

Xingyi Guo

List of Publications by Year in descending order

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Version: 2024-02-01

83
papers

4,474
citations

147801

31
h-index

114465

63
g-index

92
all docs

92
docs citations

92
times ranked

9646
citing authors

#	ARTICLE	IF	CITATIONS
1	An overview of human proteins and genes involved in SARS-CoV-2 infection. <i>Gene</i> , 2022, 808, 145963.	2.2	22
2	Disentangling genetic feature selection and aggregation in transcriptome-wide association studies. <i>Genetics</i> , 2022, 220, .	2.9	21
3	Circular RNA circDVL1 inhibits clear cell renal cell carcinoma progression through the miR-412-3p/PCDH7 axis. <i>International Journal of Biological Sciences</i> , 2022, 18, 1491-1507.	6.4	13
4	Distinct Genomic Landscapes in Early-Onset and Late-Onset Endometrial Cancer. <i>JCO Precision Oncology</i> , 2022, 6, e2100401.	3.0	3
5	The putative oncogenic role of <i>WDTC1</i> in colorectal cancer. <i>Carcinogenesis</i> , 2022, , .	2.8	2
6	Large-scale Integrated Analysis of Genetics and Metabolomic Data Reveals Potential Links Between Lipids and Colorectal Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, 31, 1216-1226.	2.5	3
7	Evaluating breast cancer predisposition genes in women of African ancestry. <i>Genetics in Medicine</i> , 2022, 24, 1468-1475.	2.4	2
8	The mutational landscape of early- and typical-onset oral tongue squamous cell carcinoma. <i>Cancer</i> , 2021, 127, 544-553.	4.1	27
9	Identifying Novel Susceptibility Genes for Colorectal Cancer Risk From a Transcriptome-Wide Association Study of 125,478 Subjects. <i>Gastroenterology</i> , 2021, 160, 1164-1178.e6.	1.3	36
10	Association between lincRNA expression and overall survival for patients with triple-negative breast cancer. <i>Breast Cancer Research and Treatment</i> , 2021, 186, 769-777.	2.5	11
11	Multi-omics analysis to identify susceptibility genes for colorectal cancer. <i>Human Molecular Genetics</i> , 2021, 30, 321-330.	2.9	13
12	Functional Genomic Analyses of the 21q22.3 Locus Identifying Functional Variants and Candidate Gene YBEY for Breast Cancer Risk. <i>Cancers</i> , 2021, 13, 2037.	3.7	2
13	Low Grade Papillary Sinonasal (Schneiderian) Carcinoma: A Series of Five Cases of a Unique Malignant Neoplasm with Comparison to Inverted Papilloma and Conventional Nonkeratinizing Squamous Cell Carcinoma. <i>Head and Neck Pathology</i> , 2021, 15, 1221-1234.	2.6	8
14	Abstract 101: Racial differences in somatic mutations among patients with early-onset colorectal cancer. , 2021, , .		1
15	Regional Differences in Epidemiological and Clinical Characteristics, Treatment, and Clinical Outcomes of COVID-19 in Wuhan and Remote Areas of Hubei Province. <i>Frontiers in Medicine</i> , 2021, 8, 667623.	2.6	3
16	Discovery of structural deletions in breast cancer predisposition genes using whole genome sequencing data from 2000 women of African-ancestry. <i>Human Genetics</i> , 2021, 140, 1449-1457.	3.8	4
17	Genetic variations of DNA bindings of FOXA1 and co-factors in breast cancer susceptibility. <i>Nature Communications</i> , 2021, 12, 5318.	12.8	14
18	Integrating Genome and Methylome Data to Identify Candidate DNA Methylation Biomarkers for Pancreatic Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 2079-2087.	2.5	10

