Joshy George

List of Publications by Year in descending order

62 papers	12,265 citations	94381 37 h-index	143943 57 g-index
62 all docs	62 docs citations	62 times ranked	19411 citing authors

#	Article	IF	Citations
1	The Oct4 and Nanog transcription network regulates pluripotency in mouse embryonic stem cells. Nature Genetics, 2006, 38, 431-440.	9.4	2,162
2	Novel Molecular Subtypes of Serous and Endometrioid Ovarian Cancer Linked to Clinical Outcome. Clinical Cancer Research, 2008, 14, 5198-5208.	3.2	1,312
3	Whole–genome characterization of chemoresistant ovarian cancer. Nature, 2015, 521, 489-494.	13.7	1,206
4	From The Cover: An expression signature for p53 status in human breast cancer predicts mutation status, transcriptional effects, and patient survival. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 13550-13555.	3.3	1,109
5	*BRCA* Mutation Frequency and Patterns of Treatment Response in *BRCA* Mutation–Positive Women With Ovarian Cancer: A Report From the Australian Ovarian Cancer Study Group. Journal of Clinical Oncology, 2012, 30, 2654-2663.	0.8	1,018
6	Genetic Reclassification of Histologic Grade Delineates New Clinical Subtypes of Breast Cancer. Cancer Research, 2006, 66, 10292-10301.	0.4	606
7	Jmjd1a and Jmjd2c histone H3 Lys 9 demethylases regulate self-renewal in embryonic stem cells. Genes and Development, 2007, 21, 2545-2557.	2.7	447
8	Single-cell transcriptomes identify human islet cell signatures and reveal cell-type–specific expression changes in type 2 diabetes. Genome Research, 2017, 27, 208-222.	2.4	440
9	Whole-Genome Cartography of Estrogen Receptor α Binding Sites. PLoS Genetics, 2007, 3, e87.	1.5	400
10	Integrated Genome-Wide DNA Copy Number and Expression Analysis Identifies Distinct Mechanisms of Primary Chemoresistance in Ovarian Carcinomas. Clinical Cancer Research, 2009, 15, 1417-1427.	3.2	266
11	IL6-STAT3-HIF Signaling and Therapeutic Response to the Angiogenesis Inhibitor Sunitinib in Ovarian Clear Cell Cancer. Clinical Cancer Research, 2011, 17, 2538-2548.	3.2	217
12	MicroRNA-134 Modulates the Differentiation of Mouse Embryonic Stem Cells, Where It Causes Post-Transcriptional Attenuation of Nanog and LRH1. Stem Cells, 2008, 26, 17-29.	1.4	213
13	Synthetic lethality between *CCNE1* amplification and loss of *BRCA1*. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19489-19494.	3.3	201
14	Host Gene Expression Profiling of Dengue Virus Infection in Cell Lines and Patients. PLoS Neglected Tropical Diseases, 2007, 1, e86.	1.3	196
15	Genome-wide Mapping of RELA(p65) Binding Identifies E2F1 as a Transcriptional Activator Recruited by NF-κB upon TLR4 Activation. Molecular Cell, 2007, 27, 622-635.	4.5	180
16	Deregulation of MYCN, LIN28B and LET7 in a Molecular Subtype of Aggressive High-Grade Serous Ovarian Cancers. PLoS ONE, 2011, 6, e18064.	1.1	172
17	The chromatin accessibility signature of human immune aging stems from CD8+ T cells. Journal of Experimental Medicine, 2017, 214, 3123-3144.	4.2	150
18	Single-cell analysis of human glioma and immune cells identifies S100A4 as an immunotherapy target. Nature Communications, 2022, 13, 767.	5.8	128

