Jason Li

List of Publications by Year in descending order

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70 papers	4,939 citations	94433 37 h-index	95266 68 g-index
72 all docs	72 docs citations	72 times ranked	11884 citing authors

#	Article	IF	Citations
1	CONTRA: copy number analysis for targeted resequencing. Bioinformatics, 2012, 28, 1307-1313.	4.1	308
2	UV-Associated Mutations Underlie the Etiology of MCV-Negative Merkel Cell Carcinomas. Cancer Research, 2015, 75, 5228-5234.	0.9	270
3	BET-Bromodomain Inhibitors Engage the Host Immune System and Regulate Expression of the Immune Checkpoint Ligand PD-L1. Cell Reports, 2017, 18, 2162-2174.	6.4	244
4	Response of BRAF-Mutant Melanoma to BRAF Inhibition Is Mediated by a Network of Transcriptional Regulators of Glycolysis. Cancer Discovery, 2014, 4, 423-433.	9.4	242
5	Sequence artefacts in a prospective series of formalin-fixed tumours tested for mutations in hotspot regions by massively parallel sequencing. BMC Medical Genomics, 2014, 7, 23.	1.5	200
6	Exome Sequencing Identifies Rare Deleterious Mutations in DNA Repair Genes FANCC and BLM as Potential Breast Cancer Susceptibility Alleles. PLoS Genetics, 2012, 8, e1002894.	3.5	186
7	A role for pericytes as microenvironmental regulators of human skin tissue regeneration. Journal of Clinical Investigation, 2009, 119, 2795-806.	8.2	178
8	The Architecture and Evolution of Cancer Neochromosomes. Cancer Cell, 2014, 26, 653-667.	16.8	161
9	Functional and molecular characterisation of EO771.LMB tumours, a new C57BL/6-mouse-derived model of spontaneously metastatic mammary cancer. DMM Disease Models and Mechanisms, 2015, 8, 237-51.	2.4	154
10	Dynamic molecular monitoring reveals that SWIâ€“SNF mutations mediate resistance to ibrutinib plus venetoclax in mantle cell lymphoma. Nature Medicine, 2019, 25, 119-129.	30.7	147
11	Molecular profiling of low grade serous ovarian tumours identifies novel candidate driver genes. Oncotarget, 2015, 6, 37663-37677.	1.8	142
12	Mutational landscape of mucinous ovarian carcinoma and its neoplastic precursors. Genome Medicine, 2015, 7, 87.	8.2	126
13	Whole exome sequencing reveals activating JAK1 and STAT3 mutations in breast implant-associated anaplastic large cell lymphoma anaplastic large cell lymphoma. Haematologica, 2016, 101, e387-e390.	3.5	124
14	BRAF/NRAS Wild-Type Melanomas Have a High Mutation Load Correlating with Histologic and Molecular Signatures of UV Damage. Clinical Cancer Research, 2013, 19, 4589-4598.	7.0	115
15	Patient-derived Xenografts Reveal that Intraductal Carcinoma of the Prostate Is a Prominent Pathology in BRCA2 Mutation Carriers with Prostate Cancer and Correlates with Poor Prognosis. European Urology, 2015, 67, 496-503.	1.9	112
16	The molecular origin and taxonomy of mucinous ovarian carcinoma. Nature Communications, 2019, 10, 3935.	12.8	110
17	Inferring copy number and genotype in tumour exome data. BMC Genomics, 2014, 15, 732.	2.8	102
18	Decreased Prostate Cancer-Specific Survival of Men with BRCA2 Mutations from Multiple Breast Cancer Families. Cancer Prevention Research, 2011, 4, 1002-1010.	1.5	100

