

Yakov Tsepilov

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

48
papers

489
citations

11
h-index

21
g-index

66
ext. papers

791
ext. citations

4.3
avg, IF

3.92
L-index

#	Paper	IF	Citations
48	Mendelian randomization of genetically independent aging phenotypes identifies LPA and VCAM1 as biological targets for human aging. <i>Nature Aging</i> , 2022 , 2, 19-30		3
47	In silico genome-wide gene-based association analysis reveals new genes predisposing to coronary artery disease. <i>Clinical Genetics</i> , 2022 , 101, 78-86	4	0
46	Genetic regulation of post-translational modification of two distinct proteins.. <i>Nature Communications</i> , 2022 , 13, 1586	17.4	0
45	A protocol for recruiting and analyzing the disease-oriented Russian disc degeneration study (RuDDS) biobank for functional omics studies of lumbar disc degeneration.. <i>PLoS ONE</i> , 2022 , 17, e0267384	3.7	0
44	Mendelian randomization analysis of plasma levels of CD209 and MICB proteins and the risk of varicose veins of lower extremities.. <i>PLoS ONE</i> , 2022 , 17, e0268725	3.7	
43	sumSTAAR: A flexible framework for gene-based association studies using GWAS summary statistics. <i>PLoS Computational Biology</i> , 2022 , 18, e1010172	5	0
42	Negative heterosis for meiotic recombination rate in spermatocytes of the domestic chicken <i>Gallus gallus</i> . <i>Vavilovskii Zhurnal Genetiki i Seleksii</i> , 2021 , 25, 661-668	0.9	0
41	Sex- and age-specific genetic analysis of chronic back pain. <i>Pain</i> , 2021 , 162, 1176-1187	8	6
40	Multivariate genome-wide analysis of immunoglobulin G N-glycosylation identifies new loci pleiotropic with immune function. <i>Human Molecular Genetics</i> , 2021 , 30, 1259-1270	5.6	0
39	Genome-wide association study identifies locus as associated with chronic widespread musculoskeletal pain. <i>Annals of the Rheumatic Diseases</i> , 2021 , 80, 1227-1235	2.4	4
38	Number of Genes Associated with Neuroticism due to Their Polymorphisms. <i>Russian Journal of Genetics</i> , 2021 , 57, 863-866	0.6	
37	Replication of 15 loci involved in human plasma protein N-glycosylation in 4802 samples from four cohorts. <i>Glycobiology</i> , 2021 , 31, 82-88	5.8	9
36	Nontrivial Replication of Loci Detected by Multi-Trait Methods. <i>Frontiers in Genetics</i> , 2021 , 12, 627989	4.5	0
35	Genome-wide association studies of low back pain and lumbar spinal disorders using electronic health record data identify a locus associated with lumbar spinal stenosis. <i>Pain</i> , 2021 , 162, 2263-2272	8	2
34	Gene-based association analysis identifies 190 genes affecting neuroticism. <i>Scientific Reports</i> , 2021 , 11, 2484	4.9	4
33	Prioritization of causal genes for coronary artery disease based on cumulative evidence from experimental and in silico studies. <i>Scientific Reports</i> , 2020 , 10, 10486	4.9	8
32	Analysis of genetically independent phenotypes identifies shared genetic factors associated with chronic musculoskeletal pain conditions. <i>Communications Biology</i> , 2020 , 3, 329	6.7	12