#	ARTICLE	IF	CITATIONS
19	IL1 Receptor Antagonist Controls Transcriptional Signature of Inflammation in Patients with Metastatic Breast Cancer. Cancer Research, 2018, 78, 5243-5258.	0.4	119
20	Mutation of ERBB2 Provides a Novel Alternative Mechanism for the Ubiquitous Activation of RAS-MAPK in Ovarian Serous Low Malignant Potential Tumors. Molecular Cancer Research, 2008, 6, 1678-1690.	1.5	108
21	RCP is a human breast cancer–promoting gene with Ras-activating function. Journal of Clinical Investigation, 2009, 119, 2171-83.	3.9	107
22	LRP1B Deletion in High-Grade Serous Ovarian Cancers Is Associated with Acquired Chemotherapy Resistance to Liposomal Doxorubicin. Cancer Research, 2012, 72, 4060-4073.	0.4	100
23	Resistance to CDK2 Inhibitors Is Associated with Selection of Polyploid Cells in <i>CCNE1</i>-Amplified Ovarian Cancer. Clinical Cancer Research, 2013, 19, 5960-5971.	3.2	97
24	Amplicon-Dependent CCNE1 Expression Is Critical for Clonogenic Survival after Cisplatin Treatment and Is Correlated with 20q11 Gain in Ovarian Cancer. PLoS ONE, 2010, 5, e15498.	1.1	92
25	Copy Number Analysis Identifies Novel Interactions Between Genomic Loci in Ovarian Cancer. PLoS ONE, 2010, 5, e11408.	1.1	83
26	Tandem duplication of chromosomal segments is common in ovarian and breast cancer genomes. Journal of Pathology, 2012, 227, 446-455.	2.1	81
27	Efficient molecular subtype classification of high–grade serous ovarian cancer. Journal of Pathology, 2015, 236, 272-277.	2.1	81
28	Homologous Recombination DNA Repair Pathway Disruption and Retinoblastoma Protein Loss Are Associated with Exceptional Survival in High-Grade Serous Ovarian Cancer. Clinical Cancer Research, 2018, 24, 569-580.	3.2	79
29	Nonequivalent Gene Expression and Copy Number Alterations in High-Grade Serous Ovarian Cancers with <i>BRCA1</i> and <i>BRCA2</i> Mutations. Clinical Cancer Research, 2013, 19, 3474-3484.	3.2	76
30	Poison Exon Splicing Regulates a Coordinated Network of SR Protein Expression during Differentiation and Tumorigenesis. Molecular Cell, 2020, 80, 648-665.e9.	4.5	76
31	Targeting myostatin/activin A protects against skeletal muscle and bone loss during spaceflight. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 23942-23951.	3.3	71
32	Differential Functions of Splicing Factors in Mammary Transformation and Breast Cancer Metastasis. Cell Reports, 2019, 29, 2672-2688.e7.	2.9	70
33	CUP-AI-Dx: A tool for inferring cancer tissue of origin and molecular subtype using RNA gene-expression data and artificial intelligence. EBioMedicine, 2020, 61, 103030.	2.7	67
34	A Signature Predicting Poor Prognosis in Gastric and Ovarian Cancer Represents a Coordinated Macrophage and Stromal Response. Clinical Cancer Research, 2014, 20, 2761-2772.	3.2	60
35	<i>EIF1AX</i> and <i>NRAS</i> Mutations Co-occur and Cooperate in Low-Grade Serous Ovarian Carcinomas. Cancer Research, 2017, 77, 4268-4278.	0.4	56
36	Leukaemia cell of origin identified by chromatin landscape of bulk tumour cells. Nature Communications, 2016, 7, 12166.	5.8	47

