

Alexander Gusev

List of Publications by Year in descending order

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Version: 2024-02-01

67
papers

14,500
citations

116194

36
h-index

107981

68
g-index

105
all docs

105
docs citations

105
times ranked

21700
citing authors

#	ARTICLE	IF	CITATIONS
1	Association of Cutaneous Immune-Related Adverse Events With Increased Survival in Patients Treated With Anti-Programmed Cell Death 1 and Anti-Programmed Cell Death Ligand 1 Therapy. <i>JAMA Dermatology</i> , 2022, 158, 189.	2.0	60
2	Functional characterisation of the amyotrophic lateral sclerosis risk locus GPX3/TNIP1. <i>Genome Medicine</i> , 2022, 14, 7.	3.6	12
3	Pre-Existing Autoimmune Disease and Mortality in Patients Treated with Anti-PD-1 and Anti-PD-L1 Therapy. <i>Journal of the National Cancer Institute</i> , 2022, 114, 1200-1202.	3.0	9
4	Variation in targetable genomic alterations in non-small cell lung cancer by genetic ancestry, sex, smoking history, and histology. <i>Genome Medicine</i> , 2022, 14, 39.	3.6	22
5	Germline predisposition to pediatric Ewing sarcoma is characterized by inherited pathogenic variants in DNA damage repair genes. <i>American Journal of Human Genetics</i> , 2022, 109, 1026-1037.	2.6	19
6	Cutaneous Toxicities Associated with Immune Checkpoint Inhibitors: An Observational, Pharmacovigilance Study. <i>Journal of Investigative Dermatology</i> , 2022, 142, 2896-2908.e4.	0.3	9
7	Allelic imbalance of chromatin accessibility in cancer identifies candidate causal risk variants and their mechanisms. <i>Nature Genetics</i> , 2022, 54, 837-849.	9.4	11
8	DeCAF: a novel method to identify cell-type specific regulatory variants and their role in cancer risk. <i>Genome Biology</i> , 2022, 23, .	3.8	1
9	Genetic Ancestry Contributes to Somatic Mutations in Lung Cancers from Admixed Latin American Populations. <i>Cancer Discovery</i> , 2021, 11, 591-598.	7.7	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. <i>Cell Reports</i> , 2021, 34, 108926.	2.9	16
12	Leveraging expression from multiple tissues using sparse canonical correlation analysis and aggregate tests improves the power of transcriptome-wide association studies. <i>PLoS Genetics</i> , 2021, 17, e1008973.	1.5	35
13	Clinical Inflection Point Detection on the Basis of EHR Data to Identify Clinical Trial-Ready Patients With Cancer. <i>JCO Clinical Cancer Informatics</i> , 2021, 5, 622-630.	1.0	3
14	Gene Fusions Create Partner and Collateral Dependencies Essential to Cancer Cell Survival. <i>Cancer Research</i> , 2021, 81, 3971-3984.	0.4	11
15	<i>CDKN2A</i> Alterations and Response to Immunotherapy in Solid Tumors. <i>Clinical Cancer Research</i> , 2021, 27, 4025-4035.	3.2	51
16	Allele-specific epigenetic activity in prostate cancer and normal prostate tissue implicates prostate cancer risk mechanisms. <i>American Journal of Human Genetics</i> , 2021, 108, 2071-2085.	2.6	3
17	Tumor Mutations Across Racial Groups in a Real-World Data Registry. <i>JCO Precision Oncology</i> , 2021, 5, 1654-1658.	1.5	16
18	Predicting master transcription factors from pan-cancer expression data. <i>Science Advances</i> , 2021, 7, eabf6123.	4.7	30

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19	Constructing germline research cohorts from the discarded reads of clinical tumor sequences. <i>Genome Medicine</i> , 2021, 13, 179.	3.6	25
20	Germline Testing Data Validate Inferences of Mutational Status for Variants Detected From Tumor-Only Sequencing. <i>JCO Precision Oncology</i> , 2021, 5, 1749-1757.	1.5	10
21	H3K27ac HiChIP in prostate cell lines identifies risk genes for prostate cancer susceptibility. <i>American Journal of Human Genetics</i> , 2021, 108, 2284-2300.	2.6	31
22	Artificial intelligence-aided clinical annotation of a large multi-cancer genomic dataset. <i>Nature Communications</i> , 2021, 12, 7304.	5.8	17
23	Annotations capturing cell type-specific TF binding explain a large fraction of disease heritability. <i>Human Molecular Genetics</i> , 2020, 29, 1057-1067.	1.4	16
24	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. <i>Nature Genetics</i> , 2020, 52, 790-799.	9.4	174
25	Identity-by-descent detection across 487,409 British samples reveals fine scale population structure and ultra-rare variant associations. <i>Nature Communications</i> , 2020, 11, 6130.	5.8	62
26	Quantifying genetic effects on disease mediated by assayed gene expression levels. <i>Nature Genetics</i> , 2020, 52, 626-633.	9.4	191
27	Transcriptome-wide association study of breast cancer risk by estrogen receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	0.6	32
28	Germline Features Associated with Immune Infiltration in Solid Tumors. <i>Cell Reports</i> , 2020, 30, 2900-2908.e4.	2.9	35
29	Allele-Specific QTL Fine Mapping with PLASMA. <i>American Journal of Human Genetics</i> , 2020, 106, 170-187.	2.6	14
30	Non-coding somatic mutations converge on the PAX8 pathway in ovarian cancer. <i>Nature Communications</i> , 2020, 11, 2020.	5.8	52
31	Genome-wide germline correlates of the epigenetic landscape of prostate cancer. <i>Nature Medicine</i> , 2019, 25, 1615-1626.	15.2	45
32	A transcriptome-wide association study of high-grade serous epithelial ovarian cancer identifies new susceptibility genes and splice variants. <i>Nature Genetics</i> , 2019, 51, 815-823.	9.4	89
33	Probabilistic fine-mapping of transcriptome-wide association studies. <i>Nature Genetics</i> , 2019, 51, 675-682.	9.4	275
34	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. <i>Nature Genetics</i> , 2018, 50, 621-629.	9.4	807
35	Transcriptome-wide association study of schizophrenia and chromatin activity yields mechanistic disease insights. <i>Nature Genetics</i> , 2018, 50, 538-548.	9.4	406
36	Large-scale transcriptome-wide association study identifies new prostate cancer risk regions. <i>Nature Communications</i> , 2018, 9, 4079.	5.8	121

