

Sean Davis

List of Publications by Year in descending order

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Version: 2024-02-01

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 | NCBI GEO: archive for functional genomics data sets update. <i>Nucleic Acids Research</i> , 2012, 41, D991-D995. | 6.5 | 7,174 |
| 2 | Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816. | 13.7 | 4,709 |
| 3 | Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , 2015, 12, 115-121. | 9.0 | 3,070 |
| 4 | GEOquery: a bridge between the Gene Expression Omnibus (GEO) and BioConductor. <i>Bioinformatics</i> , 2007, 23, 1846-1847. | 1.8 | 2,083 |
| 5 | BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. <i>Bioinformatics</i> , 2005, 21, 3439-3440. | 1.8 | 1,781 |
| 6 | Rare Structural Variants Disrupt Multiple Genes in Neurodevelopmental Pathways in Schizophrenia. <i>Science</i> , 2008, 320, 539-543. | 6.0 | 1,654 |
| 7 | High-Resolution Mapping and Characterization of Open Chromatin across the Genome. <i>Cell</i> , 2008, 132, 311-322. | 13.5 | 1,246 |
| 8 | Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. <i>Nature</i> , 2018, 555, 371-376. | 13.7 | 649 |
| 9 | A Single IGF1 Allele Is a Major Determinant of Small Size in Dogs. <i>Science</i> , 2007, 316, 112-115. | 6.0 | 587 |
| 10 | RCircos: an R package for Circos 2D track plots. <i>BMC Bioinformatics</i> , 2013, 14, 244. | 1.2 | 502 |
| 11 | Exome sequencing identifies GRIN2A as frequently mutated in melanoma. <i>Nature Genetics</i> , 2011, 43, 442-446. | 9.4 | 449 |
| 12 | Genome-wide mapping of DNase hypersensitive sites using massively parallel signature sequencing (MPSS). <i>Genome Research</i> , 2005, 16, 123-131. | 2.4 | 431 |
| 13 | Super-enhancers delineate disease-associated regulatory nodes in T cells. <i>Nature</i> , 2015, 520, 558-562. | 13.7 | 323 |
| 14 | Gene Expression Profiling of Human Sarcomas: Insights into Sarcoma Biology. <i>Cancer Research</i> , 2005, 65, 9226-9235. | 0.4 | 312 |
| 15 | Interaction of the Glucocorticoid Receptor with the Chromatin Landscape. <i>Molecular Cell</i> , 2008, 29, 611-624. | 4.5 | 285 |
| 16 | Interferon- β links ultraviolet radiation to melanomagenesis in mice. <i>Nature</i> , 2011, 469, 548-553. | 13.7 | 264 |
| 17 | Epigenomic alterations and gene expression profiles in respiratory epithelia exposed to cigarette smoke condensate. <i>Oncogene</i> , 2010, 29, 3650-3664. | 2.6 | 245 |
| 18 | The Exomes of the NCI-60 Panel: A Genomic Resource for Cancer Biology and Systems Pharmacology. <i>Cancer Research</i> , 2013, 73, 4372-4382. | 0.4 | 239 |

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|----|---|------|-----------|
| 19 | High prevalence of MAP2K1 mutations in variant and IGHV4-34â€œexpressing hairy-cell leukemias. Nature Genetics, 2014, 46, 8-10. | 9.4 | 236 |
| 20 | Canine tumor cross-species genomics uncovers targets linked to osteosarcoma progression. BMC Genomics, 2009, 10, 625. | 1.2 | 228 |
| 21 | DNase-chip: a high-resolution method to identify DNase I hypersensitive sites using tiled microarrays. Nature Methods, 2006, 3, 503-509. | 9.0 | 222 |
| 22 | 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 |
| 23 | Genome-Wide Analysis of Menin Binding Provides Insights into MEN1 Tumorigenesis. PLoS Genetics, 2006, 2, e51. | 1.5 | 193 |
| 24 | 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 |
| 25 | A Polymorphism in IRF4 Affects Human Pigmentation through a Tyrosinase-Dependent MITF/TFAP2A Pathway. Cell, 2013, 155, 1022-1033. | 13.5 | 184 |
| 26 | 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 |
| 27 | 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 |
| 28 | Evidence for an Unanticipated Relationship between Undifferentiated Pleomorphic Sarcoma and Embryonal Rhabdomyosarcoma. Cancer Cell, 2011, 19, 177-191. | 7.7 | 167 |
| 29 | Homozygosity mapping of Hallervordenâ€œSpatz syndrome to chromosome 20p12.3â€œp13. Nature Genetics, 1996, 14, 479-481. | 9.4 | 158 |
| 30 | A Molecular Function Map of Ewing's Sarcoma. PLoS ONE, 2009, 4, e5415. | 1.1 | 158 |
| 31 | 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 |
| 32 | 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 |
| 33 | 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 |
| 34 | Analysis of the matrix metalloproteinase family reveals that MMP8 is often mutated in melanoma. Nature Genetics, 2009, 41, 518-520. | 9.4 | 145 |
| 35 | 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 |
| 36 | GEOmetadb: powerful alternative search engine for the Gene Expression Omnibus. Bioinformatics, 2008, 24, 2798-2800. | 1.8 | 128 |

