Sean Davis

List of Publications by Citations

109 papers	23,221 citations	53 h-index	137 g-index
137 ext. papers	28,713 ext. citations	11.9 avg, IF	6.11 L-index

#	Paper	IF	Citations
109	NCBI GEO: archive for functional genomics data sets--update. *Nucleic Acids Research*, **2013**, 41, D991-5	20.1	4393
108	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature*, **2007**, 447, 799-816	50.4	4121
107	Orchestrating high-throughput genomic analysis with Bioconductor. *Nature Methods*, **2015**, 12, 115-21	21.6	1949
106	Rare structural variants disrupt multiple genes in neurodevelopmental pathways in schizophrenia. *Science*, **2008**, 320, 539-43	33.3	1443
105	GEOquery: a bridge between the Gene Expression Omnibus (GEO) and BioConductor. *Bioinformatics*, **2007**, 23, 1846-7	7.2	1086
104	BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. *Bioinformatics*, **2005**, 21, 3439-40	7.2	1069
103	High-resolution mapping and characterization of open chromatin across the genome. *Cell*, **2008**, 132, 311-22	56.2	988
102	A single IGF1 allele is a major determinant of small size in dogs. *Science*, **2007**, 316, 112-5	33.3	472
101	Exome sequencing identifies GRIN2A as frequently mutated in melanoma. *Nature Genetics*, **2011**, 43, 442-6	36.3	385
100	Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. *Nature*, **2018**, 555, 371-376	50.4	380
99	Genome-wide mapping of DNase hypersensitive sites using massively parallel signature sequencing (MPSS). *Genome Research*, **2006**, 16, 123-31	9.7	363
98	Gene expression profiling of human sarcomas: insights into sarcoma biology. *Cancer Research*, **2005**, 65, 9226-35	10.1	287
97	Interaction of the glucocorticoid receptor with the chromatin landscape. *Molecular Cell*, **2008**, 29, 611-24	17.6	263
96	Super-enhancers delineate disease-associated regulatory nodes in T cells. *Nature*, **2015**, 520, 558-62	50.4	247
95	RCircos: an R package for Circos 2D track plots. *BMC Bioinformatics*, **2013**, 14, 244	3.6	246
94	Epigenomic alterations and gene expression profiles in respiratory epithelia exposed to cigarette smoke condensate. *Oncogene*, **2010**, 29, 3650-64	9.2	214
93	Interferon-□links ultraviolet radiation to melanomagenesis in mice. *Nature*, **2011**, 469, 548-53	50.4	209

92	The exomes of the NCI-60 panel: a genomic resource for cancer biology and systems pharmacology. *Cancer Research*, **2013**, 73, 4372-82	10.1	207
91	DNase-chip: a high-resolution method to identify DNase I hypersensitive sites using tiled microarrays. *Nature Methods*, **2006**, 3, 503-9	21.6	188
90	Canine tumor cross-species genomics uncovers targets linked to osteosarcoma progression. *BMC Genomics*, **2009**, 10, 625	4.5	184
89	High prevalence of MAP2K1 mutations in variant and IGHV4-34-expressing hairy-cell leukemias. *Nature Genetics*, **2014**, 46, 8-10	36.3	183
88	Genome-wide analysis of menin binding provides insights into MEN1 tumorigenesis. *PLoS Genetics*, **2006**, 2, e51	6	172
87	Analyses of resected human brain metastases of breast cancer reveal the association between up-regulation of hexokinase 2 and poor prognosis. *Molecular Cancer Research*, **2009**, 7, 1438-45	6.6	163
86	Genetic susceptibility for human familial essential hypertension in a region of homology with blood pressure linkage on rat chromosome 10. *Human Molecular Genetics*, **1997**, 6, 2077-85	5.6	162
85	Identification of an inhibitor of the EWS-FLI1 oncogenic transcription factor by high-throughput screening. *Journal of the National Cancer Institute*, **2011**, 103, 962-78	9.7	156
84	Point Mutations in Exon 1B of APC Reveal Gastric Adenocarcinoma and Proximal Polyposis of the Stomach as a Familial Adenomatous Polyposis Variant. *American Journal of Human Genetics*, **2016**, 98, 830-842	11	153
83	Evidence for an unanticipated relationship between undifferentiated pleomorphic sarcoma and embryonal rhabdomyosarcoma. *Cancer Cell*, **2011**, 19, 177-91	24.3	142
82	Homozygosity mapping of Hallervorden-Spatz syndrome to chromosome 20p12.3-p13. *Nature Genetics*, **1996**, 14, 479-81	36.3	139
81	TRAIL induces apoptosis in triple-negative breast cancer cells with a mesenchymal phenotype. *Breast Cancer Research and Treatment*, **2009**, 113, 217-30	4.4	138
80	A molecular function map of Ewing's sarcoma. *PLoS ONE*, **2009**, 4, e5415	3.7	135
79	Analysis of the matrix metalloproteinase family reveals that MMP8 is often mutated in melanoma. *Nature Genetics*, **2009**, 41, 518-20	36.3	131
78	Linkage and association between inflammatory bowel disease and a locus on chromosome 12. *American Journal of Human Genetics*, **1998**, 63, 95-100	11	131
77	Whole-genome sequencing identifies a recurrent functional synonymous mutation in melanoma. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 13481-6	11.5	127
76	A polymorphism in IRF4 affects human pigmentation through a tyrosinase-dependent MITF/TFAP2A pathway. *Cell*, **2013**, 155, 1022-33	56.2	127
75	Vorinostat inhibits brain metastatic colonization in a model of triple-negative breast cancer and induces DNA double-strand breaks. *Clinical Cancer Research*, **2009**, 15, 6148-57	12.9	119

