Sean Davis

List of Publications by Year
in descending order

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127 papers	31,974 citations	28190 55 h-index	32761 100 g-index
137 all docs	137 docs citations	137 times ranked	52815 citing authors

#	Article	IF	Citations
1	Ten simple rules for large-scale data processing. PLoS Computational Biology, 2022, 18, e1009757.	1.5	1
2	GenomicSuperSignature facilitates interpretation of RNA-seq experiments through robust, efficient comparison to public databases. Nature Communications, 2022, 13, .	5.8	6
3	Toward a gold standard for benchmarking gene set enrichment analysis. Briefings in Bioinformatics, 2021, 22, 545-556.	3.2	83
4	Melanoblast transcriptome analysis reveals pathways promoting melanoma metastasis. Nature Communications, 2020, 11, 333.	5.8	65
5	HGNChelper: identification and correction of invalid gene symbols for human and mouse. F1000Research, 2020, 9, 1493.	0.8	17
6	restfulSE: A semantically rich interface for cloud-scale genomics with Bioconductor. F1000Research, 2019, 8, 21.	0.8	0
7	BiocPkgTools: Toolkit for mining the Bioconductor package ecosystem. F1000Research, 2019, 8, 752.	0.8	0
8	Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. Nature, 2018, 555, 371-376.	13.7	649
9	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.	1.5	0
10	Orchestrating a community-developed computational workshop and accompanying training materials. F1000Research, 2018, 7, 1656.	0.8	1
11	RARRES2 functions as a tumor suppressor by promoting Î²-catenin phosphorylation/degradation and inhibiting p38 phosphorylation in adrenocortical carcinoma. Oncogene, 2017, 36, 3541-3552.	2.6	47
12	Autoreactive T Cells and Chronic Fungal Infection Drive Esophageal Carcinogenesis. Cell Host and Microbe, 2017, 21, 478-493.e7.	5.1	44
13	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.	0.4	20
14	Software for the Integration of Multiomics Experiments in Bioconductor. Cancer Research, 2017, 77, e39-e42.	0.4	80
15	Resources for Interpreting Variants in Precision Genomic Oncology Applications. Frontiers in Oncology, 2017, 7, 214.	1.3	18
16	Abstract 3004: Comparison of somatic alterations in the genome and transcriptome of 1,705 pediatric leukemia and solid tumors: a report from the Childrenâ€™s Oncology Group (COG) - NCI TARGET Project. , 2017, , .		0
17	On the Selective Packaging of Genomic RNA by HIV-1. Viruses, 2016, 8, 246.	1.5	66
18	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.	2.6	201

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19	TNF-Î± modulates genome-wide redistribution of Î”Np63Î±/TAp73 and NF-ÎºB cREL interactive binding on TP53 and AP-1 motifs to promote an oncogenic gene program in squamous cancer. Oncogene, 2016, 35, 5781-5794.	2.6	33
20	Upregulation of IFN-Inducible and Damage-Response Pathways in Chronic Graft-versus-Host Disease. Journal of Immunology, 2016, 197, 3490-3503.	0.4	50
21	caOmicsV: an R package for visualizing multidimensional cancer genomic data. BMC Bioinformatics, 2016, 17, 141.	1.2	4
22	Public data and open source tools for multi-assay genomic investigation of disease. Briefings in Bioinformatics, 2016, 17, 603-615.	3.2	46
23	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.	1.1	21
24	Abstract 2717: Reintroduction of DAXX suppresses alternative lengthening of telomeres in osteosarcoma. , 2016, , .		0
25	Inhibition of Survivin with YM155 Induces Durable Tumor Response in Anaplastic Thyroid Cancer. Clinical Cancer Research, 2015, 21, 4123-4132.	3.2	31
26	miR30a Inhibits LOX Expression and Anaplastic Thyroid Cancer Progression. Cancer Research, 2015, 75, 367-377.	0.4	67
27	Super-enhancers delineate disease-associated regulatory nodes in T cells. Nature, 2015, 520, 558-562.	13.7	323
28	Orchestrating high-throughput genomic analysis with Bioconductor. Nature Methods, 2015, 12, 115-121.	9.0	3,070
29	Antagonistic Cross-Regulation between Sox9 and Sox10 Controls an Anti-tumorigenic Program in Melanoma. PLoS Genetics, 2015, 11, e1004877.	1.5	85
30	A Genome-Wide Scan Identifies Variants in NFIB Associated with Metastasis in Patients with Osteosarcoma. Cancer Discovery, 2015, 5, 920-931.	7.7	88
31	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.	1.1	7
32	The Bioconductor channel in F1000Research. F1000Research, 2015, 4, 217.	0.8	6
33	The Bioconductor channel in F1000Research. F1000Research, 2015, 4, 217.	0.8	4
34	Characterization of Genomic Alterations in Radiation-Associated Breast Cancer among Childhood Cancer Survivors, Using Comparative Genomic Hybridization (CGH) Arrays. PLoS ONE, 2015, 10, e0116078.	1.1	10
35	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, 9073-9085.	0.8	54
36	Downregulation of IGFBP2 is associated with resistance to IGF1R therapy in rhabdomyosarcoma. Oncogene, 2014, 33, 5697-5705.	2.6	23