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|----|--|-----|-----------|
| 37 | SRADB: query and use public next-generation sequencing data from within R. BMC Bioinformatics, 2013, 14, 19. | 1.2 | 120 |
| 38 | Genome-wide depletion of replication initiation events in highly transcribed regions. Genome Research, 2011, 21, 1822-1832. | 2.4 | 112 |
| 39 | Database of mRNA gene expression profiles of multiple human organs. Genome Research, 2005, 15, 443-450. | 2.4 | 110 |
| 40 | Oncogenic ETS fusions deregulate E2F3 target genes in Ewing sarcoma and prostate cancer. Genome Research, 2013, 23, 1797-1809. | 2.4 | 99 |
| 41 | Archival Fine-Needle Aspiration Cytopathology (FNAC) Samples. Journal of Molecular Diagnostics, 2010, 12, 739-745. | 1.2 | 97 |
| 42 | Nonparametric simulation-based statistics for detecting linkage in general pedigrees. American Journal of Human Genetics, 1996, 58, 867-80. | 2.6 | 97 |
| 43 | 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 |
| 44 | Kinetic Complexity of the Global Response to Glucocorticoid Receptor Action. Endocrinology, 2009, 150, 1766-1774. | 1.4 | 91 |
| 45 | A Genome-Wide Scan Identifies Variants in <i>NFIB</i> Associated with Metastasis in Patients with Osteosarcoma. Cancer Discovery, 2015, 5, 920-931. | 7.7 | 88 |
| 46 | Lineage of origin in rhabdomyosarcoma informs pharmacological response. Genes and Development, 2014, 28, 1578-1591. | 2.7 | 87 |
| 47 | Chromothripsis and Focal Copy Number Alterations Determine Poor Outcome in Malignant Melanoma. Cancer Research, 2013, 73, 1454-1460. | 0.4 | 86 |
| 48 | Antagonistic Cross-Regulation between Sox9 and Sox10 Controls an Anti-tumorigenic Program in Melanoma. PLoS Genetics, 2015, 11, e1004877. | 1.5 | 85 |
| 49 | [14] Statistics for ChIP-chip and DNase Hypersensitivity Experiments on NimbleGen Arrays. Methods in Enzymology, 2006, 411, 270-282. | 0.4 | 83 |
| 50 | Toward a gold standard for benchmarking gene set enrichment analysis. Briefings in Bioinformatics, 2021, 22, 545-556. | 3.2 | 83 |
| 51 | Software for the Integration of Multiomics Experiments in Bioconductor. Cancer Research, 2017, 77, e39-e42. | 0.4 | 80 |
| 52 | 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 |
| 53 | miR30a Inhibits LOX Expression and Anaplastic Thyroid Cancer Progression. Cancer Research, 2015, 75, 367-377. | 0.4 | 67 |
| 54 | On the Selective Packaging of Genomic RNA by HIV-1. Viruses, 2016, 8, 246. | 1.5 | 66 |