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19	OUP accepted manuscript. Carcinogenesis, 2021, , .	2.8	0
20	Genetically Predicted Levels of DNA Methylation Biomarkers and Breast Cancer Risk: Data From 228â€™951 Women of European Descent. Journal of the National Cancer Institute, 2020, 112, 295-304.	6.3	35
21	Evaluation of associations between genetically predicted circulating protein biomarkers and breast cancer risk. International Journal of Cancer, 2020, 146, 2130-2138.	5.1	13
22	Identification of Novel Loci and New Risk Variant in Known Loci for Colorectal Cancer Risk in East Asians. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 477-486.	2.5	25
23	Discovery of rare coding variants in <i>OGDHL</i> and <i>BRCA2</i> in relation to breast cancer risk in Chinese women. International Journal of Cancer, 2020, 146, 2175-2181.	5.1	8
24	An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. Nature Communications, 2020, 11, 3905.	12.8	28
25	Investigation of the genetic variation in ACE2 on the structural recognition by the novel coronavirus (SARS-CoV-2). Journal of Translational Medicine, 2020, 18, 321.	4.4	39
26	From tobacco smoking to cancerâ€™mutational signature: a mediation analysis strategy to explore the role of epigenetic changes. BMC Cancer, 2020, 20, 880.	2.6	9
27	Identification of novel breast cancer susceptibility loci in meta-analyses conducted among Asian and European descendants. Nature Communications, 2020, 11, 1217.	12.8	46
28	Differences in gene-expression profiles in breast cancer between African and European-ancestry women. Carcinogenesis, 2020, 41, 887-893.	2.8	8
29	Evaluation of pathogenetic mutations in breast cancer predisposition genes in population-based studies conducted among Chinese women. Breast Cancer Research and Treatment, 2020, 181, 465-473.	2.5	16
30	Spectrum of Somatic Cancer Gene Variations Among Adults With Appendiceal Cancer by Age. JAMA Network Open, 2020, 3, e2028644.	5.9	9
31	Associations between Genetically Predicted Blood Protein Biomarkers and Pancreatic Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1501-1508.	2.5	18
32	Transcriptome-Wide Association Study Identifies Susceptibility Loci and Genes for Age at Natural Menopause. Reproductive Sciences, 2019, 26, 496-502.	2.5	13
33	Identifying Putative Susceptibility Genes and Evaluating Their Associations with Somatic Mutations in Human Cancers. American Journal of Human Genetics, 2019, 105, 477-492.	6.2	27
34	Analysis of Over 140,000 European Descendants Identifies Genetically Predicted Blood Protein Biomarkers Associated with Prostate Cancer Risk. Cancer Research, 2019, 79, 4592-4598.	0.9	16
35	HDAC5-mediated deacetylation and nuclear localisation of SOX9 is critical for tamoxifen resistance in breast cancer. British Journal of Cancer, 2019, 121, 1039-1049.	6.4	34
36	Integrative genomic analyses of APOBEC-mutational signature, expression and germline deletion of APOBEC3 genes, and immunogenicity in multiple cancer types. BMC Medical Genomics, 2019, 12, 131.	1.5	47

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37	Calcium: magnesium intake ratio and colorectal carcinogenesis, results from the prostate, lung, colorectal, and ovarian cancer screening trial. <i>British Journal of Cancer</i> , 2019, 121, 796-804.	6.4	19
38	Discovery of a Pathogenic Variant rs139379666 (p. P2974L) in <i>ATM</i> for Breast Cancer Risk in Chinese Populations. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 1308-1315.	2.5	3
39	Identification of Novel Susceptibility Loci and Genes for Prostate Cancer Risk: A Transcriptome-Wide Association Study in Over 140,000 European Descendants. <i>Cancer Research</i> , 2019, 79, 3192-3204.	0.9	43
40	Genetic variant predictors of gene expression provide new insight into risk of colorectal cancer. <i>Human Genetics</i> , 2019, 138, 307-326.	3.8	44
41	Large-Scale Genome-Wide Association Study of East Asians Identifies Loci Associated With Risk for Colorectal Cancer. <i>Gastroenterology</i> , 2019, 156, 1455-1466.	1.3	111
42	De novo assembly and analysis of the <i>Artemisia argyi</i> transcriptome and identification of genes involved in terpenoid biosynthesis. <i>Scientific Reports</i> , 2018, 8, 5824.	3.3	30
43	Use of deep whole-genome sequencing data to identify structure risk variants in breast cancer susceptibility genes. <i>Human Molecular Genetics</i> , 2018, 27, 853-859.	2.9	20
44	A Comprehensive cis-eQTL Analysis Revealed Target Genes in Breast Cancer Susceptibility Loci Identified in Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2018, 102, 890-903.	6.2	72
45	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. <i>Cancer Research</i> , 2018, 78, 5419-5430.	0.9	54
46	Gene expression in triple-negative breast cancer in relation to survival. <i>Breast Cancer Research and Treatment</i> , 2018, 171, 199-207.	2.5	35
47	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.	21.4	184
48	In Utero Exposure to a High-Fat Diet Programs Hepatic Hypermethylation and Gene Dysregulation and Development of Metabolic Syndrome in Male Mice. <i>Endocrinology</i> , 2017, 158, 2860-2872.	2.8	42
49	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. <i>International Journal of Cancer</i> , 2016, 139, 1303-1317.	5.1	51
50	Long-term soy consumption and tumor tissue MicroRNA and gene expression in triple-negative breast cancer. <i>Cancer</i> , 2016, 122, 2544-2551.	4.1	20
51	Long intergenic non-coding RNA expression signature in human breast cancer. <i>Scientific Reports</i> , 2016, 6, 37821.	3.3	26
52	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. <i>Breast Cancer Research</i> , 2016, 18, 64.	5.0	31
53	Prediction of breast cancer risk based on common genetic variants in women of East Asian ancestry. <i>Breast Cancer Research</i> , 2016, 18, 124.	5.0	52
54	A novel patient-derived cell line originated at the time of crizotinib resistance displays a mesenchymal phenotype. <i>Journal of Thoracic Oncology</i> , 2016, 11, S16-S17.	1.1	1

