Yakov Tsepilov

List of Publications by Year
in descending order

48 papers	935 citations	623188 14 h-index
66 all docs	66 docs citations	66 times ranked

552369 26 g-index	1846 citing authors

#	Article	IF	Citations
1	Genome-wide meta-analysis of 158,000 individuals of European ancestry identifies three loci associated with chronic back pain. PLoS Genetics, 2018, 14, e1007601.	1.5	112
2	Glycosylation of immunoglobulin G is regulated by a large network of genes pleiotropic with inflammatory diseases. Science Advances, 2020, 6, eaax0301.	4.7	90
3	Identification of 12 genetic loci associated with human healthspan. Communications Biology, 2019, 2, 41.	2.0	89
4	Insight into the genetic architecture of back pain and its risk factors from a study of 509,000 individuals. Pain, 2019, 160, 1361-1373.	2.0	74
5	Varicose veins of lower extremities: Insights from the first large-scale genetic study. PLoS Genetics, 2019, 15, e1008110.	1.5	48
6	Analysis of genetically independent phenotypes identifies shared genetic factors associated with chronic musculoskeletal pain conditions. Communications Biology, 2020, 3, 329.	2.0	42
7	Defining the genetic control of human blood plasma N-glycome using genome-wide association study. Human Molecular Genetics, 2019, 28, 2062-2077.	1.4	40
8	Candidate genes for age at menarche are associated with endometriosis. Reproductive BioMedicine Online, 2020, 41, 943-956.	1.1	37
9	ISSLS Prize in Clinical Science 2020. Examining causal effects of body mass index on back pain: a Mendelian randomization study. European Spine Journal, 2020, 29, 686-691.	1.0	32
10	Genome-wide association study identifies *RNF123* locus as associated with chronic widespread musculoskeletal pain. Annals of the Rheumatic Diseases, 2021, 80, 1227-1235.	0.5	31
11	Nonadditive Effects of Genes in Human Metabolomics. Genetics, 2015, 200, 707-718.	1.2	24
12	Prioritization of causal genes for coronary artery disease based on cumulative evidence from experimental and in silico studies. Scientific Reports, 2020, 10, 10486.	1.6	22
13	Sex- and age-specific genetic analysis of chronic back pain. Pain, 2021, 162, 1176-1187.	2.0	21
14	Genetic regulation of post-translational modification of two distinct proteins. Nature Communications, 2022, 13, 1586.	5.8	19
15	Genome-wide association study in ethnic Russians suggests an association of the MHC class III genomic region with the risk of primary varicose veins. Gene, 2018, 659, 93-99.	1.0	17
16	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. Pain, 2021, 162, 2263-2272.	2.0	17
17	Mendelian randomization of genetically independent aging phenotypes identifies LPA and VCAM1 as biological targets for human aging. Nature Aging, 2022, 2, 19-30.	5.3	17
18	Polymorphisms of genes involved in inflammation and blood vessel development influence the risk of varicose veins. Clinical Genetics, 2018, 94, 191-199.	1.0	15