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|----|---|-----|-----------|
| 55 | Melanoblast transcriptome analysis reveals pathways promoting melanoma metastasis. <i>Nature Communications</i> , 2020, 11, 333. | 5.8 | 65 |
| 56 | Molecular Grading of Ductal Carcinoma <i>In situ</i> of the Breast. <i>Clinical Cancer Research</i> , 2008, 14, 8244-8252. | 3.2 | 60 |
| 57 | Genome-Wide Methylation Patterns in Papillary Thyroid Cancer Are Distinct Based on Histological Subtype and Tumor Genotype. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2014, 99, E329-E337. | 1.8 | 55 |
| 58 | Assessment of Automated Image Analysis of Breast Cancer Tissue Microarrays for Epidemiologic Studies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 992-999. | 1.1 | 54 |
| 59 | Dual inhibition of HDAC and EGFR signaling with CUDC-101 induces potent suppression of tumor growth and metastasis in anaplastic thyroid cancer. <i>Oncotarget</i> , 2015, 6, 9073-9085. | 0.8 | 54 |
| 60 | Upregulation of IFN-Inducible and Damage-Response Pathways in Chronic Graft-versus-Host Disease. <i>Journal of Immunology</i> , 2016, 197, 3490-3503. | 0.4 | 50 |
| 61 | High frequencies of leukemia stem cells in poor-outcome childhood precursor-B acute lymphoblastic leukemias. <i>Leukemia</i> , 2010, 24, 1859-1866. | 3.3 | 49 |
| 62 | Preferential Localization of Human Origins of DNA Replication at the 5' Ends of Expressed Genes and at Evolutionarily Conserved DNA Sequences. <i>PLoS ONE</i> , 2011, 6, e17308. | 1.1 | 47 |
| 63 | RARRES2 functions as a tumor suppressor by promoting β -catenin phosphorylation/degradation and inhibiting p38 phosphorylation in adrenocortical carcinoma. <i>Oncogene</i> , 2017, 36, 3541-3552. | 2.6 | 47 |
| 64 | Large-Scale Profiling of Archival Lymph Nodes Reveals Pervasive Remodeling of the Follicular Lymphoma Methyome. <i>Cancer Research</i> , 2009, 69, 758-764. | 0.4 | 46 |
| 65 | Public data and open source tools for multi-assay genomic investigation of disease. <i>Briefings in Bioinformatics</i> , 2016, 17, 603-615. | 3.2 | 46 |
| 66 | Autoreactive T Cells and Chronic Fungal Infection Drive Esophageal Carcinogenesis. <i>Cell Host and Microbe</i> , 2017, 21, 478-493.e7. | 5.1 | 44 |
| 67 | NCI-60 Whole Exome Sequencing and Pharmacological CellMiner Analyses. <i>PLoS ONE</i> , 2014, 9, e101670. | 1.1 | 38 |
| 68 | 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. <i>Journal of Biological Chemistry</i> , 2012, 287, 17812-17822. | 1.6 | 37 |
| 69 | Constitutive Fms-like tyrosine kinase 3 activation results in specific changes in gene expression in myeloid leukaemic cells. <i>British Journal of Haematology</i> , 2007, 138, 603-615. | 1.2 | 34 |
| 70 | TNF- α modulates genome-wide redistribution of Np63/TAp73 and NF- κ B cREL interactive binding on TP53 and AP-1 motifs to promote an oncogenic gene program in squamous cancer. <i>Oncogene</i> , 2016, 35, 5781-5794. | 2.6 | 33 |
| 71 | Comparative exome sequencing of metastatic lesions provides insights into the mutational progression of melanoma. <i>BMC Genomics</i> , 2012, 13, 505. | 1.2 | 31 |
| 72 | Inhibition of Survivin with YM155 Induces Durable Tumor Response in Anaplastic Thyroid Cancer. <i>Clinical Cancer Research</i> , 2015, 21, 4123-4132. | 3.2 | 31 |

