Kevin M Brown

List of Publications by Year
in descending order

68 papers	6,871 citations	136950 32 h-index	106344 65 g-index
79 all docs	79 docs citations	79 times ranked	11458 citing authors

#	Article	IF	Citations
1	Novel MAPK/AKT-impairing germline NRAS variant identified in a melanoma-prone family. Familial Cancer, 2022, 21, 347-355.	1.9	1
2	Integrated Analysis of Coexpression and Exome Sequencing to Prioritize Susceptibility Genes for Familial Cutaneous Melanoma. Journal of Investigative Dermatology, 2022, 142, 2464-2475.e5.	0.7	4
3	Defining novel causal SNPs and linked phenotypes at melanoma-associated loci. Human Molecular Genetics, 2022, 31, 2845-2856.	2.9	3
4	Arginylâ€tRNAâ€protein transferase 1 (ATE1) promotes melanoma cell growth and migration. FEBS Letters, 2022, 596, 1468-1480.	2.8	1
5	ezQTL: A Web Platform for Interactive Visualization and Colocalization of QTLs and GWAS Loci. Genomics, Proteomics and Bioinformatics, 2022, 20, 541-548.	6.9	17
6	Investigating the genetic architecture of eye colour in a Canadian cohort. IScience, 2022, 25, 104485.	4.1	2
7	Rare germline deleterious variants increase susceptibility for lung cancer. Human Molecular Genetics, 2022, 31, 3558-3565.	2.9	5
8	Cancer regulatory variation. Current Opinion in Genetics and Development, 2021, 66, 41-49.	3.3	6
9	Large-scale cross-cancer fine-mapping of the 5p15.33 region reveals multiple independent signals. Human Genetics and Genomics Advances, 2021, 2, 100041.	1.7	6
10	Altered regulation of DPF3, a member of the SWI/SNF complexes, underlies the 14q24 renal cancer susceptibility locus. American Journal of Human Genetics, 2021, 108, 1590-1610.	6.2	9
11	Genomic and evolutionary classification of lung cancer in never smokers. Nature Genetics, 2021, 53, 1348-1359.	21.4	81
12	Cell-type-specific meQTLs extend melanoma GWAS annotation beyond eQTLs and inform melanocyte gene-regulatory mechanisms. American Journal of Human Genetics, 2021, 108, 1631-1646.	6.2	12
13	The ubiquitin ligase RNF5 determines acute myeloid leukemia growth and susceptibility to histone deacetylase inhibitors. Nature Communications, 2021, 12, 5397.	12.8	20
14	A UVB-responsive common variant at chromosome band 7p21.1 confers tanning response and melanoma risk via regulation of the aryl hydrocarbon receptor, AHR. American Journal of Human Genetics, 2021, 108, 1611-1630.	6.2	7
15	OUP accepted manuscript. Human Molecular Genetics, 2021, , .	2.9	2
16	A large Canadian cohort provides insights into the genetic architecture of human hair colour. Communications Biology, 2021, 4, 1253.	4.4	11
17	Neural crest-derived tumor neuroblastoma and melanoma share 1p13.2 as susceptibility locus that shows a long-range interaction with the SLC16A1 gene. Carcinogenesis, 2020, 41, 284-295.	2.8	18
18	A Transcriptome-Wide Association Study Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer. Journal of the National Cancer Institute, 2020, 112, 1003-1012.	6.3	59

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19	Siah2 control of T-regulatory cells limits anti-tumor immunity. Nature Communications, 2020, 11, 99.	12.8	15
20	Overlapping genetic architecture between Parkinson disease and melanoma. Acta Neuropathologica, 2020, 139, 347-364.	7.7	23
21	Massively parallel reporter assays of melanoma risk variants identify MX2 as a gene promoting melanoma. Nature Communications, 2020, 11, 2718.	12.8	53
22	SPANX Control of Lamin A/C Modulates Nuclear Architecture and Promotes Melanoma Growth. Molecular Cancer Research, 2020, 18, 1560-1573.	3.4	13
23	Regulation of eIF2Î± by RNF4 Promotes Melanoma Tumorigenesis and Therapy Resistance. Journal of Investigative Dermatology, 2020, 140, 2466-2477.	0.7	13
24	The genomic and epigenomic evolutionary history of papillary renal cell carcinomas. Nature Communications, 2020, 11, 3096.	12.8	19
25	Analysis of DNA methylation patterns in the tumor immune microenvironment of metastatic melanoma. Molecular Oncology, 2020, 14, 933-950.	4.6	29
26	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. Nature Genetics, 2020, 52, 494-504.	21.4	138
27	RNF5 Defines Acute Myeloid Leukemia Growth and Susceptibility to Histone Deacetylase Inhibitors. Blood, 2020, 136, 31-32.	1.4	0
28	Inherited Contributions to Melanoma Risk. , 2019, , 225-248.		0
29	Meta-analysis of GWA studies provides new insights on the genetic architecture of skin pigmentation in recently admixed populations. BMC Genetics, 2019, 20, 59.	2.7	32
30	Sex specific associations in genome wide association analysis of renal cell carcinoma. European Journal of Human Genetics, 2019, 27, 1589-1598.	2.8	27
31	Genetic Heterogeneity of BRAF Fusion Kinases in Melanoma Affects Drug Responses. Cell Reports, 2019, 29, 573-588.e7.	6.4	62
32	A Dynamic Cis-Regulation Pattern Underlying Epithelial Ovarian Cancer Susceptibility. Cancer Research, 2019, 79, 439-440.	0.9	2
33	Gut microbiota dependent anti-tumor immunity restricts melanoma growth in Rnf5â^'/â^' mice. Nature Communications, 2019, 10, 1492.	12.8	114
34	Evaluation of the contribution of germline variants in BRCA1 and BRCA2 to uveal and cutaneous melanoma. Melanoma Research, 2019, 29, 483-490.	1.2	13
35	The influence of obesity-related factors in the etiology of renal cell carcinomaâ€"A mendelian randomization study. PLoS Medicine, 2019, 16, e1002724.	8.4	59
36	Characterising cis-regulatory variation in the transcriptome of histologically normal and tumour-derived pancreatic tissues. Gut, 2018, 67, 521-533.	12.1	26