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37	Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. <i>Nature Genetics</i> , 2018, 50, 1483-1493.	9.4	55
38	Transcriptome-wide association studies accounting for colocalization using Egger regression. <i>Genetic Epidemiology</i> , 2018, 42, 418-433.	0.6	59
39	Leveraging molecular quantitative trait loci to understand the genetic architecture of diseases and complex traits. <i>Nature Genetics</i> , 2018, 50, 1041-1047.	9.4	154
40	Methods for fine-mapping with chromatin and expression data. <i>PLoS Genetics</i> , 2018, 14, e1007240.	1.5	5
41	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. <i>Nature Genetics</i> , 2018, 50, 968-978.	9.4	184
42	Integrating Gene Expression with Summary Association Statistics to Identify Genes Associated with 30 Complex Traits. <i>American Journal of Human Genetics</i> , 2017, 100, 473-487.	2.6	248
43	Functional Architectures of Local and Distal Regulation of Gene Expression in Multiple Human Tissues. <i>American Journal of Human Genetics</i> , 2017, 100, 605-616.	2.6	76
44	Genetic Mechanisms Leading to Sex Differences Across Common Diseases and Anthropometric Traits. <i>Genetics</i> , 2017, 205, 979-992.	1.2	64
45	Mixed Model Association with Family-Biased Case-Control Ascertainment. <i>American Journal of Human Genetics</i> , 2017, 100, 31-39.	2.6	14
46	Linkage disequilibrium-dependent architecture of human complex traits shows action of negative selection. <i>Nature Genetics</i> , 2017, 49, 1421-1427.	9.4	400
47	A Frameshift in CSF2RB Predominant Among Ashkenazi Jews Increases Risk for Crohn's Disease and Reduces Monocyte Signaling via GM-CSF. <i>Gastroenterology</i> , 2016, 151, 710-723.e2.	0.6	51
48	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. <i>Nature Communications</i> , 2016, 7, 10979.	5.8	50
49	Deep targeted sequencing of 12 breast cancer susceptibility regions in 4611 women across four different ethnicities. <i>Breast Cancer Research</i> , 2016, 18, 109.	2.2	6
50	Integrative approaches for large-scale transcriptome-wide association studies. <i>Nature Genetics</i> , 2016, 48, 245-252.	9.4	1,618
51	Leveraging local ancestry to detect gene-gene interactions in genome-wide data. <i>BMC Genetics</i> , 2015, 16, 124.	2.7	14
52	Leveraging Distant Relatedness to Quantify Human Mutation and Gene-Conversion Rates. <i>American Journal of Human Genetics</i> , 2015, 97, 775-789.	2.6	77
53	Mixed Model with Correction for Case-Control Ascertainment Increases Association Power. <i>American Journal of Human Genetics</i> , 2015, 96, 720-730.	2.6	60
54	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , 2015, 97, 576-592.	2.6	1,098

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55	Partitioning heritability by functional annotation using genome-wide association summary statistics. <i>Nature Genetics</i> , 2015, 47, 1228-1235.	9.4	2,045
56	An atlas of genetic correlations across human diseases and traits. <i>Nature Genetics</i> , 2015, 47, 1236-1241.	9.4	3,145
57	Contrasting genetic architectures of schizophrenia and other complex diseases using fast variance-components analysis. <i>Nature Genetics</i> , 2015, 47, 1385-1392.	9.4	431
58	New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. <i>International Journal of Epidemiology</i> , 2015, 44, 1706-1721.	0.9	53
59	Fast and accurate imputation of summary statistics enhances evidence of functional enrichment. <i>Bioinformatics</i> , 2014, 30, 2906-2914.	1.8	173
60	Leveraging population admixture to characterize the heritability of complex traits. <i>Nature Genetics</i> , 2014, 46, 1356-1362.	9.4	69
61	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. <i>American Journal of Human Genetics</i> , 2014, 95, 535-552.	2.6	569
62	Genome-wide mapping of IBD segments in an Ashkenazi PD cohort identifies associated haplotypes. <i>Human Molecular Genetics</i> , 2014, 23, 4693-4702.	1.4	49
63	Quantifying Missing Heritability at Known GWAS Loci. <i>PLoS Genetics</i> , 2013, 9, e1003993.	1.5	115
64	The Architecture of Long-Range Haplotypes Shared within and across Populations. <i>Molecular Biology and Evolution</i> , 2012, 29, 473-486.	3.5	93
65	DASH: A Method for Identical-by-Descent Haplotype Mapping Uncovers Association with Recent Variation. <i>American Journal of Human Genetics</i> , 2011, 88, 706-717.	2.6	77
66	Whole population, genome-wide mapping of hidden relatedness. <i>Genome Research</i> , 2009, 19, 318-326.	2.4	411
67	Highly Scalable Genotype Phasing by Entropy Minimization. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008, 5, 252-261.	1.9	17