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37	Lineage of origin in rhabdomyosarcoma informs pharmacological response. Genes and Development, 2014, 28, 1578-1591.	2.7	87
38	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-E337.	1.8	55
39	High prevalence of MAP2K1 mutations in variant and IGHV4-34â€“expressing hairy-cell leukemias. Nature Genetics, 2014, 46, 8-10.	9.4	236
40	Novel Proteasome Inhibitor Carfilzomib in Combination with Survivin Inhibitor YM155 Induces Enhanced Cytotoxicity in Anaplastic Thyroid Cancer. Journal of the American College of Surgeons, 2014, 219, S125.	0.2	0
41	NCI-60 Whole Exome Sequencing and Pharmacological CellMiner Analyses. PLoS ONE, 2014, 9, e101670.	1.1	38
42	Abstract 994: Integrated embryonic transcriptome analyses identify key melanoma metastasis regulator. , 2014, , .		0
43	Abstract 4367: Tumor suppressor miR-30a inhibits LOX expression and progression in anaplastic thyroid cancer. , 2014, , .		0
44	Abstract 4167: Harvesting knowledge from unexploited genomic data: Estimating relative telomere length from targeted-resequencing. , 2014, , .		0
45	Abstract 4873: IKKÎ± bridges central tolerance to innate immunity and inflammation. , 2014, , .		0
46	Abstract IA22: Modeling recurrent metastatic melanoma in the mouse. , 2014, , .		0
47	SRAdb: query and use public next-generation sequencing data from within R. BMC Bioinformatics, 2013, 14, 19.	1.2	120
48	The Exomes of the NCI-60 Panel: A Genomic Resource for Cancer Biology and Systems Pharmacology. Cancer Research, 2013, 73, 4372-4382.	0.4	239
49	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, 13481-13486.	3.3	147
50	A Polymorphism in IRF4 Affects Human Pigmentation through a Tyrosinase-Dependent MITF/TFAP2A Pathway. Cell, 2013, 155, 1022-1033.	13.5	184
51	RCircos: an R package for Circos 2D track plots. BMC Bioinformatics, 2013, 14, 244.	1.2	502
52	Harnessing genomics to identify environmental determinants of heritable disease. Mutation Research - Reviews in Mutation Research, 2013, 752, 6-9.	2.4	25
53	Rb1 loss modifies but does not initiate alveolar rhabdomyosarcoma. Skeletal Muscle, 2013, 3, 27.	1.9	9
54	Oncogenic ETS fusions deregulate E2F3 target genes in Ewing sarcoma and prostate cancer. Genome Research, 2013, 23, 1797-1809.	2.4	99

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55	Chromothripsis and Focal Copy Number Alterations Determine Poor Outcome in Malignant Melanoma. Cancer Research, 2013, 73, 1454-1460.	0.4	86
56	Prohibitin expression is associated with high grade breast cancer but is not a driver of amplification at 17q21.33. Pathology, 2013, 45, 629-636.	0.3	10
57	Whole Genome and Transcriptome Sequencing of a B3 Thymoma. PLoS ONE, 2013, 8, e60572.	1.1	28
58	NCBI GEO: archive for functional genomics data setsâ€"update. Nucleic Acids Research, 2012, 41, D991-D995.	6.5	7,174
59	In Vivo Role of Alternative Splicing and Serine Phosphorylation of the Microphthalmia-Associated Transcription Factor. Genetics, 2012, 191, 133-144.	1.2	10
60	Advanced Bone Formation in Mice with a Dominant-negative Mutation in the Thyroid Hormone Receptor Î² Gene due to Activation of Wnt/Î²-Catenin Protein Signaling. Journal of Biological Chemistry, 2012, 287, 17812-17822.	1.6	37
61	Comparative exome sequencing of metastatic lesions provides insights into the mutational progression of melanoma. BMC Genomics, 2012, 13, 505.	1.2	31
62	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, 403-418.	2.6	20
63	Exclusion of the 750â€kb genetically unstable region at Xq27 as a candidate locus for prostate malignancy in HPCX1â€linked families. Genes Chromosomes and Cancer, 2012, 51, 933-948.	1.5	7
64	Genome-Wide Methylation Profiling in Archival Formalin-Fixed Paraffin-Embedded Tissue Samples. Methods in Molecular Biology, 2012, 823, 107-118.	0.4	5
65	Abstract 4856: Using embryonic melanoblast transcriptome analysis to identify novel mechanisms promoting metastatic melanoma. Cancer Research, 2012, 72, 4856-4856.	0.4	14
66	Abstract 4193: TNF-Î± dynamically modulates genome-wide cross-regulation of cRel, Î”Np63 and TAp73 promoter binding and gene expression in head and neck cancer: TP53 and NFÎºB ChIP-Seq in HNSCC. , 2012, , .		2
67	Abstract 2116:CHEK2(Chk2) endogenous activation is associated with p53 deficiency and downregulation ofBRCA2and Fanconi Anemia pathway gene members in the National Cancer Institute Anticancer Tumor Cell Line Panel (NCI-60). , 2012, , .		0
68	Abstract 5070: Paired-end RNA-sequencing reveals novel fusion genes and SNVs in osteosarcoma. , 2012, , .		0
69	Abstract 1879: The exomes of the NCI60 and their implications for cancer pharmacogenomics. , 2012, , .		0
70	Abstract 1113: Role of the microRNA-23aˆ¼27aˆ¼24 clusters in osteosarcoma. , 2012, , .		1
71	A Methyl-Deviator Epigenotype of Estrogen Receptorâ€"Positive Breast Carcinoma Is Associated with Malignant Biology. American Journal of Pathology, 2011, 179, 55-65.	1.9	15
72	Preferential Localization of Human Origins of DNA Replication at the 5â€²-Ends of Expressed Genes and at Evolutionarily Conserved DNA Sequences. PLoS ONE, 2011, 6, e17308.	1.1	47