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|----|---|-----|-----------|
| 73 | Whole Genome and Transcriptome Sequencing of a B3 Thymoma. PLoS ONE, 2013, 8, e60572. | 1.1 | 28 |
| 74 | Harnessing genomics to identify environmental determinants of heritable disease. Mutation Research - Reviews in Mutation Research, 2013, 752, 6-9. | 2.4 | 25 |
| 75 | Downregulation of IGFBP2 is associated with resistance to IGF1R therapy in rhabdomyosarcoma. Oncogene, 2014, 33, 5697-5705. | 2.6 | 23 |
| 76 | 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 |
| 77 | 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 |
| 78 | 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 |
| 79 | 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 |
| 80 | 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 |
| 81 | Resources for Interpreting Variants in Precision Genomic Oncology Applications. Frontiers in Oncology, 2017, 7, 214. | 1.3 | 18 |
| 82 | Modeling Synovial Sarcoma: Timing Is Everything. Cancer Cell, 2007, 11, 305-307. | 7.7 | 17 |
| 83 | HGNChelper: identification and correction of invalid gene symbols for human and mouse. F1000Research, 2020, 9, 1493. | 0.8 | 17 |
| 84 | A Methyl-Deviant Epigenotype of Estrogen Receptor-Positive Breast Carcinoma Is Associated with Malignant Biology. American Journal of Pathology, 2011, 179, 55-65. | 1.9 | 15 |
| 85 | Abstract 4856: Using embryonic melanoblast transcriptome analysis to identify novel mechanisms promoting metastatic melanoma. Cancer Research, 2012, 72, 4856-4856. | 0.4 | 14 |
| 86 | HGNChelper: identification and correction of invalid gene symbols for human and mouse. F1000Research, 0, 9, 1493. | 0.8 | 11 |
| 87 | <i>In Vivo</i> Role of Alternative Splicing and Serine Phosphorylation of the Microphthalmia-Associated Transcription Factor. Genetics, 2012, 191, 133-144. | 1.2 | 10 |
| 88 | 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 |
| 89 | 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 |
| 90 | Rb1 loss modifies but does not initiate alveolar rhabdomyosarcoma. Skeletal Muscle, 2013, 3, 27. | 1.9 | 9 |

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|-----|---|-----|-----------|
| 91 | Exclusion of the 750â€kb genetically unstable region at Xq27 as a candidate locus for prostate malignancy in HPCX1â€linked families. <i>Genes Chromosomes and Cancer</i> , 2012, 51, 933-948. | 1.5 | 7 |
| 92 | 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. <i>Breast Cancer Research and Treatment</i> , 2015, 150, 457-466. | 1.1 | 7 |
| 93 | The Bioconductor channel in F1000Research. <i>F1000Research</i> , 2015, 4, 217. | 0.8 | 6 |
| 94 | GenomicSuperSignature facilitates interpretation of RNA-seq experiments through robust, efficient comparison to public databases. <i>Nature Communications</i> , 2022, 13, . | 5.8 | 6 |
| 95 | Ewing's sarcoma: General insights from a rare model. <i>Cancer Cell</i> , 2006, 9, 331-332. | 7.7 | 5 |
| 96 | Genome-Wide Methylation Profiling in Archival Formalin-Fixed Paraffin-Embedded Tissue Samples. <i>Methods in Molecular Biology</i> , 2012, 823, 107-118. | 0.4 | 5 |
| 97 | caOmicsV: an R package for visualizing multidimensional cancer genomic data. <i>BMC Bioinformatics</i> , 2016, 17, 141. | 1.2 | 4 |
| 98 | The Bioconductor channel in F1000Research. <i>F1000Research</i> , 2015, 4, 217. | 0.8 | 4 |
| 99 | Impact of overlapping recruitment on linkage analysis of complex disorders: Simulation studies. <i>American Journal of Medical Genetics Part A</i> , 2001, 105, 141-144. | 2.4 | 3 |
| 100 | Abstract 4193: TNF-Î± dynamically modulates genome-wide cross-regulation of cRel, Î³Np63 and TAp73 promoter binding and gene expression in head and neck cancer: TP53 and NFÎ±B ChIP-Seq in HNSCC. , 2012, , . | | 2 |
| 101 | Analysis of bipolar disorder using affected relatives. , 1997, 14, 605-610. | | 1 |
| 102 | Analysis of complex oligogenic disease. , 1997, 14, 861-866. | | 1 |
| 103 | Are we there yet? genomic profiling and mechanism in cancer research. , 0, , . | | 1 |
| 104 | NCBI GEO: archive for functional genomics data setsâ€"update. , 0, . | | 1 |
| 105 | Abstract 4968: TNF-alpha promotes genome-wide replacement of TAp73 chromatin occupancy by cREL and DeltaNp63. , 2011, , . | | 1 |
| 106 | Abstract 1113: Role of the microRNA-23â€^1/427â€^1/424 clusters in osteosarcoma. , 2012, , . | | 1 |
| 107 | Orchestrating a community-developed computational workshop and accompanying training materials. <i>F1000Research</i> , 2018, 7, 1656. | 0.8 | 1 |
| 108 | Ten simple rules for large-scale data processing. <i>PLoS Computational Biology</i> , 2022, 18, e1009757. | 1.5 | 1 |

