Olga A Vsevolozhskaya

List of Publications by Year
in descending order

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	Ticagrelor Reduces ThromboinflammatoryÂMarkersÂin PatientsÂWithÂPneumonia. JACC Basic To Translational Science, 2018, 3, 435-449.	4.1	101
2	Dioxin-like PCB 126 increases intestinal inflammation and disrupts gut microbiota and metabolic homeostasis. Environmental Pollution, 2018, 242, 1022-1032.	7.5	101
3	Contrasting Linkage-Disequilibrium Patterns between Cases and Controls as a Novel Association-Mapping Method. American Journal of Human Genetics, 2006, 78, 737-746.	6.2	85
4	Epiregulin and EGFR interactions are involved in pain processing. Journal of Clinical Investigation, 2017, 127, 3353-3366.	8.2	85
5	Ranks of Genuine Associations in Whole-Genome Scans. Genetics, 2005, 171, 813-823.	2.9	81
6	Combining <i>p</i>â€values in largeâ€scale genomics experiments. Pharmaceutical Statistics, 2007, 6, 217-226.	1.3	69
7	Correlation-Based Inference for Linkage Disequilibrium With Multiple Alleles. Genetics, 2008, 180, 533-545.	2.9	65
8	The nicotinic Î±6 subunit gene determines variability in chronic pain sensitivity via cross-inhibition of P2X2/3 receptors. Science Translational Medicine, 2015, 7, 287ra72.	12.4	59
9	Bounds and normalization of the composite linkage disequilibrium coefficient. Genetic Epidemiology, 2004, 27, 252-257.	1.3	43
10	Using the False Discovery Rate Approach in the Genetic Dissection of Complex Traits: A Response to Weller et al.. Genetics, 2000, 154, 1917-1918.	2.9	41
11	<i>P</i>â€value based analysis for shared controls design in genomeâ€wide association studies. Genetic Epidemiology, 2010, 34, 725-738.	1.3	37
12	Genome-wide association reveals contribution of MRAS to painful temporomandibular disorder in males. Pain, 2019, 160, 579-591.	4.2	37
13	Transitioning from First Drug Use to Dependence Onset: Illustration of a Multiparametric Approach for Comparative Epidemiology. Neuropsychopharmacology, 2016, 41, 869-876.	5.4	27
14	Functional Analysis of Variance for Association Studies. PLoS ONE, 2014, 9, e105074.	2.5	24
15	Novel Rank-Based Approaches for Discovery and Replication in Genome-Wide Association Studies. Genetics, 2011, 189, 329-340.	2.9	15
16	Confidence interval estimation in R-DAS.. Drug and Alcohol Dependence, 2014, 143, 95-104.	3.2	13
17	Coronary artery calcification predicts cardiovascular complications after sepsis. Journal of Critical Care, 2018, 44, 261-266.	2.2	13
18	A functional polymorphism in the ATP-Binding Cassette B1 transporter predicts pharmacologic response to combination of nortriptyline and morphine in neuropathic pain patients. Pain, 2020, 161, 619-629.	4.2	13

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19	A family-based, genome-wide association study of young-onset breast cancer: inherited variants and maternally mediated effects. European Journal of Human Genetics, 2016, 24, 1316-1323.	2.8	11
20	Previous GWAS hits in relation to young-onset breast cancer. Breast Cancer Research and Treatment, 2017, 161, 333-344.	2.5	11
21	Uncovering Local Trends in Genetic Effects of Multiple Phenotypes via Functional Linear Models. Genetic Epidemiology, 2016, 40, 210-221.	1.3	10
22	Resampling-based multiple comparison procedure with application to point-wise testing with functional data. Environmental and Ecological Statistics, 2015, 22, 45-59.	3.5	9
23	Estimated probability of becoming a case of drug dependence in relation to duration of drug-taking experience: a functional analysis approach. International Journal of Methods in Psychiatric Research, 2017, 26, e1513.	2.1	9
24	Detecting Weak Signals by Combining Small P-Values in Genetic Association Studies. Frontiers in Genetics, 2019, 10, 1051.	2.3	8
25	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). Nutrition Research, 2020, 74, 78-86.	2.9	7
26	DOT: Gene-set analysis by combining decorrelated association statistics. PLoS Computational Biology, 2020, 16, e1007819.	3.2	7
27	Multi-ethnic GWAS and meta-analysis of sleep quality identify MPP6 as a novel gene that functions in sleep center neurons. Sleep, 2021, 44, .	1.1	5
28	Assessing the Probability that a Finding Is Genuine for Large-Scale Genetic Association Studies. PLoS ONE, 2015, 10, e0124107.	2.5	5
29	Investigating the impact of caregiver transportation needs on Children's response to behavioral and mental health treatment: A longitudinal analysis. Journal of Transport and Health, 2021, 23, 101262.	2.2	4
30	The more you test, the more you find: The smallest Pâ€values become increasingly enriched with real findings as more tests are conducted. Genetic Epidemiology, 2017, 41, 726-743.	1.3	3
31	Immune System Activation in Perioperative Thrombectomy Patients: Preliminary Retrospective Study. World Neurosurgery, 2019, 128, e966-e969.	1.3	3
32	Early signatures of bleeding and mortality in patients on left ventricular assist device support: novel methods for personalized risk-stratification. Biomarkers, 2019, 24, 448-456.	1.9	3
33	E-Cigarette Demand: Impact of Commodity Definitions and Testâ€"Retest Reliability. Nicotine and Tobacco Research, 2021, 23, 557-565.	2.6	3
34	The impact of genetic structure on sequencing analysis. BMC Proceedings, 2016, 10, 171-174.	1.6	1
35	Inter-relationships Linking Probability of Becoming a Case of Nicotine Dependence With Frequency of Tobacco Cigarette Smoking. Nicotine and Tobacco Research, 2016, 18, 2278-2282.	2.6	0
36	Considering the impact of vaping-associated pulmonary illness reports on e-cigarette harm perceptions and tobacco use patterns. Drug and Alcohol Dependence, 2020, 207, 107797.	3.2	0

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37	Quantifying posterior effect size distribution of susceptibility loci by common summary statistics. Genetic Epidemiology, 2020, 44, 339-351.	1.3	0
38	DOT: Gene-set analysis by combining decorrelated association statistics. , 2020, 16, e1007819.		0
39	DOT: Gene-set analysis by combining decorrelated association statistics. , 2020, 16, e1007819.		0
40	DOT: Gene-set analysis by combining decorrelated association statistics. , 2020, 16, e1007819.		0
41	DOT: Gene-set analysis by combining decorrelated association statistics. , 2020, 16, e1007819.		0
42	DOT: Gene-set analysis by combining decorrelated association statistics. , 2020, 16, e1007819.		0
43	DOT: Gene-set analysis by combining decorrelated association statistics. , 2020, 16, e1007819.		0