74	Database of mRNA gene expression profiles of multiple human organs. *Genome Research*, **2005**, 15, 443-50	9.7	101
73	Genome-wide depletion of replication initiation events in highly transcribed regions. *Genome Research*, **2011**, 21, 1822-32	9.7	95
72	GEOmetadb: powerful alternative search engine for the Gene Expression Omnibus. *Bioinformatics*, **2008**, 24, 2798-800	7.2	93
71	Nonparametric simulation-based statistics for detecting linkage in general pedigrees. *American Journal of Human Genetics*, **1996**, 58, 867-80	11	90
70	Comparison of nonparametric statistics for detection of linkage in nuclear families: single-marker evaluation. *American Journal of Human Genetics*, **1997**, 61, 1431-44	11	84
69	Archival fine-needle aspiration cytopathology (FNAC) samples: untapped resource for clinical molecular profiling. *Journal of Molecular Diagnostics*, **2010**, 12, 739-45	5.1	83
68	Identification of Novel Targets for Lung Cancer Therapy Using an Induced Pluripotent Stem Cell Model. *Annals of the American Thoracic Society*, **2018**, 15, S127-S128	4.7	78
67	Kinetic complexity of the global response to glucocorticoid receptor action. *Endocrinology*, **2009**, 150, 1766-74	4.8	78
66	Statistics for ChIP-chip and DNase hypersensitivity experiments on NimbleGen arrays. *Methods in Enzymology*, **2006**, 411, 270-82	1.7	76
65	Oncogenic ETS fusions deregulate E2F3 target genes in Ewing sarcoma and prostate cancer. *Genome Research*, **2013**, 23, 1797-809	9.7	75
64	SRAdb: query and use public next-generation sequencing data from within R. *BMC Bioinformatics*, **2013**, 14, 19	3.6	73
63	Chromothripsis and focal copy number alterations determine poor outcome in malignant melanoma. *Cancer Research*, **2013**, 73, 1454-60	10.1	72
62	A Genome-Wide Scan Identifies Variants in NFIB Associated with Metastasis in Patients with Osteosarcoma. *Cancer Discovery*, **2015**, 5, 920-31	24.4	71
61	Suppressor role of activating transcription factor 2 (ATF2) in skin cancer. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 1674-9	11.5	65
60	Lineage of origin in rhabdomyosarcoma informs pharmacological response. *Genes and Development* , **2014**, 28, 1578-91	12.6	64
59	Antagonistic cross-regulation between Sox9 and Sox10 controls an anti-tumorigenic program in melanoma. *PLoS Genetics*, **2015**, 11, e1004877	6	59
58	miR30a inhibits LOX expression and anaplastic thyroid cancer progression. *Cancer Research*, **2015**, 75, 367-77	10.1	55
57	Software for the Integration of Multiomics Experiments in Bioconductor. *Cancer Research*, **2017**, 77, e39-42	10.1	53