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37	Analysis of NRAS gain in 657 patients with melanoma and evaluation of its sensitivity to a MEK inhibitor. European Journal of Cancer, 2018, 89, 90-101.	2.8	19
38	Cell-typeâ€“specific eQTL of primary melanocytes facilitates identification of melanoma susceptibility genes. Genome Research, 2018, 28, 1621-1635.	5.5	67
39	Regulation of S100A8 Stability by RNF5 in Intestinal Epithelial Cells Determines Intestinal Inflammation and Severity of Colitis. Cell Reports, 2018, 24, 3296-3311.e6.	6.4	39
40	Somatic inactivating PTPRJ mutations and dysregulated pathways identified in canine malignant melanoma by integrated comparative genomic analysis. PLoS Genetics, 2018, 14, e1007589.	3.5	56
41	Diagnosis of Idiopathic Pulmonary Fibrosis. An Official ATS/ERS/JRS/ALAT Clinical Practice Guideline. American Journal of Respiratory and Critical Care Medicine, 2018, 198, e44-e68.	5.6	2,678
42	Combining common genetic variants and non-genetic risk factors to predict risk of cutaneous melanoma. Human Molecular Genetics, 2018, 27, 4145-4156.	2.9	34
43	Assessing the Incremental Contribution of Common Genomic Variants to Melanoma Risk Prediction in Two Population-Based Studies. Journal of Investigative Dermatology, 2018, 138, 2617-2624.	0.7	52
44	Inherited Contributions to Melanoma Risk. , 2018, , 1-23.		1
45	SDHDPromoter Mutations Ablate GABP Transcription Factor Binding in Melanoma. Cancer Research, 2017, 77, 1649-1661.	0.9	9
46	Functional characterization of a multi-cancer risk locus on chr5p15.33 reveals regulation of TERT by ZNF148. Nature Communications, 2017, 8, 15034.	12.8	40
47	Genome-wide association study identifies multiple risk loci for renal cell carcinoma. Nature Communications, 2017, 8, 15724.	12.8	106
48	Loci associated with skin pigmentation identified in African populations. Science, 2017, 358, .	12.6	260
49	A common intronic variant of PARP1 confers melanoma risk and mediates melanocyte growth via regulation of MITF. Nature Genetics, 2017, 49, 1326-1335.	21.4	51
50	Genetic Variants Related to Longer Telomere Length are Associated with Increased Risk of Renal Cell Carcinoma. European Urology, 2017, 72, 747-754.	1.9	39
51	SHARPIN-mediated regulation of protein arginine methyltransferase 5 controls melanoma growth. Journal of Clinical Investigation, 2017, 128, 517-530.	8.2	36
52	An interaction proteomics survey of transcription factor binding at recurrent TERT promoter mutations. Proteomics, 2016, 16, 417-426.	2.2	50
53	A Transcriptionally Inactive ATF2 Variant Drives Melanomagenesis. Cell Reports, 2016, 15, 1884-1892.	6.4	21
54	The genomic landscape of cutaneous melanoma. Pigment Cell and Melanoma Research, 2016, 29, 266-283.	3.3	144

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55	A melanin-bleaching methodology for molecular and histopathological analysis of formalin-fixed paraffin-embedded tissue. Laboratory Investigation, 2016, 96, 1116-1127.	3.7	17
56	Germline TERT promoter mutations are rare in familial melanoma. Familial Cancer, 2016, 15, 139-144.	1.9	51
57	Downregulation of the Ubiquitin Ligase RNF125 Underlies Resistance of Melanoma Cells to BRAF Inhibitors via JAK1 Deregulation. Cell Reports, 2015, 11, 1458-1473.	6.4	55
58	Nonsense Mutations in the Shelterin Complex Genes ACD and TERF2IP in Familial Melanoma. Journal of the National Cancer Institute, 2015, 107, .	6.3	134
59	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. Nature Genetics, 2015, 47, 987-995.	21.4	218
60	Fine mapping of genetic susceptibility loci for melanoma reveals a mixture of single variant and multiple variant regions. International Journal of Cancer, 2015, 136, 1351-1360.	5.1	30
61	Identification of a melanoma susceptibility locus and somatic mutation inTET2. Carcinogenesis, 2014, 35, 2097-2101.	2.8	41
62	A variant in FTO shows association with melanoma risk not due to BMI. Nature Genetics, 2013, 45, 428-432.	21.4	111
63	Genome-wide association study identifies novel loci predisposing to cutaneous melanomaâ€. Human Molecular Genetics, 2011, 20, 5012-5023.	2.9	187
64	Genome-wide association study identifies three new melanoma susceptibility loci. Nature Genetics, 2011, 43, 1108-1113.	21.4	230
65	A novel recurrent mutation in MITF predisposes to familial and sporadic melanoma. Nature, 2011, 480, 99-103.	27.8	413
66	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. Nature Genetics, 2011, 43, 1114-1118.	21.4	140
67	Genome-wide association study identifies three loci associated with melanoma risk. Nature Genetics, 2009, 41, 920-925.	21.4	422
68	Common sequence variants on 20q11.22 confer melanoma susceptibility. Nature Genetics, 2008, 40, 838-840.	21.4	209