31	Candidate genes for age at menarche are associated with endometriosis. <i>Reproductive BioMedicine Online</i> , 2020 , 41, 943-956	4	18
30	Glycosylation of immunoglobulin G is regulated by a large network of genes pleiotropic with inflammatory diseases. <i>Science Advances</i> , 2020 , 6, eaax0301	14.3	38
29	The GWAS-MAP platform for aggregation of results of genome-wide association studies and the GWAS-MAP homo database of 70 billion genetic associations of human traits.. <i>Vavilovskii Zhurnal Genetiki i Seleksii</i> , 2020 , 24, 876-884	0.9	1
28	ISSLS Prize in Clinical Science 2020. Examining causal effects of body mass index on back pain: a Mendelian randomization study. <i>European Spine Journal</i> , 2020 , 29, 686-691	2.7	10
27	Identification of 12 genetic loci associated with human healthspan. <i>Communications Biology</i> , 2019 , 2, 41	6.7	49
26	Male Meiotic Recombination in the Steppe Agama, <i>Trapelus sanguinolentus</i> (Agamidae, Iguania, Reptilia). <i>Cytogenetic and Genome Research</i> , 2019 , 157, 107-114	1.9	5
25	Varicose veins of lower extremities: Insights from the first large-scale genetic study. <i>PLoS Genetics</i> , 2019 , 15, e1008110	6	28
24	Defining the genetic control of human blood plasma N-glycome using genome-wide association study. <i>Human Molecular Genetics</i> , 2019 , 28, 2062-2077	5.6	28
23	Recent advances in understanding genetic variants associated with growth, carcass and meat productivity traits in sheep (<i>Ovis aries</i>): an update. <i>Archives Animal Breeding</i> , 2019 , 62, 579-583	1.6	2
22	Interbreed variation in meiotic recombination rate and distribution in the domestic chicken. <i>Archives Animal Breeding</i> , 2019 , 62, 403-411	1.6	1
21	PSX-14 Recent advances in understanding genetic variants associated with growth, carcass and meat productivity traits in sheep (<i>Ovis aries</i>): an update. <i>Journal of Animal Science</i> , 2019 , 97, 461-461	0.7	78
20	Insight into the genetic architecture of back pain and its risk factors from a study of 509,000 individuals. <i>Pain</i> , 2019 , 160, 1361-1373	8	34
19	Polymorphisms of genes involved in inflammation and blood vessel development influence the risk of varicose veins. <i>Clinical Genetics</i> , 2018 , 94, 191-199	4	8
18	Polymorphisms in inflammation-related genes and the risk of primary varicose veins in ethnic Russians. <i>Immunologic Research</i> , 2018 , 66, 141-150	4.3	3
17	Genome-wide association study in ethnic Russians suggests an association of the MHC class III genomic region with the risk of primary varicose veins. <i>Gene</i> , 2018 , 659, 93-99	3.8	8
16	<i>Mycoplasma hyorhinis</i> reduces sensitivity of human lung carcinoma cells to Nutlin-3 and promotes their malignant phenotype. <i>Journal of Cancer Research and Clinical Oncology</i> , 2018 , 144, 1289-1300	4.9	6
15	Associations of polymorphisms in the gene promoters of cytokines and matrix metalloproteinases with bone mineral density in postmenopausal type 2 diabetic women. <i>Diabetes Mellitus</i> , 2018 , 21, 26-33	1.6	1
14	A network-based conditional genetic association analysis of the human metabolome. <i>GigaScience</i> , 2018 , 7,	7.6	7

13	Genome-wide meta-analysis of 158,000 individuals of European ancestry identifies three loci associated with chronic back pain. <i>PLoS Genetics</i> , 2018 , 14, e1007601	6	60
12	Population specific analysis of Yakut exomes. <i>Doklady Biochemistry and Biophysics</i> , 2017 , 474, 213-216	0.8	
11	Apoptosis as the basic mechanism of cytotoxic action of ursolic and pomolic acids in glioma cells. <i>Molecular Biology</i> , 2017 , 51, 705-711	1.2	9
10	Nonadditive Effects of Genes in Human Metabolomics. <i>Genetics</i> , 2015 , 200, 707-18	4	14
9	Development and application of genomic control methods for genome-wide association studies using non-additive models. <i>PLoS ONE</i> , 2013 , 8, e81431	3.7	13
8	Defining the genetic control of human blood plasma N-glycome using genome-wide association study		1
7	Varicose veins of lower extremities: insights from the first large-scale genetic study		1
6	Sequence variation at 8q24.21 and risk of back pain. <i>F1000Research</i> , 9 , 424	3.6	1
5	Analysis of genetically independent phenotypes identifies shared genetic factors associated with chronic musculoskeletal pain at different anatomic sites		2
4	Beyond power: Multivariate discovery, replication, and interpretation of pleiotropic loci using summary association statistics		8
3	Genome-wide association study identifies RNF123 locus as associated with chronic widespread musculoskeletal pain		2
2	Genome-wide Meta-analysis of 158,000 Individuals of European Ancestry Identifies Three Loci Associated with Chronic Back Pain		1
1	Identification of 12 genetic loci associated with human healthspan		3