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73	Exome sequencing identifies GRIN2A as frequently mutated in melanoma. Nature Genetics, 2011, 43, 442-446.	9.4	449
74	Interferon-Î³ links ultraviolet radiation to melanomagenesis in mice. Nature, 2011, 469, 548-553.	13.7	264
75	Evidence for an Unanticipated Relationship between Undifferentiated Pleomorphic Sarcoma and Embryonal Rhabdomyosarcoma. Cancer Cell, 2011, 19, 177-191.	7.7	167
76	Identification of an Inhibitor of the EWS-FLI1 Oncogenic Transcription Factor by High-Throughput Screening. Journal of the National Cancer Institute, 2011, 103, 962-978.	3.0	174
77	Genome-wide depletion of replication initiation events in highly transcribed regions. Genome Research, 2011, 21, 1822-1832.	2.4	112
78	Abstract 4968: TNF-alpha promotes genome-wide replacement of TAp73 chromatin occupancy by cREL and DeltaNp63. , 2011, , .		1
79	Abstract 3934: Identification of novel cancer DNA sequence variants in human sarcomas. , 2011, , .		0
80	Abstract 2846: Pigment epithelium-derived factor (PEDF) functions as a brain metastasis suppressor of breast cancer. , 2011, , .		0
81	Epigenomic alterations and gene expression profiles in respiratory epithelia exposed to cigarette smoke condensate. Oncogene, 2010, 29, 3650-3664.	2.6	245
82	High frequencies of leukemia stem cells in poor-outcome childhood precursor-B acute lymphoblastic leukemias. Leukemia, 2010, 24, 1859-1866.	3.3	49
83	Assessment of Automated Image Analysis of Breast Cancer Tissue Microarrays for Epidemiologic Studies. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 992-999.	1.1	54
84	28 Ultraviolet B-induced inflammatory microenvironment promotes melanocyte survival and melanoma susceptibility. European Journal of Cancer, Supplement, 2010, 8, 8.	2.2	0
85	Archival Fine-Needle Aspiration Cytopathology (FNAC) Samples. Journal of Molecular Diagnostics, 2010, 12, 739-745.	1.2	97
86	Abstract 2213: Identification of novel cancer mutations in sarcomas. , 2010, , .		0
87	Abstract 3024: miRNA expression profiles in sarcomas. , 2010, , .		0
88	Vorinostat Inhibits Brain Metastatic Colonization in a Model of Triple-Negative Breast Cancer and Induces DNA Double-Strand Breaks. Clinical Cancer Research, 2009, 15, 6148-6157.	3.2	132
89	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, 1438-1445.	1.5	185
90	Kinetic Complexity of the Global Response to Glucocorticoid Receptor Action. Endocrinology, 2009, 150, 1766-1774.	1.4	91