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19	Massivelyâ€parallel sequencing assists the diagnosis and guided treatment of cancers of unknown primary. Journal of Pathology, 2013, 231, 413-423.	4.5	94
20	Reducing Sequence Artifacts in Amplicon-Based Massively Parallel Sequencing of Formalin-Fixed Paraffin-Embedded DNA by Enzymatic Depletion of Uracil-Containing Templates. Clinical Chemistry, 2013, 59, 1376-1383.	3.2	94
21	Splice site identification using probabilistic parameters and SVM classification. BMC Bioinformatics, 2006, 7, S15.	2.6	93
22	Loss of heterozygosity: what is it good for?. BMC Medical Genomics, 2015, 8, 45.	1.5	85
23	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.	7.0	79
24	Identification of Pik3ca Mutation as a Genetic Driver of Prostate Cancer That Cooperates with Pten Loss to Accelerate Progression and Castration-Resistant Growth. Cancer Discovery, 2018, 8, 764-779.	9.4	72
25	CoNVEX: copy number variation estimation in exome sequencing data using HMM. BMC Bioinformatics, 2013, 14, S2.	2.6	61
26	The genomic landscape of phaeochromocytoma. Journal of Pathology, 2015, 236, 78-89.	4.5	61
27	Functional Characterization of Quiescent Keratinocyte Stem Cells and Their Progeny Reveals a Hierarchical Organization in Human Skin Epidermis. Stem Cells, 2011, 29, 1256-1268.	3.2	59
28	Are there any more ovarian tumor suppressor genes? A new perspective using ultra highâ€resolution copy number and loss of heterozygosity analysis. Genes Chromosomes and Cancer, 2009, 48, 931-942.	2.8	56
29	EIF1AX and NRAS Mutations Co-occur and Cooperate in Low-Grade Serous Ovarian Carcinomas. Cancer Research, 2017, 77, 4268-4278.	0.9	56
30	Circulating Tumor DNA Analysis and Functional Imaging Provide Complementary Approaches for Comprehensive Disease Monitoring in Metastatic Melanoma. JCO Precision Oncology, 2017, 1, 1-14.	3.0	51
31	Therapeutic options for mucinous ovarian carcinoma. Gynecologic Oncology, 2020, 156, 552-560.	1.4	49
32	Alternative Transcript Initiation and Splicing as a Response to DNA Damage. PLoS ONE, 2011, 6, e25758.	2.5	45
33	TERT structural rearrangements in metastatic pheochromocytomas. Endocrine-Related Cancer, 2018, 25, 1-9.	3.1	45
34	Targeted-capture massively-parallel sequencing enables robust detection of clinically informative mutations from formalin-fixed tumours. Scientific Reports, 2013, 3, 3494.	3.3	44
35	Bcor loss perturbs myeloid differentiation and promotes leukaemogenesis. Nature Communications, 2019, 10, 1347.	12.8	41
36	Whole exome sequencing identifies a recurrentRQCD1P131L mutation in cutaneous melanoma. Oncotarget, 2015, 6, 1115-1127.	1.8	40

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37	Intraductal carcinoma of the prostate can evade androgen deprivation, with emergence of castrateâ€tolerant cells. BJU International, 2018, 121, 971-978.	2.5	39
38	Genome-wide functional analysis reveals central signaling regulators of lymphatic endothelial cell migration and remodeling. Science Signaling, 2017, 10, .	3.6	37
39	Prevalence of PALB2 mutations in Australian familial breast cancer cases and controls. Breast Cancer Research, 2015, 17, 111.	5.0	36
40	Survival Following Chemotherapy in Ovarian Clear Cell Carcinoma Is Not Associated with Pathological Misclassification of Tumor Histotype. Clinical Cancer Research, 2019, 25, 3962-3973.	7.0	36
41	Identification of a radiation sensitivity gene expression profile in primary fibroblasts derived from patients who developed radiotherapy-induced fibrosis. Radiotherapy and Oncology, 2014, 111, 186-193.	0.6	34
42	Genomic characterisation of EÎ¼-Myc mouse lymphomas identifies Bcor as a Myc co-operative tumour-suppressor gene. Nature Communications, 2017, 8, 14581.	12.8	33
43	Genome-Wide Transcription Responses to Synchrotron Microbeam Radiotherapy. Radiation Research, 2012, 178, 249.	1.5	31
44	DNA Repair Genes: Alternative Transcription and Gene Expression at the Exon Level in Response to the DNA Damaging Agent, Ionizing Radiation. PLoS ONE, 2012, 7, e53358.	2.5	30
45	Next-Generation Sequence Analysis of Cancer Xenograft Models. PLoS ONE, 2013, 8, e74432.	2.5	30
46	Pericytes Promote Malignant Ovarian Cancer Progression in Mice and Predict Poor Prognosis in Serous Ovarian Cancer Patients. Clinical Cancer Research, 2016, 22, 1813-1824.	7.0	30
47	Id2 and E Proteins Orchestrate the Initiation and Maintenance of MLL-Rearranged Acute Myeloid Leukemia. Cancer Cell, 2016, 30, 59-74.	16.8	29
48	Reevaluation of the BRCA2 truncating allele c.9976Aâ€‰>â€‰T (p.Lys3326Ter) in a familial breast cancer context. Scientific Reports, 2015, 5, 14800.	3.3	26
49	A pharmacogenomic approach validates AG-221 as an effective and on-target therapy in IDH2 mutant AML. Leukemia, 2017, 31, 1466-1470.	7.2	25
50	PathOS: a decision support system for reporting high throughput sequencing of cancers in clinical diagnostic laboratories. Genome Medicine, 2017, 9, 38.	8.2	25
51	HDAC Inhibitor Panobinostat Engages Host Innate Immune Defenses to Promote the Tumoricidal Effects of Trastuzumab in HER2+ Tumors. Cancer Research, 2017, 77, 2594-2606.	0.9	23
52	Foxp3 Expression in Macrophages Associated with RENCA Tumors in Mice. PLoS ONE, 2014, 9, e108670.	2.5	23
53	Mutational profiling of familial male breast cancers reveals similarities with luminal A female breast cancer with rare TP53 mutations. British Journal of Cancer, 2014, 111, 2351-2360.	6.4	22
54	Long term, continuous exposure to panobinostat induces terminal differentiation and long term survival in the THâ€MYCN neuroblastoma mouse model. International Journal of Cancer, 2016, 139, 194-204.	5.1	22

