

Dmitri V Zaykin

List of Publications by Year in descending order

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Version: 2024-02-01

69
papers

4,514
citations

185998

28
h-index

128067

60
g-index

75
all docs

75
docs citations

75
times ranked

6881
citing authors

#	ARTICLE	IF	CITATIONS
1	Multi-ethnic GWAS and meta-analysis of sleep quality identify MPP6 as a novel gene that functions in sleep center neurons. <i>Sleep</i> , 2021, 44, .	0.6	5
2	Investigating the impact of caregiver transportation needs on Children's response to behavioral and mental health treatment: A longitudinal analysis. <i>Journal of Transport and Health</i> , 2021, 23, 101262.	1.1	4
3	A functional polymorphism in the ATP-Binding Cassette B1 transporter predicts pharmacologic response to combination of nortriptyline and morphine in neuropathic pain patients. <i>Pain</i> , 2020, 161, 619-629.	2.0	13
4	Quantifying posterior effect size distribution of susceptibility loci by common summary statistics. <i>Genetic Epidemiology</i> , 2020, 44, 339-351.	0.6	0
5	DOT: Gene-set analysis by combining decorrelated association statistics. <i>PLoS Computational Biology</i> , 2020, 16, e1007819.	1.5	7
6	DOT: Gene-set analysis by combining decorrelated association statistics. , 2020, 16, e1007819.		0
7	DOT: Gene-set analysis by combining decorrelated association statistics. , 2020, 16, e1007819.		0
8	DOT: Gene-set analysis by combining decorrelated association statistics. , 2020, 16, e1007819.		0
9	DOT: Gene-set analysis by combining decorrelated association statistics. , 2020, 16, e1007819.		0
10	DOT: Gene-set analysis by combining decorrelated association statistics. , 2020, 16, e1007819.		0
11	DOT: Gene-set analysis by combining decorrelated association statistics. , 2020, 16, e1007819.		0
12	Detecting Weak Signals by Combining Small P-Values in Genetic Association Studies. <i>Frontiers in Genetics</i> , 2019, 10, 1051.	1.1	8
13	Genome-wide association reveals contribution of MRAS to painful temporomandibular disorder in males. <i>Pain</i> , 2019, 160, 579-591.	2.0	37
14	A study in scarlet: MC1R as the main predictor of red hair and exemplar of the flip-flop effect. <i>Human Molecular Genetics</i> , 2019, 28, 2093-2106.	1.4	11
15	The more you test, the more you find: The smallest P -values become increasingly enriched with real findings as more tests are conducted. <i>Genetic Epidemiology</i> , 2017, 41, 726-743.	0.6	3
16	Previous GWAS hits in relation to young-onset breast cancer. <i>Breast Cancer Research and Treatment</i> , 2017, 161, 333-344.	1.1	11
17	Genome-Wide Association Analysis of the Sense of Smell in U.S. Older Adults: Identification of Novel Risk Loci in African-Americans and European-Americans. <i>Molecular Neurobiology</i> , 2017, 54, 8021-8032.	1.9	17
18	Bayesian prediction intervals for assessing P-value variability in prospective replication studies. <i>Translational Psychiatry</i> , 2017, 7, 1271.	2.4	3

