# Vladimir Vacic

List of Publications by Year
in descending order



| | | | |
|---|---|---|---|
| 47 papers | 10,249 citations | 126858 33 h-index | 233338 45 g-index |
| 49 all docs | 49 docs citations | 49 times ranked | 19062 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Identification of novel risk loci, causal insights, and heritable risk for Parkinson's disease: a meta-analysis of genome-wide association studies. Lancet Neurology, The, 2019, 18, 1091-1102. | 4.9 | 1,414 |
| 2 | DisProt: the Database of Disordered Proteins. Nucleic Acids Research, 2007, 35, D786-D793. | 6.5 | 711 |
| 3 | Analysis of Molecular Recognition Features (MoRFs). Journal of Molecular Biology, 2006, 362, 1043-1059. | 2.0 | 672 |
| 4 | Microduplications of 16p11.2 are associated with schizophrenia. Nature Genetics, 2009, 41, 1223-1227. | 9.4 | 646 |
| 5 | Genome-wide analysis of insomnia in 1,331,010 individuals identifies new risk loci and functional pathways. Nature Genetics, 2019, 51, 394-403. | 9.4 | 593 |
| 6 | Identification, analysis, and prediction of protein ubiquitination sites. Proteins: Structure, Function and Bioinformatics, 2010, 78, 365-380. | 1.5 | 513 |
| 7 | The unfoldomics decade: an update on intrinsically disordered proteins. BMC Genomics, 2008, 9, S1. | 1.2 | 485 |
| 8 | Two Sample Logo: a graphical representation of the differences between two sets of sequence alignments. Bioinformatics, 2006, 22, 1536-1537. | 1.8 | 468 |
| 9 | Characterization of Molecular Recognition Features, MoRFs, and Their Binding Partners. Journal of Proteome Research, 2007, 6, 2351-2366. | 1.8 | 433 |
| 10 | Detection of a Recurrent DNAJB1-PRKACA Chimeric Transcript in Fibrolamellar Hepatocellular Carcinoma. Science, 2014, 343, 1010-1014. | 6.0 | 388 |
| 11 | Composition Profiler: a tool for discovery and visualization of amino acid composition differences. BMC Bioinformatics, 2007, 8, 211. | 1.2 | 350 |
| 12 | Immune profile and mitotic index of metastatic melanoma lesions enhance clinical staging in predicting patient survival. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 20429-20434. | 3.3 | 327 |
| 13 | Duplications of the neuropeptide receptor gene VIPR2 confer significant risk for schizophrenia. Nature, 2011, 471, 499-503. | 13.7 | 296 |
| 14 | Comparative sequencing analysis reveals high genomic concordance between matched primary and metastatic colorectal cancer lesions. Genome Biology, 2014, 15, 454. | 3.8 | 296 |
| 15 | High Frequencies of De Novo CNVs in Bipolar Disorder and Schizophrenia. Neuron, 2011, 72, 951-963. | 3.8 | 290 |
| 16 | Whole-Exome Sequencing of Metastatic Cancer and Biomarkers of Treatment Response. JAMA Oncology, 2015, 1, 466. | 3.4 | 264 |
| 17 | DisProt: a database of protein disorder. Bioinformatics, 2005, 21, 137-140. | 1.8 | 231 |
| 18 | Genomeâ€wide association study of schizophrenia in Ashkenazi Jews. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 649-659. | 1.1 | 203 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Identification of novel risk loci for restless legs syndrome in genome-wide association studies in individuals of European ancestry: a meta-analysis. Lancet Neurology, The, 2017, 16, 898-907. | 4.9 | 191 |
| 20 | A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. Biological Psychiatry, 2018, 83, 1044-1053. | 0.7 | 146 |
| 21 | Protein interaction network of alternatively spliced isoforms from brain links genetic risk factors for autism. Nature Communications, 2014, 5, 3650. | 5.8 | 131 |
| 22 | Disease-Associated Mutations Disrupt Functionally Important Regions of Intrinsic Protein Disorder. PLoS Computational Biology, 2012, 8, e1002709. | 1.5 | 123 |
| 23 | Small RNAs and the regulation of cis-natural antisense transcripts in Arabidopsis. BMC Molecular Biology, 2008, 9, 6. | 3.0 | 120 |
| 24 | Indel variant analysis of short-read sequencing data with Scalpel. Nature Protocols, 2016, 11, 2529-2548. | 5.5 | 99 |
| 25 | Disease mutations in disordered regionsâ€”exception to the rule?. Molecular BioSystems, 2012, 8, 27-32. | 2.9 | 93 |
| 26 | Genome-wide somatic variant calling using localized colored de Bruijn graphs. Communications Biology, 2018, 1, 20. | 2.0 | 85 |
| 27 | Fall risk and gait in Parkinson's disease: The role of the LRRK2 G2019S mutation. Movement Disorders, 2013, 28, 1683-1690. | 2.2 | 82 |
| 28 | Replication and characterization of CADM2 and MSRA genes on human behavior. Heliyon, 2017, 3, e00349. | 1.4 | 80 |
| 29 | Characterization of Prevalence and Health Consequences of Uniparental Disomy in Four Million Individuals from the General Population. American Journal of Human Genetics, 2019, 105, 921-932. | 2.6 | 79 |
| 30 | MSOAR: A High-Throughput Ortholog Assignment System Based on Genome Rearrangement. Journal of Computational Biology, 2007, 14, 1160-1175. | 0.8 | 67 |
| 31 | Disease variants in genomes of 44 centenarians. Molecular Genetics & Genomic Medicine, 2014, 2, 438-450. | 0.6 | 58 |
| 32 | Genome-wide mapping of IBD segments in an Ashkenazi PD cohort identifies associated haplotypes. Human Molecular Genetics, 2014, 23, 4693-4702. | 1.4 | 49 |
| 33 | Graphlet Kernels for Prediction of Functional Residues in Protein Structures. Journal of Computational Biology, 2010, 17, 55-72. | 0.8 | 44 |
| 34 | The Variance of Identity-by-Descent Sharing in the Wrightâ€“Fisher Model. Genetics, 2013, 193, 911-928. | 1.2 | 38 |
| 35 | Genome-wide Study Identifies Association between HLA-Bâˆ—55:01 and Self-Reported Penicillin Allergy. American Journal of Human Genetics, 2020, 107, 612-621. | 2.6 | 34 |
| 36 | Multiethnic GWAS Reveals Polygenic Architecture of Earlobe Attachment. American Journal of Human Genetics, 2017, 101, 913-924. | 2.6 | 29 |

