Damjan Vukcevic

List of Publications by Year
in descending order

39 papers	21,213 citations	394421 19 h-index	414414 32 g-index
45 all docs	45 docs citations	45 times ranked	30466 citing authors

#	Article	IF	Citations
1	Allele imputation for the killer cell immunoglobulin-like receptor KIR3DL1/S1. PLoS Computational Biology, 2022, 18, e1009059.	3.2	5
2	Assertion-Based Approaches to Auditing Complex Elections, with Application toÂParty-List Proportional Elections. Lecture Notes in Computer Science, 2021, , 47-62.	1.3	5
3	Large-Scale Imputation of KIR Copy Number and HLA Alleles in North American and European Psoriasis Case-Control Cohorts Reveals Association of Inhibitory KIR2DL2 With Psoriasis. Frontiers in Immunology, 2021, 12, 684326.	4.8	7
4	Auditing Hamiltonian Elections. Lecture Notes in Computer Science, 2021, , 235-250.	1.3	4
5	Multiâ€output Gaussian processes for species distribution modelling. Methods in Ecology and Evolution, 2020, 11, 1587-1598.	5.2	19
6	Epistatic interactions between killer immunoglobulin-like receptors and human leukocyte antigen ligands are associated with ankylosing spondylitis. PLoS Genetics, 2020, 16, e1008906.	3.5	12
7	A Unified Evaluation of Two-Candidate Ballot-Polling Election Auditing Methods. Lecture Notes in Computer Science, 2020, , 112-128.	1.3	5
8	Random Errors Are Not Necessarily Politically Neutral. Lecture Notes in Computer Science, 2020, , 19-35.	1.3	0
9	Title is missing!. , 2020, 16, e1008906.		0
10	Title is missing!. , 2020, 16, e1008906.		0
11	Title is missing!. , 2020, 16, e1008906.		0
12	Title is missing!. , 2020, 16, e1008906.		0
13	Genome-wide association study of eosinophilic granulomatosis with polyangiitis reveals genomic loci stratified by ANCA status. Nature Communications, 2019, 10, 5120.	12.8	160
14	Insights Into the Health of Defence Simulated Workforce Systems Using Data Farming and Analytics. , 2019, , .		1
15	Temporal clustering of rotational glitches in the Crab pulsar. Monthly Notices of the Royal Astronomical Society, 2019, 482, 3736-3743.	4.4	8
16	The Effect of ACTN3 Gene Doping on Skeletal Muscle Performance. American Journal of Human Genetics, 2018, 102, 845-857.	6.2	17
17	Genetic variation in VAC14 is associated with bacteremia secondary to diverse pathogens in African children. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3601-E3603.	7.1	12
18	The UK Biobank resource with deep phenotyping and genomic data. Nature, 2018, 562, 203-209.	27.8	5,221

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19	Bayesian modelling of lung function data from multiple‐breath washout tests. Statistics in Medicine, 2018, 37, 2016-2033.	1.6	3
20	Bayesian analysis of genetic association across tree-structured routine healthcare data in the UK Biobank. Nature Genetics, 2017, 49, 1311-1318.	21.4	56
21	Lack of transparency in software used to analyze multiple breath washout data. Pediatric Pulmonology, 2016, 51, 1108-1110.	2.0	7
22	Polymorphism in a lincRNA Associates with a Doubled Risk of Pneumococcal Bacteremia in Kenyan Children. American Journal of Human Genetics, 2016, 98, 1092-1100.	6.2	39
23	The influence of sighing respirations on infant lung function measured using multiple breath washout gas mixing techniques. Physiological Reports, 2015, 3, e12347.	1.7	6
24	Imputation of KIR Types from SNP Variation Data. American Journal of Human Genetics, 2015, 97, 593-607.	6.2	73
25	Bayesian Test for Colocalisation between Pairs of Genetic Association Studies Using Summary Statistics. PLoS Genetics, 2014, 10, e1004383.	3.5	2,012
26	The correlation between reading and mathematics ability at age twelve has a substantial genetic component. Nature Communications, 2014, 5, 4204.	12.8	72
27	Common variants in the HLA-DRB1‐HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis. Nature Genetics, 2013, 45, 208-213.	21.4	86
28	Young Writers Competition: GUESTimation: Breaking the deadlock on wedding guest lists. Significance, 2013, 10, 45-48.	0.4	0
29	Bayesian refinement of association signals for 14 loci in 3 common diseases. Nature Genetics, 2012, 44, 1294-1301.	21.4	469
30	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. Nature Genetics, 2012, 44, 1341-1348.	21.4	848
31	Quantifying the Underestimation of Relative Risks from Genome-Wide Association Studies. PLoS Genetics, 2011, 7, e1001337.	3.5	37
32	Disease model distortion in association studies. Genetic Epidemiology, 2011, 35, 278-290.	1.3	26
33	Strong genetic evidence for a selective influence of GABAA receptors on a component of the bipolar disorder phenotype. Molecular Psychiatry, 2010, 15, 146-153.	7.9	111
34	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. Nature, 2010, 464, 713-720.	27.8	737
35	<i>CISH</i> and Susceptibility to Infectious Diseases. New England Journal of Medicine, 2010, 362, 2092-2101.	27.0	129
36	Genetic utility of broadly defined bipolar schizoaffective disorder as a diagnostic concept. British Journal of Psychiatry, 2009, 195, 23-29.	2.8	83

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37	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. Nature Genetics, 2007, 39, 1329-1337.	21.4	1,298
38	Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. Nature, 2007, 447, 661-678.	27.8	8,895
39	Identification and Stoichiometry of Glycosylphosphatidylinositol-anchored Membrane Proteins of the Human Malaria Parasite Plasmodium falciparum. Molecular and Cellular Proteomics, 2006, 5, 1286-1299.	3.8	243