56	Molecular grading of ductal carcinoma in situ of the breast. *Clinical Cancer Research*, **2008**, 14, 8244-52	12.9	50
55	Dual inhibition of HDAC and EGFR signaling with CUDC-101 induces potent suppression of tumor growth and metastasis in anaplastic thyroid cancer. *Oncotarget*, **2015**, 6, 9073-85	3.3	47
54	Genome-wide methylation patterns in papillary thyroid cancer are distinct based on histological subtype and tumor genotype. *Journal of Clinical Endocrinology and Metabolism*, **2014**, 99, E329-37	5.6	46
53	Large-scale profiling of archival lymph nodes reveals pervasive remodeling of the follicular lymphoma methylome. *Cancer Research*, **2009**, 69, 758-64	10.1	46
52	High frequencies of leukemia stem cells in poor-outcome childhood precursor-B acute lymphoblastic leukemias. *Leukemia*, **2010**, 24, 1859-66	10.7	45
51	Assessment of automated image analysis of breast cancer tissue microarrays for epidemiologic studies. *Cancer Epidemiology Biomarkers and Prevention*, **2010**, 19, 992-9	4	43
50	On the Selective Packaging of Genomic RNA by HIV-1. *Viruses*, **2016**, 8,	6.2	43
49	Public data and open source tools for multi-assay genomic investigation of disease. *Briefings in Bioinformatics*, **2016**, 17, 603-15	13.4	38
48	Preferential localization of human origins of DNA replication at the 5′ ends of expressed genes and at evolutionarily conserved DNA sequences. *PLoS ONE*, **2011**, 6, e17308	3.7	37
47	Melanoblast transcriptome analysis reveals pathways promoting melanoma metastasis. *Nature Communications*, **2020**, 11, 333	17.4	33
46	RARRES2 functions as a tumor suppressor by promoting β-catenin phosphorylation/degradation and inhibiting p38 phosphorylation in adrenocortical carcinoma. *Oncogene*, **2017**, 36, 3541-3552	9.2	32
45	Advanced bone formation in mice with a dominant-negative mutation in the thyroid hormone receptor β gene due to activation of Wnt/β-catenin protein signaling. *Journal of Biological Chemistry*, **2012**, 287, 17812-17822	5.4	30
44	Upregulation of IFN-Inducible and Damage-Response Pathways in Chronic Graft-versus-Host Disease. *Journal of Immunology*, **2016**, 197, 3490-3503	5.3	30
43	Toward a gold standard for benchmarking gene set enrichment analysis. *Briefings in Bioinformatics*, **2021**, 22, 545-556	13.4	30
42	NCI-60 whole exome sequencing and pharmacological CellMiner analyses. *PLoS ONE*, **2014**, 9, e101670	3.7	29
41	Constitutive Fms-like tyrosine kinase 3 activation results in specific changes in gene expression in myeloid leukaemic cells. *British Journal of Haematology*, **2007**, 138, 603-15	4.5	27
40	Harnessing genomics to identify environmental determinants of heritable disease. *Mutation Research - Reviews in Mutation Research*, **2013**, 752, 6-9	7	25
39	Comparative exome sequencing of metastatic lesions provides insights into the mutational progression of melanoma. *BMC Genomics*, **2012**, 13, 505	4.5	25