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|---|---|---|---|
| 37 | Integrative genetic analysis of mouse and human AML identifies cooperating disease alleles. Journal of Experimental Medicine, 2016, 213, 25-34. | 4.2 | 25 |
| 38 | Genetic overlap analysis of endometriosis and asthma identifies shared loci implicating sex hormones and thyroid signalling pathways. Human Reproduction, 2022, 37, 366-383. | 0.4 | 19 |
| 39 | Association of Whole-Genome and NETRIN1 Signaling Pathwayâ€"Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. Biological Psychiatry: Cognitive Neuroscience and Neuroimaging, 2019, 4, 91-100. | 1.1 | 16 |
| 40 | The Influence of Microdeletions and Microduplications of 16p11.2 on Global Transcription Profiles. Journal of Child Neurology, 2015, 30, 1947-1953. | 0.7 | 13 |
| 41 | A Parsimony Approach to Genome-Wide Ortholog Assignment. Lecture Notes in Computer Science, 2006, , 578-594. | 1.0 | 11 |
| 42 | Differential burden of rare protein truncating variants in Alzheimerâ€™s disease patients compared to centenarians. Human Molecular Genetics, 2016, 25, ddw150. | 1.4 | 10 |
| 43 | A probabilistic method for small RNA flowgram matching. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2008, , 75-86. | 0.7 | 10 |
| 44 | Sequencing and curation strategies for identifying candidate glioblastoma treatments. BMC Medical Genomics, 2019, 12, 56. | 0.7 | 7 |
| 45 | A PROBABILISTIC METHOD FOR SMALL RNA FLOWGRAM MATCHING. , 2007, , . | | 2 |
| 46 | 65GENOME-WIDE ANALYSIS OF INSOMNIA AND SLEEP-RELATED TRAITS IN OVER 1 MILLION INDIVIDUALS IDENTIFIES NOVEL GENES AND PATHWAYS. European Neuropsychopharmacology, 2019, 29, S1104-S1105. | 0.3 | 0 |
| 47 | Integrative Analysis of the Mutational Landscape of Mouse and Human AML Identifies Functionally Relevant Leukemia Disease Alleles. Blood, 2015, 126, 1247-1247. | 0.6 | 0 |