Alexander Gusev

List of Publications by Year
in descending order

67 papers	14,500 citations	101543 36 h-index	95266 68 g-index
105 all docs	105 docs citations	105 times ranked	19548 citing authors

#	Article	IF	Citations
1	Association of Cutaneous Immune-Related Adverse Events With Increased Survival in Patients Treated With Antiâ€“Programmed Cell Death 1 and Antiâ€“Programmed Cell Death Ligand 1 Therapy. JAMA Dermatology, 2022, 158, 189.	4.1	60
2	Functional characterisation of the amyotrophic lateral sclerosis risk locus GPX3/TNIP1. Genome Medicine, 2022, 14, 7.	8.2	12
3	Pre-Existing Autoimmune Disease and Mortality in Patients Treated with Anti-PD-1 and Anti-PD-L1 Therapy. Journal of the National Cancer Institute, 2022, 114, 1200-1202.	6.3	9
4	Variation in targetable genomic alterations in non-small cell lung cancer by genetic ancestry, sex, smoking history, and histology. Genome Medicine, 2022, 14, 39.	8.2	22
5	Germline predisposition to pediatric Ewing sarcoma is characterized by inherited pathogenic variants in DNA damage repair genes. American Journal of Human Genetics, 2022, 109, 1026-1037.	6.2	19
6	Cutaneous Toxicities Associated with Immune Checkpoint Inhibitors: An Observational, Pharmacovigilance Study. Journal of Investigative Dermatology, 2022, 142, 2896-2908.e4.	0.7	9
7	Allelic imbalance of chromatin accessibility in cancer identifies candidate causal risk variants and their mechanisms. Nature Genetics, 2022, 54, 837-849.	21.4	11
8	DeCAF: a novel method to identify cell-type specific regulatory variants and their role in cancer risk. Genome Biology, 2022, 23, .	8.8	1
9	Genetic Ancestry Contributes to Somatic Mutations in Lung Cancers from Admixed Latin American Populations. Cancer Discovery, 2021, 11, 591-598.	9.4	69
10	Prediction of severe immune-related adverse events requiring hospital admission in patients on immune checkpoint inhibitors: study of a population level insurance claims database from the USA. , 2021, 9, e001935.		38
11	Trans-ethnic variation in germline variants of patients with renal cell carcinoma. Cell Reports, 2021, 34, 108926.	6.4	16
12	Leveraging expression from multiple tissues using sparse canonical correlation analysis and aggregate tests improves the power of transcriptome-wide association studies. PLoS Genetics, 2021, 17, e1008973.	3.5	35
13	Clinical Inflection Point Detection on the Basis of EHR Data to Identify Clinical Trialâ€“Ready Patients With Cancer. JCO Clinical Cancer Informatics, 2021, 5, 622-630.	2.1	3
14	Gene Fusions Create Partner and Collateral Dependencies Essential to Cancer Cell Survival. Cancer Research, 2021, 81, 3971-3984.	0.9	11
15	CDKN2A Alterations and Response to Immunotherapy in Solid Tumors. Clinical Cancer Research, 2021, 27, 4025-4035.	7.0	51
16	Allele-specific epigenetic activity in prostate cancer and normal prostate tissue implicates prostate cancer risk mechanisms. American Journal of Human Genetics, 2021, 108, 2071-2085.	6.2	3
17	Tumor Mutations Across Racial Groups in a Real-World Data Registry. JCO Precision Oncology, 2021, 5, 1654-1658.	3.0	16
18	Predicting master transcription factors from pan-cancer expression data. Science Advances, 2021, 7, eabf6123.	10.3	30

#	Article	IF	Citations
19	Constructing germline research cohorts from the discarded reads of clinical tumor sequences. Genome Medicine, 2021, 13, 179.	8.2	25
20	Germline Testing Data Validate Inferences of Mutational Status for Variants Detected From Tumor-Only Sequencing. JCO Precision Oncology, 2021, 5, 1749-1757.	3.0	10
21	H3K27ac HiChIP in prostate cell lines identifies risk genes for prostate cancer susceptibility. American Journal of Human Genetics, 2021, 108, 2284-2300.	6.2	31
22	Artificial intelligence-aided clinical annotation of a large multi-cancer genomic dataset. Nature Communications, 2021, 12, 7304.	12.8	17
23	Annotations capturing cell type-specific TF binding explain a large fraction of disease heritability. Human Molecular Genetics, 2020, 29, 1057-1067.	2.9	16
24	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. Nature Genetics, 2020, 52, 790-799.	21.4	174
25	Identity-by-descent detection across 487,409 British samples reveals fine scale population structure and ultra-rare variant associations. Nature Communications, 2020, 11, 6130.	12.8	62
26	Quantifying genetic effects on disease mediated by assayed gene expression levels. Nature Genetics, 2020, 52, 626-633.	21.4	191
27	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	1.3	32
28	Germline Features Associated with Immune Infiltration in Solid Tumors. Cell Reports, 2020, 30, 2900-2908.e4.	6.4	35
29	Allele-Specific QTL Fine Mapping with PLASMA. American Journal of Human Genetics, 2020, 106, 170-187.	6.2	14
30	Non-coding somatic mutations converge on the PAX8 pathway in ovarian cancer. Nature Communications, 2020, 11, 2020.	12.8	52
31	Genome-wide germline correlates of the epigenetic landscape of prostate cancer. Nature Medicine, 2019, 25, 1615-1626.	30.7	45
32	A transcriptome-wide association study of high-grade serous epithelial ovarian cancer identifies new susceptibility genes and splice variants. Nature Genetics, 2019, 51, 815-823.	21.4	89
33	Probabilistic fine-mapping of transcriptome-wide association studies. Nature Genetics, 2019, 51, 675-682.	21.4	275
34	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. Nature Genetics, 2018, 50, 621-629.	21.4	807
35	Transcriptome-wide association study of schizophrenia and chromatin activity yields mechanistic disease insights. Nature Genetics, 2018, 50, 538-548.	21.4	406
36	Large-scale transcriptome-wide association study identifies new prostate cancer risk regions. Nature Communications, 2018, 9, 4079.	12.8	121