#	Article	IF	Citations
19	Replication of 15 loci involved in human plasma protein N-glycosylation in 4802 samples from four cohorts. Glycobiology, 2021, 31, 82-88.	1.3	15
20	Development and Application of Genomic Control Methods for Genome-Wide Association Studies Using Non-Additive Models. PLoS ONE, 2013, 8, e81431.	1.1	14
21	A network-based conditional genetic association analysis of the human metabolome. GigaScience, 2018, 7, .	3.3	13
22	Gene-based association analysis identifies 190 genes affecting neuroticism. Scientific Reports, 2021, 11, 2484.	1.6	12
23	Causal effects of psychosocial factors on chronic back pain: a bidirectional Mendelian randomisation study. European Spine Journal, 2022, 31, 1906-1915.	1.0	12
24	Recent advances in understanding genetic variants associated with growth, carcass and meat productivity traits in sheep (&lt;i&gt;Ovis aries&lt;/i&gt;): an update. Archives Animal Breeding, 2019, 62, 579-583.	0.5	11
25	Investigation of the causal relationships between human IgG N-glycosylation and 12 common diseases associated with changes in the IgG N-glycome. Human Molecular Genetics, 2022, 31, 1545-1559.	1.4	11
26	Apoptosis as the basic mechanism of cytotoxic action of ursolic and pomolic acids in glioma cells. Molecular Biology, 2017, 51, 705-711.	0.4	10
27	Male Meiotic Recombination in the Steppe Agama, Trapelus sanguinolentus (Agamidae, Iguania, Reptilia). Cytogenetic and Genome Research, 2019, 157, 107-114.	0.6	10
28	Multivariate genome-wide analysis of immunoglobulin G N-glycosylation identifies new loci pleiotropic with immune function. Human Molecular Genetics, 2021, 30, 1259-1270.	1.4	8
29	Mycoplasma hyorhinis reduces sensitivity of human lung carcinoma cells to Nutlin-3 and promotes their malignant phenotype. Journal of Cancer Research and Clinical Oncology, 2018, 144, 1289-1300.	1.2	7
30	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. Vavilovskii Zhurnal Genetiki I Selektsii, 2020, 24, 876-884.	0.4	7
31	Polymorphisms in inflammation-related genes and the risk of primary varicose veins in ethnic Russians. Immunologic Research, 2018, 66, 141-150.	1.3	6
32	Multivariate Analysis Identifies Eight Novel Loci Associated with Meat Productivity Traits in Sheep. Genes, 2021, 12, 367.	1.0	6
33	Nontrivial Replication of Loci Detected by Multi-Trait Methods. Frontiers in Genetics, 2021, 12, 627989.	1.1	4
34	Negative heterosis for meiotic recombination rate inÂspermatocytes of the domestic chicken Gallus gallus. Vavilovskii Zhurnal Genetiki I Selektsii, 2021, 25, 661-668.	0.4	3
35	Interbreed variation in meiotic recombination rate and distribution in the domestic chicken &lt;i&gt;Gallus gallus&lt;/i&gt;. Archives Animal Breeding, 2019, 62, 403-411.	0.5	3
36	sumSTAAR: A flexible framework for gene-based association studies using GWAS summary statistics. PLoS Computational Biology, 2022, 18, e1010172.	1.5	3

#	Article	IF	Citations
37	*In silico* genome‐wide gene‐based association analysis reveals new genes predisposing to coronary artery disease. Clinical Genetics, 2022, 101, 78-86.	1.0	2
38	Associations of polymorphisms in the gene promoters of cytokines and matrix metalloproteinases with bone mineral density in postmenopausal type 2 diabetic women. Diabetes Mellitus, 2018, 21, 26-33.	0.5	2
39	Sequence variation at 8q24.21 and risk of back pain. F1000Research, 0, 9, 424.	0.8	1
40	A protocol for recruiting and analyzing the disease-oriented Russian disc degeneration study (RuDDS) biobank for functional omics studies of lumbar disc degeneration. PLoS ONE, 2022, 17, e0267384.	1.1	1
41	Mendelian randomization analysis of plasma levels of CD209 and MICB proteins and the risk of varicose veins of lower extremities. PLoS ONE, 2022, 17, e0268725.	1.1	1
42	The GWAS-MAP|ovis platform for aggregation and analysis of genome-wide association study results in sheep. Vavilovskii Zhurnal Genetiki I Selektsii, 2022, 26, 378-384.	0.4	1
43	Population specific analysis of Yakut exomes. Doklady Biochemistry and Biophysics, 2017, 474, 213-216.	0.3	0
44	Modeling the risk of osteopenia and osteoporosis in postmenopausal women with type 2 diabetes on the sets of clinical and immunogenetic parameters. , 2017, , .		0
45	PSX-14 Recent advances in understanding genetic variants associated with growth, carcass and meat productivity traits in sheep (Ovis aries): an update. Journal of Animal Science, 2019, 97, 461-461.	0.2	0
46	Number of Genes Associated with Neuroticism due to Their Polymorphisms. Russian Journal of Genetics, 2021, 57, 863-866.	0.2	0
47	A study of causal relationships between human IgG N-glycosylation traits and twelve associated diseases. , 2020, , .		0
48	A new method for combining of genetically correlated traits by maximizing of their shared heritability. , 2020, , .		0