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|-----|--|-----|-----------|
| 109 | 28 Ultraviolet B-induced inflammatory microenvironment promotes melanocyte survival and melanoma susceptibility. <i>European Journal of Cancer, Supplement</i> , 2010, 8, 8. | 2.2 | 0 |
| 110 | Novel Proteasome Inhibitor Carfilzomib in Combination with Survivin Inhibitor YM155 Induces Enhanced Cytotoxicity in Anaplastic Thyroid Cancer. <i>Journal of the American College of Surgeons</i> , 2014, 219, S125. | 0.2 | 0 |
| 111 | Identification of Novel Targets for Lung Cancer Therapy Using an Induced Pluripotent Stem Cell Model. <i>Annals of the American Thoracic Society</i> , 2018, 15, S127-S128. | 1.5 | 0 |
| 112 | Abstract 2213: Identification of novel cancer mutations in sarcomas. , 2010, , . | | 0 |
| 113 | Abstract 3024: miRNA expression profiles in sarcomas. , 2010, , . | | 0 |
| 114 | Abstract 3934: Identification of novel cancer DNA sequence variants in human sarcomas. , 2011, , . | | 0 |
| 115 | Abstract 2846: Pigment epithelium-derived factor (PEDF) functions as a brain metastasis suppressor of breast cancer. , 2011, , . | | 0 |
| 116 | Abstract 2116: CHEK2(Chk2) endogenous activation is associated with p53 deficiency and downregulation of BRCA2 and Fanconi Anemia pathway gene members in the National Cancer Institute Anticancer Tumor Cell Line Panel (NCI-60). , 2012, , . | | 0 |
| 117 | Abstract 5070: Paired-end RNA-sequencing reveals novel fusion genes and SNVs in osteosarcoma. , 2012, , . | | 0 |
| 118 | Abstract 1879: The exomes of the NCI60 and their implications for cancer pharmacogenomics. , 2012, , . | | 0 |
| 119 | Abstract 994: Integrated embryonic transcriptome analyses identify key melanoma metastasis regulator. , 2014, , . | | 0 |
| 120 | Abstract 4367: Tumor suppressor miR-30a inhibits LOX expression and progression in anaplastic thyroid cancer. , 2014, , . | | 0 |
| 121 | Abstract 4167: Harvesting knowledge from unexploited genomic data: Estimating relative telomere length from targeted-resequencing. , 2014, , . | | 0 |
| 122 | Abstract 4873: IKK \pm bridges central tolerance to innate immunity and inflammation. , 2014, , . | | 0 |
| 123 | Abstract IA22: Modeling recurrent metastatic melanoma in the mouse. , 2014, , . | | 0 |
| 124 | Abstract 2717: Reintroduction of DAXX suppresses alternative lengthening of telomeres in osteosarcoma. , 2016, , . | | 0 |
| 125 | Abstract 3004: Comparison of somatic alterations in the genome and transcriptome of 1,705 pediatric leukemia and solid tumors: a report from the Children's Oncology Group (COG) - NCI TARGET Project. , 2017, , . | | 0 |
| 126 | restfulSE: A semantically rich interface for cloud-scale genomics with Bioconductor. <i>F1000Research</i> , 2019, 8, 21. | 0.8 | 0 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 127 | BiocPkgTools: Toolkit for mining the Bioconductor package ecosystem. F1000Research, 2019, 8, 752. | 0.8 | 0 |