

Olga A Vsevolozhskaya

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

1,009
citations

623734

14
h-index

454955

30
g-index

44
all docs

44
docs citations

44
times ranked

2133
citing authors

#	ARTICLE	IF	CITATIONS
1	E-Cigarette Demand: Impact of Commodity Definitions and Testâ€“Retest Reliability. <i>Nicotine and Tobacco Research</i> , 2021, 23, 557-565.	2.6	3
2	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, .	1.1	5
3	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.	2.2	4
4	Considering the impact of vaping-associated pulmonary illness reports on e-cigarette harm perceptions and tobacco use patterns. <i>Drug and Alcohol Dependence</i> , 2020, 207, 107797.	3.2	0
5	Inflammatory properties of diet mediate the effect of depressive symptoms on Framingham risk score in men and women: Results from the National Health and Nutrition Examination Survey (2007-2014). <i>Nutrition Research</i> , 2020, 74, 78-86.	2.9	7
6	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.	4.2	13
7	Quantifying posterior effect size distribution of susceptibility loci by common summary statistics. <i>Genetic Epidemiology</i> , 2020, 44, 339-351.	1.3	0
8	DOT: Gene-set analysis by combining decorrelated association statistics. <i>PLoS Computational Biology</i> , 2020, 16, e1007819.	3.2	7
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	DOT: Gene-set analysis by combining decorrelated association statistics. , 2020, 16, e1007819.		0
13	DOT: Gene-set analysis by combining decorrelated association statistics. , 2020, 16, e1007819.		0
14	DOT: Gene-set analysis by combining decorrelated association statistics. , 2020, 16, e1007819.		0
15	Immune System Activation in Perioperative Thrombectomy Patients: Preliminary Retrospective Study. <i>World Neurosurgery</i> , 2019, 128, e966-e969.	1.3	3
16	Early signatures of bleeding and mortality in patients on left ventricular assist device support: novel methods for personalized risk-stratification. <i>Biomarkers</i> , 2019, 24, 448-456.	1.9	3
17	Detecting Weak Signals by Combining Small P-Values in Genetic Association Studies. <i>Frontiers in Genetics</i> , 2019, 10, 1051.	2.3	8
18	Genome-wide association reveals contribution of MRAS to painful temporomandibular disorder in males. <i>Pain</i> , 2019, 160, 579-591.	4.2	37

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19	Coronary artery calcification predicts cardiovascular complications after sepsis. <i>Journal of Critical Care</i> , 2018, 44, 261-266.	2.2	13
20	Ticagrelor Reduces Thromboinflammatory Markers in Patients With Pneumonia. <i>JACC Basic To Translational Science</i> , 2018, 3, 435-449.	4.1	101
21	Dioxin-like PCB 126 increases intestinal inflammation and disrupts gut microbiota and metabolic homeostasis. <i>Environmental Pollution</i> , 2018, 242, 1022-1032.	7.5	101
22	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.	1.3	3
23	Previous GWAS hits in relation to young-onset breast cancer. <i>Breast Cancer Research and Treatment</i> , 2017, 161, 333-344.	2.5	11
24	Estimated probability of becoming a case of drug dependence in relation to duration of drug-taking experience: a functional analysis approach. <i>International Journal of Methods in Psychiatric Research</i> , 2017, 26, e1513.	2.1	9
25	Epiregulin and EGFR interactions are involved in pain processing. <i>Journal of Clinical Investigation</i> , 2017, 127, 3353-3366.	8.2	85
26	Uncovering Local Trends in Genetic Effects of Multiple Phenotypes via Functional Linear Models. <i>Genetic Epidemiology</i> , 2016, 40, 210-221.	1.3	10
27	Inter-relationships Linking Probability of Becoming a Case of Nicotine Dependence With Frequency of Tobacco Cigarette Smoking. <i>Nicotine and Tobacco Research</i> , 2016, 18, 2278-2282.	2.6	0
28	The impact of genetic structure on sequencing analysis. <i>BMC Proceedings</i> , 2016, 10, 171-174.	1.6	1
29	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.	2.8	11
30	Transitioning from First Drug Use to Dependence Onset: Illustration of a Multiparametric Approach for Comparative Epidemiology. <i>Neuropsychopharmacology</i> , 2016, 41, 869-876.	5.4	27
31	The nicotinic $\alpha 6$ subunit gene determines variability in chronic pain sensitivity via cross-inhibition of P2X2/3 receptors. <i>Science Translational Medicine</i> , 2015, 7, 287ra72.	12.4	59
32	Resampling-based multiple comparison procedure with application to point-wise testing with functional data. <i>Environmental and Ecological Statistics</i> , 2015, 22, 45-59.	3.5	9
33	Assessing the Probability that a Finding Is Genuine for Large-Scale Genetic Association Studies. <i>PLoS ONE</i> , 2015, 10, e0124107.	2.5	5
34	Confidence interval estimation in R-DAS. <i>Drug and Alcohol Dependence</i> , 2014, 143, 95-104.	3.2	13
35	Functional Analysis of Variance for Association Studies. <i>PLoS ONE</i> , 2014, 9, e105074.	2.5	24
36	Novel Rank-Based Approaches for Discovery and Replication in Genome-Wide Association Studies. <i>Genetics</i> , 2011, 189, 329-340.	2.9	15

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37	<i>P</i> -value based analysis for shared controls design in genome-wide association studies. <i>Genetic Epidemiology</i> , 2010, 34, 725-738.	1.3	37
38	Correlation-Based Inference for Linkage Disequilibrium With Multiple Alleles. <i>Genetics</i> , 2008, 180, 533-545.	2.9	65
39	Combining <i>p</i> -values in large-scale genomics experiments. <i>Pharmaceutical Statistics</i> , 2007, 6, 217-226.	1.3	69
40	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.	6.2	85
41	Ranks of Genuine Associations in Whole-Genome Scans. <i>Genetics</i> , 2005, 171, 813-823.	2.9	81
42	Bounds and normalization of the composite linkage disequilibrium coefficient. <i>Genetic Epidemiology</i> , 2004, 27, 252-257.	1.3	43
43	Using the False Discovery Rate Approach in the Genetic Dissection of Complex Traits: A Response to Weller et al.. <i>Genetics</i> , 2000, 154, 1917-1918.	2.9	41