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91	Large-Scale Profiling of Archival Lymph Nodes Reveals Pervasive Remodeling of the Follicular Lymphoma Methylome. Cancer Research, 2009, 69, 758-764.	0.4	46
92	Canine tumor cross-species genomics uncovers targets linked to osteosarcoma progression. BMC Genomics, 2009, 10, 625.	1.2	228
93	TRAIL induces apoptosis in triple-negative breast cancer cells with a mesenchymal phenotype. Breast Cancer Research and Treatment, 2009, 113, 217-230.	1.1	157
94	Analysis of the matrix metalloproteinase family reveals that MMP8 is often mutated in melanoma. Nature Genetics, 2009, 41, 518-520.	9.4	145
95	A Molecular Function Map of Ewing's Sarcoma. PLoS ONE, 2009, 4, e5415.	1.1	158
96	Interaction of the Glucocorticoid Receptor with the Chromatin Landscape. Molecular Cell, 2008, 29, 611-624.	4.5	285
97	High-Resolution Mapping andÂCharacterization of Open Chromatin across the Genome. Cell, 2008, 132, 311-322.	13.5	1,246
98	Rare Structural Variants Disrupt Multiple Genes in Neurodevelopmental Pathways in Schizophrenia. Science, 2008, 320, 539-543.	6.0	1,654
99	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, 1674-1679.	3.3	78
100	Molecular Grading of Ductal Carcinoma In situ of the Breast. Clinical Cancer Research, 2008, 14, 8244-8252.	3.2	60
101	GEOmetadb: powerful alternative search engine for the Gene Expression Omnibus. Bioinformatics, 2008, 24, 2798-2800.	1.8	128
102	GEOquery: a bridge between the Gene Expression Omnibus (GEO) and BioConductor. Bioinformatics, 2007, 23, 1846-1847.	1.8	2,083
103	A Single IGF1 Allele Is a Major Determinant of Small Size in Dogs. Science, 2007, 316, 112-115.	6.0	587
104	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.	1.1	18
105	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	13.7	4,709
106	Constitutive Fmsâ€like tyrosine kinase 3 activation results in specific changes in gene expression in myeloid leukaemic cells. British Journal of Haematology, 2007, 138, 603-615.	1.2	34
107	Modeling Synovial Sarcoma: Timing Is Everything. Cancer Cell, 2007, 11, 305-307.	7.7	17
108	DNase-chip: a high-resolution method to identify DNase I hypersensitive sites using tiled microarrays. Nature Methods, 2006, 3, 503-509.	9.0	222

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109	Ewing's sarcoma: General insights from a rare model. Cancer Cell, 2006, 9, 331-332.	7.7	5
110	Genome-Wide Analysis of Menin Binding Provides Insights into MEN1 Tumorigenesis. PLoS Genetics, 2006, 2, e51.	1.5	193
111	Zoom-in comparative genomic hybridisation arrays for the characterisation of variable breakpoint contiguous gene syndromes. Journal of Medical Genetics, 2006, 44, e59-e59.	1.5	22
112	[14] Statistics for ChIPâ€chip and DNase Hypersensitivity Experiments on NimbleGen Arrays. Methods in Enzymology, 2006, 411, 270-282.	0.4	83
113	Database of mRNA gene expression profiles of multiple human organs. Genome Research, 2005, 15, 443-450.	2.4	110
114	Gene Expression Profiling of Human Sarcomas: Insights into Sarcoma Biology. Cancer Research, 2005, 65, 9226-9235.	0.4	312
115	Genome-wide mapping of DNase hypersensitive sites using massively parallel signature sequencing (MPSS). Genome Research, 2005, 16, 123-131.	2.4	431
116	BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. Bioinformatics, 2005, 21, 3439-3440.	1.8	1,781
117	Impact of overlapping recruitment on linkage analysis of complex disorders: Simulation studies. American Journal of Medical Genetics Part A, 2001, 105, 141-144.	2.4	3
118	Linkage and Association between Inflammatory Bowel Disease and a Locus on Chromosome 12. American Journal of Human Genetics, 1998, 63, 95-100.	2.6	152
119	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, 2077-2085.	1.4	172
120	Comparison of Nonparametric Statistics for Detection of Linkage in Nuclear Families: Single-Marker Evaluation. American Journal of Human Genetics, 1997, 61, 1431-1444.	2.6	94
121	Analysis of bipolar disorder using affected relatives. , 1997, 14, 605-610.		1
122	Analysis of complex oligogenic disease. , 1997, 14, 861-866.		1
123	Homozygosity mapping of Hallervordenâ€“Spatz syndrome to chromosome 20p12.3â€“p13. Nature Genetics, 1996, 14, 479-481.	9.4	158
124	Nonparametric simulation-based statistics for detecting linkage in general pedigrees. American Journal of Human Genetics, 1996, 58, 867-80.	2.6	97
125	Are we there yet? genomic profiling and mechanism in cancer research. , 0, , .		1
126	NCBI GEO: archive for functional genomics data setsâ€”update. , 0, .		1

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127	HGNChelper: identification and correction of invalid gene symbols for human and mouse. F1000Research, 0, 9, 1493.	0.8	11