

# Yuan Yuan

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9434615/publications.pdf>

Version: 2024-02-01

31  
papers

12,125  
citations

279798

23  
h-index

434195

31  
g-index

33  
all docs

33  
docs citations

33  
times ranked

22625  
citing authors

#	ARTICLE	IF	CITATIONS
1	A study to evaluate the immunogenicity and shedding of live attenuated influenza vaccine strains in children 24–48 months of age. <i>Vaccine</i> , 2020, 38, 1001-1008.	3.8	10
2	Comprehensive molecular characterization of mitochondrial genomes in human cancers. <i>Nature Genetics</i> , 2020, 52, 342-352.	21.4	256
3	Characterization of hypoxia-associated molecular features to aid hypoxia-targeted therapy. <i>Nature Metabolism</i> , 2019, 1, 431-444.	11.9	158
4	Systematic characterization of A-to-I RNA editing hotspots in microRNAs across human cancers. <i>Genome Research</i> , 2017, 27, 1112-1125.	5.5	144
5	Comprehensive Characterization of Molecular Differences in Cancer between Male and Female Patients. <i>Cancer Cell</i> , 2016, 29, 711-722.	16.8	242
6	Ablation of miR-10b Suppresses Oncogene-Induced Mammary Tumorigenesis and Metastasis and Reactivates Tumor-Suppressive Pathways. <i>Cancer Research</i> , 2016, 76, 6424-6435.	0.9	77
7	p53 deficiency linked to B cell translocation gene 2 (BTG2) loss enhances metastatic potential by promoting tumor growth in primary and metastatic sites in patient-derived xenograft (PDX) models of triple-negative breast cancer. <i>Breast Cancer Research</i> , 2016, 18, 13.	5.0	41
8	TANRIC: An Interactive Open Platform to Explore the Function of lncRNAs in Cancer. <i>Cancer Research</i> , 2015, 75, 3728-3737.	0.9	518
9	The Genomic Landscape and Clinical Relevance of A-to-I RNA Editing in Human Cancers. <i>Cancer Cell</i> , 2015, 28, 515-528.	16.8	426
10	Epstein-Barr Virus MicroRNAs are Expressed in Patients with Chronic Lymphocytic Leukemia and Correlate with Overall Survival. <i>EBioMedicine</i> , 2015, 2, 572-582.	6.1	43
11	MAD Bayes for Tumor Heterogeneity—Feature Allocation With Exponential Family Sampling. <i>Journal of the American Statistical Association</i> , 2015, 110, 503-514.	3.1	22
12	BM-SNP: A Bayesian Model for SNP Calling Using High Throughput Sequencing Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 1038-1044.	3.0	3
13	miR-100 Induces Epithelial-Mesenchymal Transition but Suppresses Tumorigenesis, Migration and Invasion. <i>PLoS Genetics</i> , 2014, 10, e1004177.	3.5	110
14	miR-205 acts as a tumour radiosensitizer by targeting ZEB1 and Ubc13. <i>Nature Communications</i> , 2014, 5, 5671.	12.8	148
15	Î±-catenin acts as a tumour suppressor in E-cadherin-negative basal-like breast cancer by inhibiting NF-Î²B signalling. <i>Nature Cell Biology</i> , 2014, 16, 245-254.	10.3	74
16	Gene co-expression network analysis reveals common system-level properties of prognostic genes across cancer types. <i>Nature Communications</i> , 2014, 5, 3231.	12.8	385
17	A community computational challenge to predict the activity of pairs of compounds. <i>Nature Biotechnology</i> , 2014, 32, 1213-1222.	17.5	264
18	ATM-mediated stabilization of ZEB1 promotes DNA damage response and radioresistance through CHK1. <i>Nature Cell Biology</i> , 2014, 16, 864-875.	10.3	367

#	ARTICLE	IF	CITATIONS
19	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. <i>Cell</i> , 2014, 158, 929-944.	28.9	1,242
20	Assessing the clinical utility of cancer genomic and proteomic data across tumor types. <i>Nature Biotechnology</i> , 2014, 32, 644-652.	17.5	257
21	The Pan-Cancer analysis of pseudogene expression reveals biologically and clinically relevant tumour subtypes. <i>Nature Communications</i> , 2014, 5, 3963.	12.8	143
22	A community effort to assess and improve drug sensitivity prediction algorithms. <i>Nature Biotechnology</i> , 2014, 32, 1202-1212.	17.5	653
23	The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , 2013, 45, 1113-1120.	21.4	6,265
24	Enabling transparent and collaborative computational analysis of 12 tumor types within The Cancer Genome Atlas. <i>Nature Genetics</i> , 2013, 45, 1121-1126.	21.4	102
25	Nonparametric Bayesian Bi-Clustering for Next Generation Sequencing Count Data. <i>Bayesian Analysis</i> , 2013, 8, 759-780.	3.0	12
26	A Bayesian graphical model for integrative analysis of TCGA data. , 2012, 2012, 135-138.		9
27	Predicting the lethal phenotype of the knockout mouse by integrating comprehensive genomic data. <i>Bioinformatics</i> , 2012, 28, 1246-1252.	4.1	34
28	A Bayesian model for SNP discovery based on next-generation sequencing data. , 2012, 2012, 42-45.		1
29	BM-Map: an efficient software package for accurately allocating multireads of RNA-sequencing data. <i>BMC Genomics</i> , 2012, 13, S9.	2.8	6
30	Stochastic models for virus and immune system dynamics. <i>Mathematical Biosciences</i> , 2011, 234, 84-94.	1.9	85
31	BM-Map: Bayesian Mapping of Multireads for Next-Generation Sequencing Data. <i>Biometrics</i> , 2011, 67, 1215-1224.	1.4	23