38	Autoreactive T Cells and Chronic Fungal Infection Drive Esophageal Carcinogenesis. *Cell Host and Microbe*, **2017**, 21, 478-493.e7	23.4	24
37	Inhibition of Survivin with YM155 Induces Durable Tumor Response in Anaplastic Thyroid Cancer. *Clinical Cancer Research*, **2015**, 21, 4123-32	12.9	23
36	TNF- modulates genome-wide redistribution of Np63/TAp73 and NF-B cREL interactive binding on TP53 and AP-1 motifs to promote an oncogenic gene program in squamous cancer. *Oncogene*, **2016**, 35, 5781-5794	9.2	23
35	Downregulation of IGFBP2 is associated with resistance to IGF1R therapy in rhabdomyosarcoma. *Oncogene*, **2014**, 33, 5697-705	9.2	22
34	Whole genome and transcriptome sequencing of a B3 thymoma. *PLoS ONE*, **2013**, 8, e60572	3.7	21
33	Zoom-in comparative genomic hybridisation arrays for the characterisation of variable breakpoint contiguous gene syndromes. *Journal of Medical Genetics*, **2007**, 44, e59	5.8	19
32	CHEK2 genomic and proteomic analyses reveal genetic inactivation or endogenous activation across the 60 cell lines of the US National Cancer Institute. *Oncogene*, **2012**, 31, 403-18	9.2	18
31	Whole Genome Sequencing of Newly Established Pancreatic Cancer Lines Identifies Novel Somatic Mutation (c.2587G>A) in Axon Guidance Receptor Plexin A1 as Enhancer of Proliferation and Invasion. *PLoS ONE*, **2016**, 11, e0149833	3.7	17
30	Resources for Interpreting Variants in Precision Genomic Oncology Applications. *Frontiers in Oncology*, **2017**, 7, 214	5.3	15
29	Modeling synovial sarcoma: timing is everything. *Cancer Cell*, **2007**, 11, 305-7	24.3	15
28	Detection of novel amplicons in prostate cancer by comprehensive genomic profiling of prostate cancer cell lines using oligonucleotide-based arrayCGH. *PLoS ONE*, **2007**, 2, e769	3.7	14
27	A methyl-deviator epigenotype of estrogen receptor-positive breast carcinoma is associated with malignant biology. *American Journal of Pathology*, **2011**, 179, 55-65	5.8	13
26	ASXL3 Is a Novel Pluripotency Factor in Human Respiratory Epithelial Cells and a Potential Therapeutic Target in Small Cell Lung Cancer. *Cancer Research*, **2017**, 77, 6267-6281	10.1	12
25	Prohibitin expression is associated with high grade breast cancer but is not a driver of amplification at 17q21.33. *Pathology*, **2013**, 45, 629-36	1.6	8
24	In vivo role of alternative splicing and serine phosphorylation of the microphthalmia-associated transcription factor. *Genetics*, **2012**, 191, 133-44	4	8
23	Characterization of genomic alterations in radiation-associated breast cancer among childhood cancer survivors, using comparative genomic hybridization (CGH) arrays. *PLoS ONE*, **2015**, 10, e0116078	3.7	8
22	Rb1 loss modifies but does not initiate alveolar rhabdomyosarcoma. *Skeletal Muscle*, **2013**, 3, 27	5.1	7
21	Abstract 4856: Using embryonic melanoblast transcriptome analysis to identify novel mechanisms promoting metastatic melanoma **2012**,		7

20	Integrated analysis of DNA methylation, immunohistochemistry and mRNA expression, data identifies a methylation expression index (MEI) robustly associated with survival of ER-positive breast cancer patients. *Breast Cancer Research and Treatment*, **2015**, 150, 457-466	4.4	6
19	Exclusion of the 750-kb genetically unstable region at Xq27 as a candidate locus for prostate malignancy in HPCX1-linked families. *Genes Chromosomes and Cancer*, **2012**, 51, 933-48	5	6
18	Ewing's sarcoma: general insights from a rare model. *Cancer Cell*, **2006**, 9, 331-2	24.3	5
17	Genome-wide methylation profiling in archival formalin-fixed paraffin-embedded tissue samples. *Methods in Molecular Biology*, **2012**, 823, 107-18	1.4	5
16	caOmicsV: an R package for visualizing multidimensional cancer genomic data. *BMC Bioinformatics*, **2016**, 17, 141	3.6	4
15	The Bioconductor channel in F1000Research. *F1000Research*, **2015**, 4, 217	3.6	4
14	HGNChelper: identification and correction of invalid gene symbols for human and mouse. *F1000Research*, **2020**, 9, 1493	3.6	3
13	The Bioconductor channel in F1000Research. *F1000Research*, **2015**, 4, 217	3.6	3
12	Software for the integration of multi-omics experiments in Bioconductor		3
11	recount-brain: a curated repository of human brain RNA-seq datasets metadata		3
10	Analysis of bipolar disorder using affected relatives. *Genetic Epidemiology*, **1997**, 14, 605-10	2.6	1
9	Analysis of a complex oligogenic disease. *Genetic Epidemiology*, **1997**, 14, 861-6	2.6	1
8	Impact of overlapping recruitment on linkage analysis of complex disorders: simulation studies. *American Journal of Medical Genetics Part A*, **2001**, 105, 141-4		1
7	Orchestrating a community-developed computational workshop and accompanying training materials. *F1000Research*, **2018**, 7, 1656	3.6	1
6	NCBI GEO: archive for functional genomics data sets—update		1
5	GenomicDataCommons: a Bioconductor Interface to the NCI Genomic Data Commons		1
4	HGNChelper: identification and correction of invalid gene symbols for human and mouse		1
3	Towards a gold standard for benchmarking gene set enrichment analysis		1

2	restfulSE: A semantically rich interface for cloud-scale genomics with Bioconductor. *F1000Research*, **2019**, 8, 21	3.6
1	BiocPkgTools: Toolkit for mining the package ecosystem. *F1000Research*, **2019**, 8, 752	3.6