Vladimir Vacic

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Work Experience

- **Senior Scientist, Computational Biology, 23andMe, Inc.**, Mountain View, CA — 2015 - present
- **Manager, Computational Biology, New York Genome Center**, New York, NY — 2013-2015
  Bioinformatics Scientist — 2012-2013
- **Intern, Siemens Corporate Research**, Princeton, NJ — 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
  Interned 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 the development of the enterprise portal product.
- **Director of Technology, ArtXone Inc.**, Westport, CT — 1999-2000
  Managed all aspects of technology for a small 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 diseases 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 — 2013
  From Scientist to CSO: A leadership course for scientists in business, academia, government and research institutes.
- New York Academy of Sciences, New York, NY — 2012
  From Idea to IPO: The technology venture course.

Service

- Program committee member for the Intelligent Systems for Molecular Biology - ISMB (2016), 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 →

1. 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. (2018) Genome-wide analysis of insomnia (N=1,331,010) identifies novel loci and functional pathways. *bioRxiv preprint*.
2. Narzisi G, Corvelo A, Arora K, Bergmann E, Shah M, Musunuri R, Emde AK, Robine N, **Vacic V**, Zody MC. (2018) Lancet: genome-wide somatic variant calling using localized colored DeBruijn graphs. *Commun Biology*. 1:20.
3. Fejzo MS, Sazonova OV, Sathirapongsasuti JF, Hallgrimsdottir 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. *Nat Commun*. 9(1):1178.
4. 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 J, 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 platforms and human-machine analyses for calling actionable variants in glioblastoma. *Neurol Genet*. 3(4):e164.
5. Fang H, Bergmann EA, Arora K, **Vacic V**, Zody MC, Iossifov I, O'Rowe JA, Wu Y, Jimenez Barron LT, Rosenbaum J, Ronemus M, Lee Y, Wang Z, Dikoglu E, Jobanputra V, Lyon GJ, Schatz MC, Narzisi G. (2016) Indel variant analysis of short-read sequencing data with Scalpel. *Nat Protoc*. 11(12):2529-2548.
6. Bagrodia A, Lee B, Lee W, Cha E, Sfakianos J, Gao SP, Iyer G, Zabor E, Ostrovnaya I, Kaffenberger S, Syed A, Arcila M, Chaganti RS, Kundra R, Eng J, Hreiki J, **Vacic V**, Arora K, Oschwald DM, Seshan V, Shen R, Berger M, Bajorin DF, Bains M, Schultz N, Reuter VE, Sheinfeld J, Bosl G, Al-Ahmadie H, Solit DB, Feldman DR. (2016) Genetic basis for cisplatin-resistance in patients with advanced germ cell tumors. *J Clin Oncol*. 34(33):4000-4007.
7. 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.
8. Freudenberg-Hua Y, Li W, Abhyankar A, **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. *Hum Mol Genet*. 25(14):3096-3105.
9. 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. *J Exp Med*. 213(1):25-34.
10. 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. *J Child Neurol*. 30(14):1947-53.
11. 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. *Am J Med Genet B Neuropsychiatr Genet*. 168(8):649-59.
12. 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 Oncol*. 1(4):466-474.

13. 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. *Mol Genet Genomic Med*. 2(5):438-50.
14. 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 Biol*. 15(8):454.
15. **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. (2014) Genome-wide mapping of identical-by-descent segments in an Ashkenazi Parkinson disease cohort identifies associated haplotypes. *Hum Mol Genet*. 23(17):4693-702.
16. 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. *Nat Commun*. 5:3650.
17. 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.
18. 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 Comput Biol*. 8(10):e1002709.
20. **Vacic V**, Iakoucheva LM. (2012) Disease mutations in disordered regions - exception to the rule? *Mol Biosyst*. 8(1):27-32.
21. 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. (2011) High frequencies of *de novo* CNVs in bipolar disorder and schizophrenia. *Neuron*. 72(6):951-63.
22. **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. (2011) Duplications of the neuropeptide receptor VIPR2 confer significant risk for schizophrenia. *Nature*. 471(7339):499-503.
23. Radivojac P, **Vacic V**, Haynes C, Cocklin RR, Mohan A, Heyen JW, Goebl MG, Iakoucheva LM. (2010) Identification, analysis and prediction of protein ubiquitination sites. *Proteins*, 78(2):365-380.
24. **Vacic V**, Iakoucheva LM, Lonardi S, Radivojac P. (2010) Graphlet kernels for prediction of functional residues in protein structures. *J Comput Biol*. 17(1):55-72.
25. 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. (2009) 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.
26. McCarthy S, Makarov V, Kirov G, Addington A, McClellan J, Yoon S, Perkins D, Dickel DE, Kusenda M, Kras-

toshevsky 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. (2009) Microduplications of 16p11.2 are associated with schizophrenia. *Nat Genet*. 41:1223-7.

27. Dunker AK, Oldfield CJ, Meng J, Romero P, Yang JY, Chen JW, **Vacic V**, Obradovic Z, Uversky VN. (2008) The unfoldomics decade: an update on intrinsically disordered proteins. *BMC Genomics*. 9(S2):S1.
28. Jin H, **Vacic V**, Girke T, Lonardi S, Zhu J-K. (2008) Small RNAs and the regulation of cis-natural antisense transcripts in Arabidopsis. *BMC Mol Biol*. 9:6.
29. **Vacic V**, Jin H, Zhu J-K, Lonardi S. (2008) A probabilistic method for small RNA flowgram matching. *Pac Symp Biocomput*. 13:75-86.
30. Fu Z, Chen X, **Vacic V**, Nan P, Zhong Y, Jiang T. (2007) MSOAR: A high-throughput ortholog assignment system based on genome rearrangement. *J Comput Biol*. 14(9):1160-75.
31. **Vacic V**, Uversky VN, Dunker AK, Lonardi S. (2007) Composition Profiler: a tool for discovery and visualization of amino acid composition differences. *BMC Bioinformatics*. 8:211.
32. **Vacic V**, Oldfield CJ, Mohan A, Radivojac P, Cortese MS, Uversky VN, Dunker AK. (2007) Characterization of molecular recognition features, MoRFs, and their binding partners. *J Proteome Res*. 6(6):2351-66.
33. Sickmeier M, Hamilton J, LeGall T, **Vacic V**, Uversky VN, Cortese MS, Tompa P, Obradovic Z, Dunker AK. (2007) DisProt: the database of disordered proteins. *Nucleic Acids Res*. 35:D786-93.
34. Mohan A, Oldfield CJ, Radivojac P, **Vacic V**, Cortese MS, Dunker AK, Uversky VN. (2006) Analysis of Molecular Recognition Features (MoRFs). *J Mol Biol*. 362(5):1043-59.
35. **Vacic V**, Iakoucheva LM, Radivojac P. (2006) Two Sample Logo: a graphical representation of the differences between two sets of sequence alignments. *Bioinformatics*. 22(12):1536-7.
36. Fu Z, Chen X, **Vacic V**, Nan P, Zhong Y, Jiang T. (2006) A parsimony approach to genome-wide ortholog assignment. *RECOMB'06*. Venice, Italy.
37. Vucetic S, Obradovic Z, **Vacic V**, Radivojac P, Peng K, Iakoucheva LM, Cortese MS, Lawson JD, Brown CJ, Sikes JG, Newton CD, Dunker AK. (2005) DisProt: a database of protein disorder. *Bioinformatics*. 21(1): 137-40.

Patents

- 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.

Affiliations

- International Society for Computational Biology; American Society of Human Genetics.