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55	Variant discovery and breakpoint region prediction for studying the human 22q11.2 deletion using BAC clone and whole genome sequencing analysis. <i>Human Molecular Genetics</i> , 2016, 25, 3754-3767.	2.9	20
56	Genome-wide association studies in East Asians identify new loci for waist-hip ratio and waist circumference. <i>Scientific Reports</i> , 2016, 6, 17958.	3.3	58
57	An integrative genomics approach for identifying novel functional consequences of PBRM1 truncated mutations in clear cell renal cell carcinoma (ccRCC). <i>BMC Genomics</i> , 2016, 17, 515.	2.8	24
58	Genome-wide association study in East Asians identifies two novel breast cancer susceptibility loci. <i>Human Molecular Genetics</i> , 2016, 25, 3361-3371.	2.9	40
59	Identification of Susceptibility Loci and Genes for Colorectal Cancer Risk. <i>Gastroenterology</i> , 2016, 150, 1633-1645.	1.3	97
60	Evaluation of potential regulatory function of breast cancer risk locus at 6q25.1. <i>Carcinogenesis</i> , 2016, 37, 163-168.	2.8	16
61	Colony stimulating factor-1 receptor signaling networks inhibit mouse macrophage inflammatory responses by induction of microRNA-21. <i>Blood</i> , 2015, 125, e1-e13.	1.4	120
62	Integrative genomic analysis reveals functional diversification of APOBEC gene family in breast cancer. <i>Human Genomics</i> , 2015, 9, 34.	2.9	32
63	Tumor tissue microRNA expression in association with triple-negative breast cancer outcomes. <i>Breast Cancer Research and Treatment</i> , 2015, 152, 183-191.	2.5	59
64	In-depth genomic data analyses revealed complex transcriptional and epigenetic dysregulations of BRAF V600E in melanoma. <i>Molecular Cancer</i> , 2015, 14, 60.	19.2	30
65	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1680-1691.	2.5	24
66	Snowball: resampling combined with distance-based regression to discover transcriptional consequences of a driver mutation. <i>Bioinformatics</i> , 2015, 31, 84-93.	4.1	5
67	Characterization of Human Pseudogene-Derived Non-Coding RNAs for Functional Potential. <i>PLoS ONE</i> , 2014, 9, e93972.	2.5	51
68	Meta-analysis of genome-wide association studies in East Asian-ancestry populations identifies four new loci for body mass index. <i>Human Molecular Genetics</i> , 2014, 23, 5492-5504.	2.9	192
69	Architectural Niche Organization by LHX2 Is Linked to Hair Follicle Stem Cell Function. <i>Cell Stem Cell</i> , 2013, 13, 314-327.	11.1	84
70	<i>Nfatc1</i> orchestrates aging in hair follicle stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4950-9.	7.1	146
71	A core erythroid transcriptional network is repressed by a master regulator of myelo-lymphoid differentiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3832-3837.	7.1	71
72	Development of Patient-Specific Neurons in Schizophrenia Using Induced Pluripotent Stem Cells. <i>Journal of Neurogenetics</i> , 2011, 25, 88-103.	1.4	121

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73	Genome-wide Maps of Histone Modifications Unwind In Vivo Chromatin States of the Hair Follicle Lineage. <i>Cell Stem Cell</i> , 2011, 9, 219-232.	11.1	187
74	Characterization of the past and current duplication activities in the human 22q11.2 region. <i>BMC Genomics</i> , 2011, 12, 71.	2.8	25
75	A Large Gene Network in Immature Erythroid Cells Is Controlled by the Myeloid and B Cell Transcriptional Regulator PU.1. <i>PLoS Genetics</i> , 2011, 7, e1001392.	3.5	40
76	Î²-Catenin Promoter CHIP-Chip Reveals Potential Schizophrenia and Bipolar Disorder Gene Network. <i>Journal of Neurogenetics</i> , 2010, 24, 182-193.	1.4	29
77	ETV1 is a lineage survival factor that cooperates with KIT in gastrointestinal stromal tumours. <i>Nature</i> , 2010, 467, 849-853.	27.8	279
78	Distinct Factors Control Histone Variant H3.3 Localization at Specific Genomic Regions. <i>Cell</i> , 2010, 140, 678-691.	28.9	1,069
79	Small RNAs Originated from Pseudogenes: cis- or trans-Acting?. <i>PLoS Computational Biology</i> , 2009, 5, e1000449.	3.2	69
80	Molecular evidence for post-domestication selection in the Waxy gene of Chinese waxy maize. <i>Molecular Breeding</i> , 2008, 22, 329-338.	2.1	49
81	Chloroplast DNA insertions into the nuclear genome of rice: the genes, sites and ages of insertion involved. <i>Functional and Integrative Genomics</i> , 2008, 8, 101-108.	3.5	29
82	Evidence of selectively driven codon usage in rice: Implications for GC content evolution of Gramineae genes. <i>FEBS Letters</i> , 2007, 581, 1015-1021.	2.8	42
83	Molecular evolution and selection of a gene encoding two tandem microRNAs in rice. <i>FEBS Letters</i> , 2007, 581, 4789-4793.	2.8	37