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55	Evaluating the breast cancer predisposition role of rare variants in genes associated with low-penetrance breast cancer risk SNPs. Breast Cancer Research, 2018, 20, 3.	5.0	19
56	Mutations in RECQL are not associated with breast cancer risk in an Australian population. Nature Genetics, 2018, 50, 1346-1348.	21.4	19
57	Bioinformatics Pipelines for Targeted Resequencing and Whole-Exome Sequencing of Human and Mouse Genomes: A Virtual Appliance Approach for Instant Deployment. PLoS ONE, 2014, 9, e95217.	2.5	17
58	CNspector: a web-based tool for visualisation and clinical diagnosis of copy number variation from next generation sequencing. Scientific Reports, 2019, 9, 6426.	3.3	17
59	Integrated mutation, copy number and expression profiling in resectable non-small cell lung cancer. BMC Cancer, 2011, 11, 93.	2.6	16
60	Assessment of DNA methylation profiling and copy number variation as indications of clonal relationship in ipsilateral and contralateral breast cancers to distinguish recurrent breast cancer from a second primary tumour. BMC Cancer, 2015, 15, 669.	2.6	14
61	Studying Cancer Genomics Through Next-Generation DNA Sequencing and Bioinformatics. Methods in Molecular Biology, 2014, 1168, 83-98.	0.9	12
62	Deciphering clonality in aneuploid breast tumors using SNP array and sequencing data. Genome Biology, 2014, 15, 470.	8.8	11
63	Gene function prediction based on genomic context clustering and discriminative learning: an application to bacteriophages. BMC Bioinformatics, 2007, 8, S6.	2.6	10
64	Genome classification by gene distribution: An overlapping subspace clustering approach. BMC Evolutionary Biology, 2008, 8, 116.	3.2	10
65	Altered significance of <scp>D</scp>'<scp>A</scp>mico risk classification in patients with prostate cancer linked to a familial breast cancer (k<scp>C</scp>on<scp>F</scp>ab) cohort. BJU International, 2015, 116, 207-212.	2.5	7
66	Polynomial kernel adaptation and extensions to the SVM classifier learning. Neural Computing and Applications, 2007, 17, 19-25.	5.6	5
67	Cooperation of the BTB-Zinc finger protein, Abrupt, with cytoskeletal regulators inDrosophilaepithelial tumorigenesis. Biology Open, 2015, 4, 1024-1039.	1.2	5
68	Searching for candidate genes in familial BRCAX mutation carriers with prostate cancer. Urologic Oncology: Seminars and Original Investigations, 2016, 34, 120.e9-120.e16.	1.6	4
69	TRACEBACK: Testing of Historical Tubo-Ovarian Cancer Patients for Hereditary Risk Genes as a Cancer Prevention Strategy in Family Members. Journal of Clinical Oncology, 2022, , JCO2102108.	1.6	3
70	Improving Training Speed of Support Vector Machines by Creating Exploitable Trends of Lagrangian Variables: An Application to DNA Splice Site Detection. , 2007, , .		0