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19	[P2 $\hat{\alpha}$ €“109]: CEREBROSPINAL FLUID BIOMARKER SIGNATURE IN ALZHEIMER'S DISEASE GENETIC ASSOCIATION LANDSCAPE BY FUNCTIONAL LINEAR MODELS. <i>Alzheimer's and Dementia</i> , 2017, 13, P648.	0.4	0
20	Epiregulin and EGFR interactions are involved in pain processing. <i>Journal of Clinical Investigation</i> , 2017, 127, 3353-3366.	3.9	85
21	Uncovering Local Trends in Genetic Effects of Multiple Phenotypes via Functional Linear Models. <i>Genetic Epidemiology</i> , 2016, 40, 210-221.	0.6	10
22	A family-based, genome-wide association study of young-onset breast cancer: inherited variants and maternally mediated effects. <i>European Journal of Human Genetics</i> , 2016, 24, 1316-1323.	1.4	11
23	COMT gene locus. <i>Pain</i> , 2015, 156, 2072-2083.	2.0	28
24	Response. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv228.	3.0	1
25	Is Bad Luck the Main Cause of Cancer?. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv125-djv125.	3.0	31
26	The nicotinic $\hat{\alpha}$ 6 subunit gene determines variability in chronic pain sensitivity via cross-inhibition of P2X2/3 receptors. <i>Science Translational Medicine</i> , 2015, 7, 287ra72.	5.8	59
27	Resampling-based multiple comparison procedure with application to point-wise testing with functional data. <i>Environmental and Ecological Statistics</i> , 2015, 22, 45-59.	1.9	9
28	Assessing the Probability that a Finding Is Genuine for Large-Scale Genetic Association Studies. <i>PLoS ONE</i> , 2015, 10, e0124107.	1.1	5
29	Integrative framework for identification of key cell identity genes uncovers determinants of ES cell identity and homeostasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1581-90.	3.3	26
30	Functional Analysis of Variance for Association Studies. <i>PLoS ONE</i> , 2014, 9, e105074.	1.1	24
31	Facial pain with localized and widespread manifestations: Separate pathways of vulnerability. <i>Pain</i> , 2013, 154, 2335-2343.	2.0	31
32	The Ranking Probability Approach and Its Usage in Design and Analysis of Large-Scale Studies. <i>PLoS ONE</i> , 2013, 8, e83079.	1.1	2
33	Genetically determined P2X7 receptor pore formation regulates variability in chronic pain sensitivity. <i>Nature Medicine</i> , 2012, 18, 595-599.	15.2	335
34	Large candidate gene association study reveals genetic risk factors and therapeutic targets for fibromyalgia. <i>Arthritis and Rheumatism</i> , 2012, 64, 584-593.	6.7	78
35	Potential Genetic Risk Factors for Chronic TMD: Genetic Associations from the OPPERA Case Control Study. <i>Journal of Pain</i> , 2011, 12, T92-T101.	0.7	157
36	Optimally weighted Z-test is a powerful method for combining probabilities in meta-analysis. <i>Journal of Evolutionary Biology</i> , 2011, 24, 1836-1841.	0.8	214

