N, Germer S, Emde AK, **Vacic V,** Bloom T, Darnell R.
- WO 2012094681 A1. Compositions and methods for the diagnosis of schizophrenia. **Vacic V,** McCarthy S, Malhotra D, Murray F, Chou HH, Larach-Walters V, Insel PA, Karayiorgou M, DeLisi LE, Sebat J.

**SOFTWARE AND DATABASES**

- Lancet is a microassembly-based somatic SNV and indel caller.
- Conpair is concordance and contamination estimator for tumor and matched normal pairs of DNA samples.
- Graphlet kernel is a graph classification method based on efficient enumeration of small local subgraphs (graphlets).
- UbPred is a sequence-based predictor of protein ubiquitination sites.
- Composition Profiler is a web-based tool that automates detection of enrichment or depletion patterns of individual amino acids or groups of amino acids classified by several physico-chemical and structural properties.
- Two Sample Logo is a procedure for discovery of statistically significant position-specific differences in residue compositions between two multiple sequence alignments.
- DisProt is a curated database of intrinsically disordered proteins.