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37	Expression and function of ABCG2 and XIAP in glioblastomas. Journal of Neuro-Oncology, 2017, 133, 47-57.	1.4	43
38	Development and Validation of the Gene Expression Predictor of High-grade Serous Ovarian Carcinoma Molecular SubTYPE (PrOTYPE). Clinical Cancer Research, 2020, 26, 5411-5423.	3.2	43
39	Comparison of Expression Profiles in Ovarian Epithelium In Vivo and Ovarian Cancer Identifies Novel Candidate Genes Involved in Disease Pathogenesis. PLoS ONE, 2011, 6, e17617.	1.1	36
40	Pericytes Promote Malignant Ovarian Cancer Progression in Mice and Predict Poor Prognosis in Serous Ovarian Cancer Patients. Clinical Cancer Research, 2016, 22, 1813-1824.	3.2	30
41	Comprehensive Molecular Characterization of Adenocarcinoma of the Gastroesophageal Junction Between Esophageal and Gastric Adenocarcinomas. Annals of Surgery, 2022, 275, 706-717.	2.1	30
42	Genomic data analysis workflows for tumors from patient-derived xenografts (PDXs): challenges and guidelines. BMC Medical Genomics, 2019, 12, 92.	0.7	29
43	Enhanced *GAB2* Expression Is Associated with Improved Survival in High-Grade Serous Ovarian Cancer and Sensitivity to PI3K Inhibition. Molecular Cancer Therapeutics, 2015, 14, 1495-1503.	1.9	26
44	Genomewide Expression Analysis in Zebrafish mind bomb Alleles with Pancreas Defects of Different Severity Identifies Putative Notch Responsive Genes. PLoS ONE, 2008, 3, e1479.	1.1	15
45	High-resolution deconstruction of evolution induced by chemotherapy treatments in breast cancer xenografts. Scientific Reports, 2018, 8, 17937.	1.6	15
46	Transcriptional profiling of macrophages in situ in metastatic melanoma reveals localization-dependent phenotypes and function. Cell Reports Medicine, 2022, 3, 100621.	3.3	15
47	multiClust: An R-package for Identifying Biologically Relevant Clusters in Cancer Transcriptome Profiles. Cancer Informatics, 2016, 15, CIN.S38000.	0.9	14
48	Classification of Molecular Subtypes of High-Grade Serous Ovarian Cancer by MALDI-Imaging. Cancers, 2021, 13, 1512.	1.7	14
49	High-throughput visual assessment of sleep stages in mice using machine learning. Sleep, 2022, 45, .	0.6	9
50	A Genomics Approach to Understanding Host Response during Dengue Infection. Novartis Foundation Symposium, 2008, 277, 206-217.	1.2	8
51	Transcriptome Analysis. , 2019, , 792-805.		8
52	A computational method to aid the design and analysis of single cell RNA-seq experiments for cell type identification. BMC Bioinformatics, 2019, 20, 275.	1.2	8
53	3D patient-derived tumor models to recapitulate pediatric brain tumors In Vitro. Translational Oncology, 2022, 20, 101407.	1.7	8
54	Computational inference of a genomic pluripotency signature in human and mouse stem cells. Biology Direct, 2016, 11, 47.	1.9	5

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55	Human KIT+ myeloid cells facilitate visceral metastasis by melanoma. Journal of Experimental Medicine, 2021, 218, .	4.2	5
56	Local versus systemic control of bone and skeletal muscle mass by components of the transforming growth factor-Î² signaling pathway. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	5
57	Supervised learning with word embeddings derived from PubMed captures latent knowledge about protein kinases and cancer. NAR Genomics and Bioinformatics, 2021, 3, lqab113.	1.5	4
58	Cancer Stem Cells, not Bulk Tumor Cells, Determine Mechanisms of Resistance to SMO Inhibitors. Cancer Research Communications, 2022, 2, 402-416.	0.7	2
59	RAD21 cohesin overexpression is a prognostic and predictive marker exacerbating poor prognosis in kras mutant colorectal carcinomas. Pathology, 2015, 47, S53-S54.	0.3	0
60	Leukemia cell-of-origin identified by chromatin landscape of bulk tumor cells. Experimental Hematology, 2016, 44, S104.	0.2	0
61	A computational method to aid in the design and analysis of single cell RNA-seq experiments. , 2017, , .		0
62	Identifying Associations Between Genomic Alterations in Tumors. Methods in Molecular Biology, 2013, 1049, 9-19.	0.4	0