

Kevin Litchfield

List of Publications by Year in descending order

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43
papers

6,068
citations

147801

31
h-index

254184

43
g-index

50
all docs

50
docs citations

50
times ranked

10737
citing authors

#	ARTICLE	IF	CITATIONS
1	Spatial patterns of tumour growth impact clonal diversification in a computational model and the TRACERx Renal study. <i>Nature Ecology and Evolution</i> , 2022, 6, 88-102.	7.8	30
2	Meta-analysis of tumor- and T cell-intrinsic mechanisms of sensitization to checkpoint inhibition. <i>Cell</i> , 2021, 184, 596-614.e14.	28.9	485
3	Tracking Cancer Evolution through the Disease Course. <i>Cancer Discovery</i> , 2021, 11, 916-932.	9.4	77
4	Selection of metastasis competent subclones in the tumour interior. <i>Nature Ecology and Evolution</i> , 2021, 5, 1033-1045.	7.8	50
5	E3 ubiquitin ligase HECTD2 mediates melanoma progression and immune evasion. <i>Oncogene</i> , 2021, 40, 5567-5578.	5.9	3
6	Cancer evolution: Darwin and beyond. <i>EMBO Journal</i> , 2021, 40, e108389.	7.8	118
7	Using DNA sequencing data to quantify T cell fraction and therapy response. <i>Nature</i> , 2021, 597, 555-560.	27.8	36
8	9p21 loss confers a cold tumor immune microenvironment and primary resistance to immune checkpoint therapy. <i>Nature Communications</i> , 2021, 12, 5606.	12.8	76
9	Metastasis and Immune Evasion from Extracellular cGAMP Hydrolysis. <i>Cancer Discovery</i> , 2021, 11, 1212-1227.	9.4	139
10	Determinants of anti-PD-1 response and resistance in clear cell renal cell carcinoma. <i>Cancer Cell</i> , 2021, 39, 1497-1518.e11.	16.8	126
11	Intratumor heterogeneity reflects clinical disease course. <i>Nature Cancer</i> , 2020, 1, 3-6.	13.2	44
12	Escape from nonsense-mediated decay associates with anti-tumor immunogenicity. <i>Nature Communications</i> , 2020, 11, 3800.	12.8	61
13	Pervasive chromosomal instability and karyotype order in tumour evolution. <i>Nature</i> , 2020, 587, 126-132.	27.8	221
14	Genomic landscape of platinum resistant and sensitive testicular cancers. <i>Nature Communications</i> , 2020, 11, 2189.	12.8	43
15	The T cell differentiation landscape is shaped by tumour mutations in lung cancer. <i>Nature Cancer</i> , 2020, 1, 546-561.	13.2	74
16	Abstract CT023: Phylogenetic tracking and minimal residual disease detection using ctDNA in early-stage NSCLC: A lung TRACERx study. <i>Cancer Research</i> , 2020, 80, CT023-CT023.	0.9	36
17	UVB-Induced Tumor Heterogeneity Diminishes Immune Response in Melanoma. <i>Cell</i> , 2019, 179, 219-235.e21.	28.9	270
18	A clonal expression biomarker associates with lung cancer mortality. <i>Nature Medicine</i> , 2019, 25, 1540-1548.	30.7	75

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19	Tumour mutational burden: primary versus metastatic tissue creates systematic bias. <i>Immuno-Oncology Technology</i> , 2019, 4, 8-14.	0.3	26
20	Timing the Landmark Events in the Evolution of Clear Cell Renal Cell Cancer: TRACERx Renal. <i>Cell</i> , 2018, 173, 611-623.e17.	28.9	398
21	Deterministic Evolutionary Trajectories Influence Primary Tumor Growth: TRACERx Renal. <i>Cell</i> , 2018, 173, 595-610.e11.	28.9	472
22	Tracking Cancer Evolution Reveals Constrained Routes to Metastases: TRACERx Renal. <i>Cell</i> , 2018, 173, 581-594.e12.	28.9	609
23	Large-scale Sequencing of Testicular Germ Cell Tumour (TGCT) Cases Excludes Major TGCT Predisposition Gene. <i>European Urology</i> , 2018, 73, 828-831.	1.9	54
24	Fc Effector Function Contributes to the Activity of Human Anti-CTLA-4 Antibodies. <i>Cancer Cell</i> , 2018, 33, 649-663.e4.	16.8	448
25	Promoter capture Hi-C-based identification of recurrent noncoding mutations in colorectal cancer. <i>Nature Genetics</i> , 2018, 50, 1375-1380.	21.4	49
26	Large-scale Analysis Demonstrates Familial Testicular Cancer to have Polygenic Aetiology. <i>European Urology</i> , 2018, 74, 248-252.	1.9	20
27	Validation of loci at 2q14.2 and 15q21.3 as risk factors for testicular cancer. <i>Oncotarget</i> , 2018, 9, 12630-12638.	1.8	8
28	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. <i>JAMA Oncology</i> , 2017, 3, 636.	7.1	376
29	Meta-analysis of five genome-wide association studies identifies multiple new loci associated with testicular germ cell tumor. <i>Nature Genetics</i> , 2017, 49, 1141-1147.	21.4	105
30	Identification of 19 new risk loci and potential regulatory mechanisms influencing susceptibility to testicular germ cell tumor. <i>Nature Genetics</i> , 2017, 49, 1133-1140.	21.4	120
31	The GENIE Is Out of the Bottle: Landmark Cancer Genomics Dataset Released. <i>Cancer Discovery</i> , 2017, 7, 796-798.	9.4	14
32	Insertion-and-deletion-derived tumour-specific neoantigens and the immunogenic phenotype: a pan-cancer analysis. <i>Lancet Oncology</i> , The, 2017, 18, 1009-1021.	10.7	716
33	Genomic evolution and chemoresistance in germ-cell tumours. <i>Nature</i> , 2016, 540, 114-118.	27.8	139
34	Rare disruptive mutations in ciliary function genes contribute to testicular cancer susceptibility. <i>Nature Communications</i> , 2016, 7, 13840.	12.8	32
35	Germ line mutations in shelterin complex genes are associated with familial chronic lymphocytic leukemia. <i>Blood</i> , 2016, 128, 2319-2326.	1.4	90
36	The genomic landscape of testicular germ cell tumours: from susceptibility to treatment. <i>Nature Reviews Urology</i> , 2016, 13, 409-419.	3.8	83

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37	Implementation of genome-wide complex trait analysis to quantify the heritability in multiple myeloma. Scientific Reports, 2015, 5, 12473.	3.3	16
38	Quantifying the heritability of testicular germ cell tumour using both population-based and genomic approaches. Scientific Reports, 2015, 5, 13889.	3.3	55
39	Polygenic susceptibility to testicular cancer: implications for personalised health care. British Journal of Cancer, 2015, 113, 1512-1518.	6.4	10
40	Whole-exome sequencing reveals the mutational spectrum of testicular germ cell tumours. Nature Communications, 2015, 6, 5973.	12.8	161
41	Multi-stage genome-wide association study identifies new susceptibility locus for testicular germ cell tumour on chromosome 3q25. Human Molecular Genetics, 2015, 24, 1169-1176.	2.9	31
42	Identification of four new susceptibility loci for testicular germ cell tumour. Nature Communications, 2015, 6, 8690.	12.8	36
43	Pathway-based analysis of GWAs data identifies association of sex determination genes with susceptibility to testicular germ cell tumors. Human Molecular Genetics, 2014, 23, 6061-6068.	2.9	28