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37	Novel Rank-Based Approaches for Discovery and Replication in Genome-Wide Association Studies. <i>Genetics</i> , 2011, 189, 329-340.	1.2	15
38	Using Imputed Genotypes for Relative Risk Estimation in Case-Parent Studies. <i>American Journal of Epidemiology</i> , 2011, 173, 553-559.	1.6	2
39	DOMINE: a comprehensive collection of known and predicted domain-domain interactions. <i>Nucleic Acids Research</i> , 2011, 39, D730-D735.	6.5	167
40	<i>P</i> -value based analysis for shared controls design in genome-wide association studies. <i>Genetic Epidemiology</i> , 2010, 34, 725-738.	0.6	37
41	Pain perception is altered by a nucleotide polymorphism in <i>SCN9A</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 5148-5153.	3.3	279
42	Multiple chronic pain states are associated with a common amino acid-changing allele in <i>KCNS1</i> . <i>Brain</i> , 2010, 133, 2519-2527.	3.7	224
43	Robust Tests in Genome-Wide Scans under Incomplete Linkage Disequilibrium. <i>Statistical Science</i> , 2009, 24, .	1.6	18
44	Expansion of the human μ -opioid receptor gene architecture: novel functional variants. <i>Human Molecular Genetics</i> , 2009, 18, 1037-1051.	1.4	150
45	Haplotype associations with quantitative traits in the presence of complex multilocus and heterogeneous effects. <i>Genetic Epidemiology</i> , 2009, 33, 63-78.	0.6	15
46	Genetic Flip-Flop without an Accompanying Change in Linkage Disequilibrium. <i>American Journal of Human Genetics</i> , 2008, 82, 794-796.	2.6	53
47	Correlation-Based Inference for Linkage Disequilibrium With Multiple Alleles. <i>Genetics</i> , 2008, 180, 533-545.	1.2	65
48	Use of pairwise marker combination and recursive partitioning in a pharmacogenetic genome-wide scan. <i>Pharmacogenomics Journal</i> , 2007, 7, 180-189.	0.9	12
49	Combining <i>p</i> -values in large-scale genomics experiments. <i>Pharmaceutical Statistics</i> , 2007, 6, 217-226.	0.7	69
50	A letter to the editor in reply to "susceptibility to guillain-barre syndrome is associated to polymorphisms of <i>CD1 genes</i> " by Caporale et al. in the <i>J of Neuroimmunology</i> (2006) 177:112-118. <i>Journal of Neuroimmunology</i> , 2007, 186, 201-202.	1.1	6
51	Contrasting Linkage-Disequilibrium Patterns between Cases and Controls as a Novel Association-Mapping Method. <i>American Journal of Human Genetics</i> , 2006, 78, 737-746.	2.6	85
52	Ranks of Genuine Associations in Whole-Genome Scans. <i>Genetics</i> , 2005, 171, 813-823.	1.2	81
53	Large recursive partitioning analysis of complex disease pharmacogenetic studies. II. Statistical considerations. <i>Pharmacogenomics</i> , 2005, 6, 77-89.	0.6	16
54	Effect of Two- and Three-Locus Linkage Disequilibrium on the Power to Detect Marker/Phenotype Associations. <i>Genetics</i> , 2004, 168, 1029-1040.	1.2	60

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55	Interval estimation of genetic susceptibility for retrospective case-control studies. BMC Genetics, 2004, 5, 9.	2.7	7
56	Bounds and normalization of the composite linkage disequilibrium coefficient. Genetic Epidemiology, 2004, 27, 252-257.	0.6	43
57	Selection of Genetic Markers for Association Analyses, Using Linkage Disequilibrium and Haplotypes. American Journal of Human Genetics, 2003, 73, 115-130.	2.6	137
58	Multiple Tests for Genetic Effects in Association Studies. , 2002, 184, 143-168.		58
59	Testing Association of Statistically Inferred Haplotypes with Discrete and Continuous Traits in Samples of Unrelated Individuals. Human Heredity, 2002, 53, 79-91.	0.4	628
60	Truncated product method for combining P-values. Genetic Epidemiology, 2002, 22, 170-185.	0.6	457
61	Effectiveness of computational methods in haplotype prediction. Human Genetics, 2002, 110, 148-156.	1.8	75
62	GAW12: Simulated Genome Scan, Sequence, and Family Data for a Common Disease. Genetic Epidemiology, 2001, 21, S332-S338.	0.6	26
63	Evolution of the Simulated Data Problem. Genetic Epidemiology, 2001, 21, S325-S331.	0.6	4
64	Identifying Susceptibility Genes Using Linkage and Linkage Disequilibrium Analysis in Large Pedigrees. Genetic Epidemiology, 2001, 21, S453-8.	0.6	1
65	Association mapping: where weâ€™ve been, where weâ€™re going. Expert Review of Molecular Diagnostics, 2001, 1, 334-342.	1.5	6
66	Using the False Discovery Rate Approach in the Genetic Dissection of Complex Traits: A Response to Weller et al.. Genetics, 2000, 154, 1917-1918.	1.2	41
67	Novel tests for markerâ€disease association using the collaborative study on the genetics of alcoholism data. Genetic Epidemiology, 1999, 17, S265-70.	0.6	2
68	Exact tests for association between alleles at arbitrary numbers of loci. Genetica, 1995, 96, 169-178.	0.5	190
69	Two Programs to Estimate Significance of χ^2 Values Using Pseudo-Probability Tests. Journal of Heredity, 1993, 84, 152-152.	1.0	254