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37	Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. Nature Genetics, 2018, 50, 1483-1493.	21.4	55
38	Transcriptomeâ€wide association studies accounting for colocalization using Egger regression. Genetic Epidemiology, 2018, 42, 418-433.	1.3	59
39	Leveraging molecular quantitative trait loci to understand the genetic architecture of diseases and complex traits. Nature Genetics, 2018, 50, 1041-1047.	21.4	154
40	Methods for fine-mapping with chromatin and expression data. PLoS Genetics, 2018, 14, e1007240.	3.5	5
41	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	21.4	184
42	Integrating Gene Expression with Summary Association Statistics to Identify Genes Associated with 30 Complex Traits. American Journal of Human Genetics, 2017, 100, 473-487.	6.2	248
43	Functional Architectures of Local and Distal Regulation of Gene Expression in Multiple Human Tissues. American Journal of Human Genetics, 2017, 100, 605-616.	6.2	76
44	Genetic Mechanisms Leading to Sex Differences Across Common Diseases and Anthropometric Traits. Genetics, 2017, 205, 979-992.	2.9	64
45	Mixed Model Association with Family-Biased Case-Control Ascertainment. American Journal of Human Genetics, 2017, 100, 31-39.	6.2	14
46	Linkage disequilibriumâ€“dependent architecture of human complex traits shows action of negative selection. Nature Genetics, 2017, 49, 1421-1427.	21.4	400
47	A Frameshift in CSF2RB Predominant Among Ashkenazi Jews Increases Risk for Crohn's Disease and Reduces Monocyte Signaling via GM-CSF. Gastroenterology, 2016, 151, 710-723.e2.	1.3	51
48	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979.	12.8	50
49	Deep targeted sequencing of 12 breast cancer susceptibility regions in 4611 women across four different ethnicities. Breast Cancer Research, 2016, 18, 109.	5.0	6
50	Integrative approaches for large-scale transcriptome-wide association studies. Nature Genetics, 2016, 48, 245-252.	21.4	1,618
51	Leveraging local ancestry to detect gene-gene interactions in genome-wide data. BMC Genetics, 2015, 16, 124.	2.7	14
52	Leveraging Distant Relatedness to Quantify Human Mutation and Gene-Conversion Rates. American Journal of Human Genetics, 2015, 97, 775-789.	6.2	77
53	Mixed Model with Correction for Case-Control Ascertainment Increases Association Power. American Journal of Human Genetics, 2015, 96, 720-730.	6.2	60
54	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	6.2	1,098

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55	Partitioning heritability by functional annotation using genome-wide association summary statistics. Nature Genetics, 2015, 47, 1228-1235.	21.4	2,045
56	An atlas of genetic correlations across human diseases and traits. Nature Genetics, 2015, 47, 1236-1241.	21.4	3,145
57	Contrasting genetic architectures of schizophrenia and other complex diseases using fast variance-components analysis. Nature Genetics, 2015, 47, 1385-1392.	21.4	431
58	New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. International Journal of Epidemiology, 2015, 44, 1706-1721.	1.9	53
59	Fast and accurate imputation of summary statistics enhances evidence of functional enrichment. Bioinformatics, 2014, 30, 2906-2914.	4.1	173
60	Leveraging population admixture to characterize the heritability of complex traits. Nature Genetics, 2014, 46, 1356-1362.	21.4	69
61	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	6.2	569
62	Genome-wide mapping of IBD segments in an Ashkenazi PD cohort identifies associated haplotypes. Human Molecular Genetics, 2014, 23, 4693-4702.	2.9	49
63	Quantifying Missing Heritability at Known GWAS Loci. PLoS Genetics, 2013, 9, e1003993.	3.5	115
64	The Architecture of Long-Range Haplotypes Shared within and across Populations. Molecular Biology and Evolution, 2012, 29, 473-486.	8.9	93
65	DASH: A Method for Identical-by-Descent Haplotype Mapping Uncovers Association with Recent Variation. American Journal of Human Genetics, 2011, 88, 706-717.	6.2	77
66	Whole population, genome-wide mapping of hidden relatedness. Genome Research, 2009, 19, 318-326.	5.5	411
67	Highly Scalable Genotype Phasing by Entropy Minimization. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 252-261.	3.0	17